

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Run on:      December 8, 2004, 09:16:13 ; Search time 263.185 Seconds
              (without alignments)
              866.886 Million cell updates/sec
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Title: US-09-788-051-4
Perfect score: 3354
Sequence: 1 M M G L V R L L A M L G W G C M G R . . . . . L P S C Q L P L G I P A L G I V L C A S 636

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      2002273 segs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
1: Genesepd_23Sep04:*
2: Genesepd_1980s:*
3: Genesepd_1990s:*
4: Genesepd_2000s:*
5: Genesepd_2001s:*
6: Genesepd_2002s:*
7: Genesepd_2003s:*
8: Genesepd_2004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result							Description
No.	Score	Query	Match	Length	DB	ID	
1	3354	100.0	636	7	ADD29445	ADD29445	Human cca6
2	3259	97.2	620	7	ADD29448	ADD29448	Human cca6
3	2746.5	81.9	781	5	ABBS5296	ABBS5296	Human p01
4	2746.5	81.9	781	5	PAm48736	PAm48736	Human p01
5	2746.5	81.9	781	5	ABG34078	ABG34078	Human p01
6	2746.5	81.9	781	6	ABR40114	ABR40114	Human p01
7	2746.5	81.9	781	6	ADAO3365	ADAO3365	Human p01
8	2746.5	81.9	781	6	ADA43795	ADA43795	Human sec
9	2746.5	81.9	781	6	ADA43563	ADA43563	Human sec
10	2746.5	81.9	781	6	ADA01238	ADA01238	Human p01
11	2746.5	81.9	781	7	ADA01122	ADA01122	Human sec
12	2746.5	81.9	781	7	ADA34679	ADA34679	Human sec
13	2746.5	81.9	781	7	ADA06941	ADA06941	Human p01
14	2746.5	81.9	781	7	ADA08429	ADA08429	Novel humn
15	2746.5	81.9	781	7	ADB99722	ADB99722	Human p01
16	2746.5	81.9	781	7	ADB87005	ADB87005	Human p01
17	2746.5	81.9	781	7	ADB66160	ADB66160	Human sec
18	2746.5	81.9	781	7	ADB99838	ADB99838	Human p01
19	2746.5	81.9	781	7	ADB99493	ADB99493	Novel humn
20	2746.5	81.9	781	7	ADB66044	ADB66044	Human sec
21	2746.5	81.9	781	7	ADC23442	ADC23442	Human p01
22	2746.5	81.9	781	7	ADC26135	ADC26135	Human p01
23	2746.5	81.9	781	7	ADB04962	ADB04962	Human p01
24	2746.5	81.9	781	7	ADB11268	ADB11268	Human p01
25	2746.5	81.9	781	7	ADB88199	ADB88199	Human p01

ALIGNMENTS

45	2746.5	81.9	781.8	AD519756	Human	PRO
44	2746.5	81.9	781.8	AD339681	Human	PRO
43	2746.5	81.9	781.8	AD604294	Human	PRO
42	2746.5	81.9	781.8	AD339490	Human	PRO
41	2746.5	81.9	781.8	AD575167	Human	PRO
40	2746.5	81.9	781.8	AD338078	Human	PRO
39	2746.5	81.9	781.8	AD395378	Human	SEC
38	2746.5	81.9	781.8	AD337607	Human	SEC
37	2746.5	81.9	781.8	AD537223	Human	SEC
36	2746.5	81.9	781.8	AD581665	Human	SEC
35	2746.5	81.9	781.8	AD581749	Human	SEC
34	2746.5	81.9	781.7	AD589296	Human	PRO
33	2746.5	81.9	781.7	AD582496	Human	PRO
32	2746.5	81.9	781.7	AD306545	Human	PRO
31	2746.5	81.9	781.7	AD306244	Human	SEC
30	2746.5	81.9	781.7	AD399951	Human	SEC
29	2746.5	81.9	781.7	AD388315	Human	PRO
28	2746.5	81.9	781.7	AD381919	Human	PRO
27	2746.5	81.9	781.7	AD506424	Human	PRO
26	2746.5	81.9	781.7	AD595494	Human	SEC
25	2746.5	81.9	781.7	AD595494	Human	SEC

RESULT 1

ID	ADD29445 standard; protein; 636 AA.
XX	ADD29445;
XX	AC
XX	15-JAN-2004 (first entry)
DT	
XX	Human cadherin-like protein amino acid sequence.
DE	
XX	cadherin-like protein; transmembrane protein; cadherin domain;
KW	homotypic cell-cell adhesion; cytostatic; osteopapthic cancer;
KW	osteopetrosis, Pager's disease; osteomalacia; hyperostosis; osteopetrosis
KM	metastatic tumour; human.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..16
FT	/label= Signal_peptide
FT	17..636
FT	Protein /label= Mature_human_cadherin-like_protein
XX	
FN	US2003144491-A1.
PD	
XX	31-JUL-2003.
PE	
XX	16-FEB-2001; 2001US-00788051.
XX	
XX	03-FEB-2000; 2000US-00496914.
PR	27-APR-2000; 2000US-00560875.
XX	
XX	
PA	(GODB/) GODBOLE S D.
PA	(KUOC/) KUO C.
PA	(ARTE/) ARTERBURN M C.
PA	(YEUN/) YEUNG G.
PA	(PALE/) PALENCIA S.
PA	(TANG/) TANG Y T.
PA	(LITUC/) LITU C.
PA	(DRMA/) DRMANAC R T.
XX	
XX	Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
PI	Liu C, Drmanac RT;
XX	
DR	WPI; 2003-829799/77.
XX	N-PSDB; ADD28461, ADD29446.
XX	
PT	Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 4; 63pp; English.

CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteoplastic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

SQ Sequence 636 AA;

Query Match	100.0%	Score 3354	DB 7	Length 636
Best Local Similarity	100.0%	Pred. No. 1.1e-272		
Matches 636	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	601	MOGLVYLLAAIAGCMCMRLAAPRAVAGSEHEHGPLLTPRSWMNOGFVLEAAGP	60
Dp	1	MOGLVYLLAAIAGCMCMRLAAPRAVAGSEHEHGPLLTPRSWMNOGFVLEAAGP	60
QY	61	EPVLIGKLHSDVDRGGRTRYLLTGEAGTVFVIDEATGNIVTKSLDREKQVYLLAQ	120
Dp	61	EPVLIGKLHSDVDRGGRTRYLLTGEAGTVFVIDEATGNIVTKSLDREKQVYLLAQ	120
QY	121	AVVRASNRPLEPSEFIKGGDINNPPFLPGPYHAIVPMSVNGSVIOVTHADDDP	180
Dp	121	AVVRASNRPLEPSEFIKGGDINNPPFLPGPYHAIVPMSVNGSVIOVTHADDDP	180
QY	181	SYNSAKLYYTYLDGLPFPSPDPQGVVFETALPMDRETQEEFLVVIQAKMGSGMGSL	240
Dp	181	SYNSAKLYYTYLDGLPFPSPDPQGVVFETALPMDRETQEEFLVVIQAKMGSGMGSL	240
QY	241	GSTTVYVTLSDVNDNPKFPQSLYQFSVETAGPFTLVGRADDPIDGVALMAYSILD	300
Dp	241	GSTTVYVTLSDVNDNPKFPQSLYQFSVETAGPFTLVGRADDPIDGVALMAYSILD	300
QY	301	GSESEAFSISTLQGHGILLTRKPLDSESQASYSFRYEANTLIDPAYLRGPFKQVAS	360
Dp	301	GSESEAFSISTLQGHGILLTRKPLDSESQASYSFRYEANTLIDPAYLRGPFKQVAS	360
QY	361	VRAVAVDADEPAFTQAAHYLTVPENKAPGTLVQISAADIDSPASPIRYSILPHSDPER	420
Dp	361	VRAVAVDADEPAFTQAAHYLTVPENKAPGTLVQISAADIDSPASPIRYSILPHSDPER	420
QY	421	CSISIOEEBTHITAPLREAPAMNLTVALTELIGMSGPRGVPYLVAEWSAPAPQ	480
Dp	421	CSISIOEEBTHITAPLREAPAMNLTVALTELIGMSGPRGVPYLVAEWSAPAPQ	480
QY	481	RSPVGSANGIPODSSAQSARVQVALIOTLIDENDNAPQALPEYDTFVCSAAPGQIIVIRA	540
Dp	481	RSPVGSANGIPODSSAQSARVQVALIOTLIDENDNAPQALPEYDTFVCSAAPGQIIVIRA	540
QY	541	LDRDEYGNSSHVSFGCPGPDANFVQONRDLPMWFHILMASSSLWHPZABRGNOQA	600
Dp	541	LDRDEYGNSSHVSFGCPGPDANFVQONRDLPMWFHILMASSSLWHPZABRGNOQA	600
QY	601	SGQKSSSLPCGRLPALPBGQPLIGIPALGIVLCA	636
Dp	601	SGQKSSSLPCGRLPALPBGQPLIGIPALGIVLCA	636

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RESULT 2
ADD29448
ID      ADD29448 standard; protein; 620 AA
XX

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AC	ADD29448;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Human cadherin-like mature protein.
XX	
KW	cadherin-like protein; transmembrane protein; cadherin domain;
KW	homotypic cell-cell adhesion; cytotatic; osteopapic; cancer;
KW	osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis
KW	metastatic tumour; human.

OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.

PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR

PA (GODB) GODBOLE S D.
PA (KUOC) KUO C.
PA (ARTE) ARTERBURN M C.
PA (YEUN) YEUNG G.
PA (PALE) PALENCIA S.
PA (TANG) TANG Y T.
PA (LIUC) LIU C.
PA (DEMA) DRMANAC R T.

PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.

PS Claim 11; SEQ ID NO 7; 63pp; English

CC This invention relates to a novel, isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cyrostatic or osteoparhic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the mature human secreted
CC cadherin-like protein which was used during the exemplification of the
CC invention.

Sequence 620 AA;

Query Match	97.2%;	Score 3259;	DB 7;	Length 620;
Best Local Similarity	100.0%;	Pred. No. 1e-264;		
Matches 620; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	CMGRLLAPARAAAGSEHFGPLLATRRSSWMNNOFVLYEEVAGESEPLVIGKLSHDVDVNGE	76
Dd	1	CMGRLLAPARAAAGSEHFGPLLATRRSSWMNNOFVLYEEVAGESEPLVIGKLSHDVDVNGE	60
QY	77	GRKTYLLTSEGAGTVFVIDEATGNHHTKSLDREBKAQYLLLAADVNRASNRPLEPSPSEF	126
Dd	61	GRKTYLLTSEGAGTVFVIDEATGNHHTKSLDREBKAQYLLLAADVNRASNRPLEPSPSEF	120
QY	137	IKKQDINDNPPIFLPGPYHATVPBMSNVGTSVIQVTAHADDDPSYGNSAKLYVTYVLIDGL	186
Dd	121	IKKQDINDNPPIFLPGPYHATVPBMSNVGTSVIQVTAHADDDPSYGNSAKLYVTYVLIDGL	180

QY 197 PFSSVDPQTGVVTRAI PNMRETOEELVVIQAKDMGNGHGLSGSTTVTLTDVNDNP 256
DB 181 PFSSVDPQTGVVTRAI PNMRETOEELVVIQAKDMGNGHGLSGSTTVTLTDVNDNP 240
QY 257 PKFQSLYQSFVETAPGTLVGRRAODPDLDGNLMAYSLIDGSESAFSTLQGR 316
DB 241 PKFQSLYQSFVETAPGTLVGRRAODPDLDGNLMAYSLIDGSESAFSTLQGR 300
QY 317 DGLTVKRPDLFESQSFVETAPGTLVGRRAODPDLDGNLMAYSLIDGSESAFSTLQGR 376
DB 301 DGLTVKRPDLFESQSFVETAPGTLVGRRAODPDLDGNLMAYSLIDGSESAFSTLQGR 360
QY 377 AAHVLTPENKAPGTLVGRRAODPDLDGNLMAYSLIDGSESAFSTLQGR 436
DB 361 AAHVLTPENKAPGTLVGRRAODPDLDGNLMAYSLIDGSESAFSTLQGR 420
QY 437 LDRARAHNLTVALTELGMGMPERGMPVPLVAEMGAPAPQPSVGSAGVIGPQSSA 496
DB 421 LDRARAHNLTVALTELGMGMPERGMPVPLVAEMGAPAPQPSVGSAGVIGPQSSA 480
QY 497 QASRVQVAIOTLDENDNAPOLAEPYDTFVCDSPAAGQLIOVIRALDDEVGNSSHVSFOG 556
DB 481 QASRVQVAIOTLDENDNAPOLAEPYDTFVCDSPAAGQLIOVIRALDDEVGNSSHVSFOG 540
QY 557 PLGSDANFTVODNNDLPAMFHPILMASASSWLMHPAERGQNPASQKSSSLPCGRLEGA 616
DB 541 PLGSDANFTVODNNDLPAMFHPILMASASSWLMHPAERGQNPASQKSSSLPCGRLEGA 600
QY 617 LPSCOLPLGIPALGIVLCAS 636
DB 601 LPSCOLPLGIPALGIVLCAS 620

RESULT 3
ID ABB53296
ID ABB53296 standard; protein; 781 AA.
AC ABB53296;
DT 12-FEB-2002 (first entry)
DE Human polypeptide #36.
XX Human; noctropic; neuroprotective; anticonvulsant; antidepressant;
KW neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
KW antiinflammatory; antihypertensive; hepatotropic; vitamin; antidiabetic;
KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
KW cardiovascular disease; respiratory disease; liver disease;
KW renal disease; skeletal muscle disease; gastrointestinal disease;
KW placental disease; testicular cancer; male fertility; pancreatic disease.
XX Homo sapiens.
OS Homo sapiens.
FN WO200181363-A1.
XX 01-NOV-2001.
PF 26-APR-2001; 2001WO-US013360.
XX 27-APR-2000; 2000US-0199963P.
PR 11-MAY-2000; 2000US-020336P.
PR 25-MAY-2000; 2000US-0207087P.
PR 26-MAY-2000; 2000US-0207546P.
XX (SMTK) SMITHKLINE BEECHAM CORP.
PA (SMTK) SMITHKLINE BEECHAM PLC.
XX Agarwal P, Murdoch FR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
PI Lai Y, Xie Q;
XX WPI; 2002-041392/05.
DR N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
PT and treating diseases associated with the polypeptide, e.g. Alzheimer's
PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
XX
PS Claim 1, Page 108-109; 116pp; English.
XX The invention relates to an isolated polypeptide comprising a 277, 480,
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 359, 382, 185, 586, 1026,
CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
CC 784, 252, 593, 472, 607, 781, 640, 666 or 154 amino acid sequence as
CC given in the specification. The polypeptides, modulators of the
CC polypeptides and antibodies against the polypeptides are useful for
CC treating diseases such as neurological and psychiatric diseases including
CC Alzheimer's, paraneoplastic disease, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Battenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphogranuloma; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type I and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX
SQ Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 5; Length 781;
Best Local Similarity 84.8%; Pred No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
QY 1 MMGLVRLILAMLGWCMGRALAPARAWGSEHFGPALLRTRRWVWVNFVIEYAGP 60
DB 1 MMGLVRLILAMLGWCMGRALAPARAWGSEHFGPALLRTRRWVWVNFVIEYAGP 60
QY 61 EPLTIGKHSVDVDRGGRKTYLLTGEAGTVAVIDEATNHTVSLDREKAAQVYLAQ 120
DB 61 EPLTIGKHSVDVDRGGRKTYLLTGEAGTVAVIDEATNHTVSLDREKAAQVYLAQ 120
QY 121 AVDRASNPLEPSEPIIKQDINDNPPIPLGPYHATVPENSNVTSYQVTAHADDP 180
DB 121 AVDRASNPLEPSEPIIKQDINDNPPIPLGPYHATVPENSNVTSYQVTAHADDP 180
QY 181 SYNSAKLYVTYLDGIPFSSVDPQGVVTRAI PNMRETOEELVVIQAKDMGNGHGLSG 240
DB 181 SYNSAKLYVTYLDGIPFSSVDPQGVVTRAI PNMRETOEELVVIQAKDMGNGHGLSG 240
QY 241 GSTTVTLTDVNDNPPKFPQSLYQSFVETAPGTLVGRRAODPDLDGNLMAYSLID 300
DB 241 GSTTVTLTDVNDNPPKFPQSLYQSFVETAPGTLVGRRAODPDLDGNLMAYSLID 300
QY 301 GEGSEAFSISTDIQGRDGLITVRKPLDFESQSFVETAPGTLVGRRAODPDLDGNLMAYSLID 360
DB 301 GEGSEAFSISTDIQGRDGLITVRKPLDFESQSFVETAPGTLVGRRAODPDLDGNLMAYSLID 360
QY 361 VRYAVODAPPPAPFQAAHVLTPENKAPGTLVGRRAODPDLDGNLMAYSLID 420
DB 361 VRYAVODAPPPAPFQAAHVLTPENKAPGTLVGRRAODPDLDGNLMAYSLID 420
QY 421 CFSIOPEEGTHTAAPLDREARAHNLTVALTEL 454
DB 421 CFSIOPEEGTHTAAPLDREARAHNLTVALTEL 454
QY 481 RSPVGSAGVIGPQSSAASRVQVAIOTLDENDNAPOLAEPYDTFVCDSPAAGQLIOVIRA 540
DB 481 RSPVGSAGVIGPQSSAASRVQVAIOTLDENDNAPOLAEPYDTFVCDSPAAGQLIOVIRA 502

QY 541 LDRDEVGNSHVSFGPLGPDANFTVODNRD-----LPA-----WF 576
 DB 503 LDRDEVGNSHVSFGPLGPDANFTVODNRGASLLPSPAPPRHAPYLVPIELMDWG 562
 QY 577 HPLMASASWLH-----WPPAERGQAPASOG 603
 DB 563 QPALSSTATVTVSVCRQCPDGSVASCPPEAHLISAAGLSTG 602
 RESULT 4
 ID AAM48736
 AAM48736 standard; protein; 781 AA.
 AC AAM48736;
 XX
 DT 28-MAR-2002 (first entry)
 XX
 DE Human cadherin family member 57805 protein SEQ ID NO 2.
 XX
 KW Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
 KW antidiabetic; neuroprotective; antiarthritic; antirheumatic;
 KW dermatological; immunosuppressive; antinflammatory; antipruritic;
 KW antiaesthetic; antiallergic; antileptotic; haemostatic; antipruritic;
 KW antithyroid; hypotensive; antiarteriosclerotic; cardiant; antiarrhythmic;
 KW anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
 KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 KW vital; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 EN WO200190145-A2.
 XX
 PD 29-NOV-2001.
 XX
 PE 18-MAY-2001; 2001WO-US016013.
 XX
 PR 19-MAY-2000; 2000US-0205674P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2002-083082/11.
 XX
 DR N-PSDB; ABA96406; ABA96407.
 XX
 XX
 PT New human cadherin family protein and polynucleotides, useful for
 PT diagnosing and treating disorders e.g obstructive jaundice, multiple
 PT sclerosis, encephalomyelitis and atherosclerosis and to identify
 PT modulators of therapeutic use.
 XX
 PS Claim 9; Page 105; 119pp; English.
 XX
 CC The invention relates to human cadherin family polypeptide designated
 CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarthritic, antirheumatic, dermatological,
 CC immunosuppressive, antinflammatory, antipruritic, antiaesthetic,
 CC antiallergic, antileptotic, haemostatic, antipruritic, antithyroid,
 CC hypotensive, antiarteriosclerotic, cardiant, antiarrhythmic, anorectic,
 CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy; cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders.

CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy
 XX
 SQ Sequence 781 AA;
 Query Match 81.9%; Score 2746.5; DB 5; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 MNGVLRLLAAMLGCMGCRFLAAPARAWAGREHPGALLRTSRSMWNQFFVBEVAPG 60
 DB 1 MNGVLRLLAAMLGCMGCRFLAAPARAWAGREHPGALLRTSRSMWNQFFVBEVAPG 60
 QY 61 EPLLIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNITHVTKSLDREKQAYVLLAQ 120
 DB 61 EPLLIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNITHVTKSLDREKQAYVLLAQ 120
 QY 121 AVDRASNPPLPPESEFIIKQGDINDNPPIPLGPHATVPMMSVGTSVIOVTAHDDP 180
 DB 121 AVDRASNPPLPPESEFIIKQGDINDNPPIPLGPHATVPMMSVGTSVIOVTAHDDP 180
 QY 181 SYGNSAKLVTVLDGLPFFSVDPQTGVVTRAIIPNMDETOBEFLVVIQAKMGGMGLS 240
 DB 181 SYGNSAKLVTVLDGLPFFSVDPQTGVVTRAIIPNMDETOBEFLVVIQAKMGGMGLS 240
 QY 241 GSTTTVTVLSDVNDNPPKFPQSLYQFSVETAGGTVGRIRADPDLGDAALMAYSILD 300
 DB 241 GSTTTVTVLSDVNDNPPKFPQSLYQFSVETAGGTVGRIRADPDLGDAALMAYSILD 300
 QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKXVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKXVAS 360
 QY 361 VRVAVQDAPBPAPATQAAVHLTVPENKAPGTLVQGISADIDSPASTIRISILPHSPER 420
 DB 361 VRVAVQDAPBPAPATQAAVHLTVPENKAPGTLVQGISADIDSPASTIRISILPHSPER 420
 QY 421 CFSIQPEEGTHTTAAPLDREARAHNTLVATELGMGMBERGWPVPLVAMWSAPAPQ 480
 DB 421 CFSIQPEEGTHTTAAPLDREARAHNTLVATELGMGMBERGWPVPLVAMWSAPAPQ 480
 QY 481 RSPVGSAGVIRPQSSAQSARVOVAIQTLDENDNAPQALAEFYDFVCDSPAAGQIQVIRA 540
 DB 481 RSPVGSAGVIRPQSSAQSARVOVAIQTLDENDNAPQALAEFYDFVCDSPAAGQIQVIRA 540
 QY 455 -----DSSAQSARVOVAIQTLDENDNAPQALAEFYDFVCDSPAAGQIQVIRA 502
 DB 455 -----DSSAQSARVOVAIQTLDENDNAPQALAEFYDFVCDSPAAGQIQVIRA 502
 QY 541 LDRDEVGNSHVSFGPLGPDANFTVODNRD-----LPA-----WF 576
 DB 503 LDRDEVGNSHVSFGPLGPDANFTVODNRGASLLPSPAPPRHAPYLVPIELMDWG 562
 QY 577 HPLMASASWLH-----WPPAERGQAPASOG 603
 DB 563 QPALSSTATVTVSVCRQCPDGSVASCPPEAHLISAAGLSTG 602
 RESULT 5
 ID ABG34078
 ABG34078 standard; protein; 781 AA.
 AC ABG34078;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human Pro peptide #49.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.
 XX
 OS Homo sapiens.
 XX
 EN WO200224888-A2.

XX 28-MAR-2002.
 PD
 XX
 PF 29-AUG-2001; 2001WO-US027099.
 XX
 PR 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0266421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282128P.
 PR 04-APR-2001; 2001US-0282199P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Bacon DL, Filvarcoff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI; 2002-362426/39.
 DR N-PSDB; ABR70009.
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX
 XX Claim 11; Fig 98; 218pp; English.
 XX
 CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders. In assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC diagnosis and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention
 XX
 XX Sequence 781 AA;
 SQ

Query Match 81.9%; Score 2746.5; DB 5; Length 781;
 Best Local Similarity 84.8%; Pred No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVLLIAMIWGWCWGRLLAAPARAWGSRHFGPALLTRRSWVNWQFFVIEEYAGP 60
 DB 1 MMGLVLLIAMIWGWCWGRLLAAPARAWGSRHFGPALLTRRSWVNWQFFVIEEYAGP 60

QY 61 EPLLIGKLSHDVDRGEGRTKYLITGEGAGTVFVIDEATGNTHVTKSLDRREKAQVYLLAQ 120
 DB 61 EPLLIGKLSHDVDRGEGRTKYLITGEGAGTVFVIDEATGNTHVTKSLDRREKAQVYLLAQ 120
 QY 121 AVDRASNRPLEPPESEFIKGGDINDNPPIFPGPYHATVPEMSNVGTSVITVAHADADP 180
 DB 121 AVDRASNRPLEPPESEFIKGGDINDNPPIFPGPYHATVPEMSNVGTSVITVAHADADP 180
 QY 181 SYGSAKLYTVLDGIPFESVDPQGVRTAIPNMDRETQEEFLVYIQAKMGHMGIS 240
 DB 181 SYGSAKLYTVLDGIPFESVDPQGVRTAIPNMDRETQEEFLVYIQAKMGHMGIS 240
 QY 241 GSTTVTVLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRLRAQDPDGDNALMAYSILD 300
 DB 241 GSTTVTVLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRLRAQDPDGDNALMAYSILD 300
 QY 301 GEGSEAFSISTDLQGRDGLITVRKPLDEESQSYSFVEATNTLIDPAYLRGPFKYAS 360
 DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDEESQSYSFVEATNTLIDPAYLRGPFKYAS 360
 QY 361 VRAVQDAPEPPAFQAAVHLTVPENKAPGLTVGQISAADLSPASPIRYSILPHSDPER 420
 DB 361 VRAVQDAPEPPAFQAAVHLTVPENKAPGLTVGQISAADLSPASPIRYSILPHSDPER 420
 QY 421 CFSIQPEEGTITTAAPLDREARAHNLTVLATELGMSWGPBERGWPLLVAEWSAPAPQ 480
 DB 421 CFSIQPEEGTITTAAPLDREARAHNLTVLATELGMSWGPBERGWPLLVAEWSAPAPQ 480
 QY 481 RSPVGSAGVIFODSSAQASRVQAIQTLDENNAPQALPEYTFVQDSAPQQLQVIRA 540
 DB 481 RSPVGSAGVIFODSSAQASRVQAIQTLDENNAPQALPEYTFVQDSAPQQLQVIRA 540
 QY 455 -----DSSAQASRVQAIQTLDENNAPQALPEYTFVQDSAPQQLQVIRA 502
 DB 455 -----DSSAQASRVQAIQTLDENNAPQALPEYTFVQDSAPQQLQVIRA 502
 QY 541 LDRDEVGNSSHVFSQGLPEPDANFTVQDNRD-----LPA-----WF 576
 DB 541 LDRDEVGNSSHVFSQGLPEPDANFTVQDNRD-----LPA-----WF 576
 QY 577 HPLMASASSWLH-----WPPAERGNQAPASOG 603
 DB 577 HPLMASASSWLH-----WPPAERGNQAPASOG 603
 QY 563 QPALSSTATVTVSVCRQPDGVSASCPFAHLSAAGLSYG 602
 DB 563 QPALSSTATVTVSVCRQPDGVSASCPFAHLSAAGLSYG 602

RESULT 6
 ABR40114
 ID ABR40114 standard; protein; 781 AA.
 XX
 AC ABR40114;
 XX
 DT 04-JUL-2003 (first entry)
 XX
 DE Human cell adhesion and extracellular matrix protein, CADPCM-11.
 XX
 XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
 KW anti-convulsant; nootropic; neuroprotective; immunosuppressive;
 KW dermatological; anti-inflammatory; cytosolic; antiarteriosclerotic;
 KW gene therapy; cell adhesion; extracellular matrix; CADPCM;
 KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
 KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
 KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
 KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 XX WC0203027230-A2.
 XX
 XX
 PD 03-APR-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024649.
 XX
 XX
 PR 03-AUG-2001; 2001US-0309964P.
 PR 03-AUG-2001; 2001US-0310119P.
 PR 17-AUG-2001; 2001US-0313091P.
 PR 31-AUG-2001; 2001US-0316771P.

07-SEP-2001; 2001US-0317896P.
 PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 (INCY-) INCYTE GENOMICS INC.
 Burford N, Warren BA, Duggan EM, Mason PM, Richardson TW, Yue H;
 PI Forsythe TJ, Elliott VS, Griffin JA, Gorvad AB, Azizai Y,
 PI Kallikch DA, Xu Y, Honcheil CD, Baughn ME, Gietzen KO, Lee S,
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
 XX WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 PS
 XX
 XX
 CC Claim 1; Page 192-194; 234pp; English.
 CC
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 XX
 XX
 SO Sequence 781 AA;
 Query Match 81.9%; Score 2746.5; DB 6; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221; Indels 75; Gaps 4;
 Matches 543; Conservative 5; Mismatches 17;
 QY 1 MMGLVRLILAWLGGMGCMGRLLAARAMAGSREHPGALRTSRSWWNOFFVIEBYAGP 60
 DB 1 MMGLVRLILAWLGGMGCMGRLLAARAMAGSREHPGALRTSRSWWNOFFVIEBYAGP 60
 QY 61 EPTVLIGLHSDVDNGERTKYLITGEGAGTVFVIDENTGNHNTKSLDREKQYVLLAQ 120
 DB 61 EPTVLIGLHSDVDNGERTKYLITGEGAGTVFVIDENTGNHNTKSLDREKQYVLLAQ 120
 QY 121 AVDRASNRPLEPSEPFIIKQDINDNPIPLGPHYATVEMSNNGTSVIOYTAHDADP 180
 DB 121 AVDRASNRPLEPSEPFIIKQDINDNPIPLGPHYATVEMSNNGTSVIOYTAHDADP 180
 QY 181 SYGSAKLVTYVLDGLFFESVDPOGTGYRTAIPMDRETOEELVVIQAKDGMGHGSL 240
 DB 181 SYGSAKLVTYVLDGLFFESVDPOGTGYRTAIPMDRETOEELVVIQAKDGMGHGSL 240
 QY 241 GSTTVYTLSDVDNPKFPQSLYQFSVETAGPGLTGLRAQDDPLDGNLMAYSILD 300
 DB 241 GSTTVYTLSDVDNPKFPQSLYQFSVETAGPGLTGLRAQDDPLDGNLMAYSILD 300
 QY 301 GEGSEAFSISTDIQGRDGLTVKPKLPDESQRSYFRVETNTLIDPAYLRGPFQDVA 360
 DB 301 GEGSEAFSISTDIQGRDGLTVKPKLPDESQRSYFRVETNTLIDPAYLRGPFQDVA 360
 QY 361 VRAVADQAPPEPAFTQAAHYLTPENKAPETLVGOISADLDSPASPIYSILPHSDPR 420
 DB 361 VRAVADQAPPEPAFTQAAHYLTPENKAPETLVGOISADLDSPASPIYSILPHSDPR 420
 QY 421 CFSIQPEEGTHTTAAPLDREARAHNLITVATELGWSQBERGWELVAEMSAAPAPO 480
 DB 421 CFSIQPEEGTHTTAAPLDREARAHNLITVATELGWSQBERGWELVAEMSAAPAPO 480
 454

QY 481 RSPVSAVIGIPODSSAOSRVQVAICTLIDENDNAPQALAEPTDTPVCSAARGLIQVIRA 540
 DB 455 -----DSSAQSRYVQVAICTLIDENDNAPQALAEPTDTPVCSAARGLIQVIRA 502
 QY 541 LDRDEVGNSSHVSPGPGLPDANFTVQDNRD-----LPA-----WF 576
 DB 503 LDRDEVGNSSHVSPGPGLPDANFTVQDNRDGSASILLPSRPAPRRAPVLPVLEMDWG 562
 QY 577 HPLMASASMTLH-----WPPAREGNQPAQ 603
 DB 563 QPALSTATVTVSVCRCPDGSVASCWPEAHLSAAGLSTG 602
 RESULT 7
 ADA01366
 ID ADA01366 strand; protein; 781 AA.
 AC ADA01366;
 XX
 XX
 DT 06-NOV-2003 (first entry)
 XX
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO, secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; anti-rheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 PR 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX
 DR WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 PS
 XX
 PS Claim 11; Fig 98; 307pp; English.
 CC
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a

medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 6; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWMNQFVIEEYACP 60
DB 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWMNQFVIEEYACP 60
QY 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTIVIDEATGNITHVTKSLDREERQAYVLLAQ 120
DB 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTIVIDEATGNITHVTKSLDREERQAYVLLAQ 120
QY 121 AVDAASNRPLEPSEEFITKQDINDNPNPIPLGPHATVPEMSWVGTSVIQTVAHDDDP 180
DB 121 AVDAASNRPLEPSEEFITKQDINDNPNPIPLGPHATVPEMSWVGTSVIQTVAHDDDP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPTQGVVTRAI PNMDSETOEELVVI QAKDMGGMGLS 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPTQGVVTRAI PNMDSETOEELVVI QAKDMGGMGLS 240
QY 241 GSTTWTWLTSPVNNPKPEFOSIVQSVETAGGTLVGRADDPDIGNALMAYSLTD 300
DB 241 GSTTWTWLTSPVNNPKPEFOSIVQSVETAGGTLVGRADDPDIGNALMAYSLTD 300
QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDPESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDPESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVQDAPPEPPATQAAVHLTVBENKAPGTLVQISADDDSPASIRISILPHSPER 420
DB 361 VRVAVQDAPPEPPATQAAVHLTVBENKAPGTLVQISADDDSPASIRISILPHSPER 420
QY 421 CFSIOPEBGTHTTAFLDREARAWNLTVLATELGWSMGPGRGWPLLVASWASAPAPQ 480
DB 421 CFSIOPEBGTHTTAFLDREARAWNLTVLATELGWSMGPGRGWPLLVASWASAPAPQ 480
QY 481 RSPVGSAGVIGPODSSAQASRVOVAIQTLIDENDNAPOLAEPYDTVVCSPAAGQLIQVIRA 540
DB 481 RSPVGSAGVIGPODSSAQASRVOVAIQTLIDENDNAPOLAEPYDTVVCSPAAGQLIQVIRA 540
QY 541 LDRDEVGNSSHVSRGGLGPANFLVVOONRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHVSRGGLGPANFLVVOONRD-----LPA-----WF 576
QY 576 HPLMASASWLH-----WPPAERGNOQASOG 603
DB 576 HPLMASASWLH-----WPPAERGNOQASOG 603
QY 603 QPALSTATVTVVSVCRQPDGVSASCPDEAHLISAAGSTG 602
DB 603 QPALSTATVTVVSVCRQPDGVSASCPDEAHLISAAGSTG 602

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RESULT 8
ADA43795
ID ADA43795 standard; protein; 781 AA.

ADA43795;

20-NOV-2003 (first entry)

Human secreted/transmembrane polypeptide PRO34009.

Human; PRO; secreted protein; transmembrane protein;
endothelial cell tube formation; chondrocyte cell differentiation;
microvascular endothelial cell; tumour; lung tumour; colon tumour;
breast tumour; prostate tumour; rectal tumour; kidney tumour;
liver tumour; cytostatic; vaccine.

XX Homo sapiens.
XX US2003064474-A1.
XX 03-APR-2003.
XX 16-SEP-2002; 2002US-00245859.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00157942.
XX (GENET) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX MPI; 2003-605867/57.
XX N-PSDB; ADA43794.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
XX PRO21383, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.
XX Claim 11; Fig 98; 308pp; English.
XX The invention relates to an isolated secreted/transmembrane (PRO)
XX polypeptide, having at least 80% sequence identity to a sequence selected
XX from any one of the 57 amino acid sequences given in specification, or to
XX a sequence encoded by a nucleic acid molecule selected from any one of
XX the nucleic acids deposited under any of the ATCC accession numbers given
XX in specification, or a sequence having at least 80% identity to PRO
XX lacking its associated signal peptide, an extracellular domain of PRO
XX with or without its associated signal peptide. Also included are vectors,
XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6006,
XX PRO1275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX an oligonucleotide probe derived from any one of the above nucleotide
XX sequences. PRO6018 polypeptide is useful for stimulating the
XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
XX and PRO21383 polypeptides are useful for stimulating the proliferation of
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX polypeptides are useful for inhibiting the proliferation of human
XX microvascular endothelial cells. PRO polypeptides are useful for
XX detecting the presence of tumour in a mammal, including tumours of lung,
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and
XX PRO34274 polypeptides are useful for inducing endothelial cell tube
XX formation. PRO or the antibody are useful in the preparation of a
XX medicament for treating a condition responsive to PRO polypeptide. The
XX oligonucleotide probes are useful for isolating genomic and cDNA
XX nucleotide sequences, for measuring or detecting the expression of an
XX associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX hybridisation probe, in chromosome and gene mapping, in the generation of
XX antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence represents a PRO protein.

Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 6; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWMNQFVIEEYACP 60
DB 1 MMGLVRLLLAWLGWGMCKGRLAAPARAWAGSREHHPGALLRTRRSWMNQFVIEEYACP 60
QY 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTIVIDEATGNITHVTKSLDREERQAYVLLAQ 120
DB 61 EPLVIGKLHSDVDGEGRTKYLITGEGAGTIVIDEATGNITHVTKSLDREERQAYVLLAQ 120

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Db 361 VRVAVQDAPEPPAFTQAAYHLTPENKAPGTLVNGQISADLDSDSPASPIRYSILPHSDPER 420
QY 421 CFSIOPEEGTHTTAAPLDREARAHNLTVALTELGMWKGWPERGWPLVLAWSAPAAPQ 480
Db 421 CFSIOPEEGTHTTAAPLDREARAHNLTVALTELGMWKGWPERGWPLVLAWSAPAAPQ 454
QY 481 RSPVGSANVGIPQDSSAQSARVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 540
Db 455 -----DSSAQASRVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 502
QY 541 LDRDEVNGSSHVSFCQPLGPDANFTVQDNRD-----LPA-----WF 576
Db 503 LDRDEVNGSSHVSFCQPLGPDANFTVQDNRDGASALLPSRPAPPRAHAPYLPIELMDWG 562
QY 577 HPPLMASASSWLH-----WPAERGNQSPASOG 603
Db 563 QPALSTATVTVSVCRQCPDGSVASCPPEAHLASAAGLSTG 602

RESULT 10
ADA01238 standard; protein; 781 AA.
AC ADA01238;
DT 06-NOV-2003 (first entry)
DE Human PRO polypeptide #49.
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX cancer; lung; colon; breast; prostate; rectum; kidney; liver;
XX microvascular endothelial cell; endothelial cell tube formation.
OS Homo sapiens.
FN US2003068782-A1.
PD 10-APR-2003.
PF 16-SEP-2002; 2002US-00245851.
PR 27-APR-1999; 98US-0131271P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99MO-US028551.
PR 29-AUG-2001; 2001MO-US027099.
PR 18-JUL-2002; 2002US-00197942.
PA (GETH ) GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurey AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX WPI: 2003-625487/59.
XX N-PSDB: ADA01237.
XX
XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
XX preparation of a medicament for treating a condition responsive to PRO
XX polypeptide, and as therapeutic agents e.g. vaccines.
XX
XX Claim 11; Fig 98; 308pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
XX prostate, rectal, kidney and liver tumours). The polynucleotides are
XX useful in molecular biology, including uses as hybridisation probes, in
XX chromosome and gene mapping, in generating antisense RNA and DNA and in

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CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for stimulating and inhibiting proliferation of human
CC microvascular endothelial cells and for inducing endothelial cell tube
CC formation. This sequence represents a human PRO polypeptide of the
CC invention.
XX
XX Sequence 781 AA:
SQ
XX
XX Query Match 81.9%; Score 2746.5; DB 6; Length 781;
XX Best Local Similarity 84.8%; Pred. No. 1.8e-221;
XX Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAMLGWCMGRLLAPAPAMAGSEHHPGALLRTRRSVMNQFVIEYAGP 60
Db 1 MMGLVRLLLAMLGWCMGRLLAPAPAMAGSEHHPGALLRTRRSVMNQFVIEYAGP 60
QY 61 EPLYLGLKLSDDVDRGGRTRKYLITGAGTAVFIDEATGNHVTSLDREKAQVYLAAQ 120
Db 61 EPLYLGLKLSDDVDRGGRTRKYLITGAGTAVFIDEATGNHVTSLDREKAQVYLAAQ 120
QY 121 AYDRASNRPLEPSEPIIKGQDINDNPIPLPGPYATVPENSMNVTGYIQTADADDP 180
Db 121 AYDRASNRPLEPSEPIIKGQDINDNPIPLPGPYATVPENSMNVTGYIQTADADDP 180
QY 181 SYGNSAKLYTTLVDGIPFSSVDPQTGVFRTAIPNMDREFQEBLYIQAOKMGHNGGJS 240
Db 181 SYGNSAKLYTTLVDGIPFSSVDPQTGVFRTAIPNMDREFQEBLYIQAOKMGHNGGJS 240
QY 241 GSTTAVTSLDVNDNPKPFQSLYQFSVETAGPGLVRLRAQDDLDGNLMAYSIID 300
Db 241 GSTTAVTSLDVNDNPKPFQSLYQFSVETAGPGLVRLRAQDDLDGNLMAYSIID 300
QY 301 GEGSEAFSISTDLQGRDGLTVAKPLDFESQNSYSFRVATNTLIDPAYLRGPFQDVS 360
Db 301 GEGSEAFSISTDLQGRDGLTVAKPLDFESQNSYSFRVATNTLIDPAYLRGPFQDVS 360
QY 361 VRVAVQDAPEPPAFTQAAYHLTPENKAPGTLVNGQISADLDSDSPASPIRYSILPHSDPER 420
Db 361 VRVAVQDAPEPPAFTQAAYHLTPENKAPGTLVNGQISADLDSDSPASPIRYSILPHSDPER 420
QY 421 CFSIOPEEGTHTTAAPLDREARAHNLTVALTELGMWKGWPERGWPLVLAWSAPAAPQ 480
Db 421 CFSIOPEEGTHTTAAPLDREARAHNLTVALTELGMWKGWPERGWPLVLAWSAPAAPQ 480
QY 481 RSPVGSANVGIPQDSSAQSARVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 540
Db 455 -----DSSAQASRVQVAIQTLDENNDNAPOLAEPYDTFVCDASAPGQLIOYIRA 502
QY 541 LDRDEVNGSSHVSFCQPLGPDANFTVQDNRD-----LPA-----WF 576
Db 503 LDRDEVNGSSHVSFCQPLGPDANFTVQDNRDGASALLPSRPAPPRAHAPYLPIELMDWG 562
QY 577 HPPLMASASSWLH-----WPAERGNQSPASOG 603
Db 563 QPALSTATVTVSVCRQCPDGSVASCPPEAHLASAAGLSTG 602

RESULT 11
ADA01122
ID ADA01122 standard; protein; 781 AA.
AC ADA01122;
DT 06-NOV-2003 (first entry)
DE Human secreted/transmembrane polypeptide PRO34009.
XX
XX Human; PRO; secreted protein; transmembrane protein.

```

KM endothelial cell tube formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cytostatic; vaccine.
 XX Homo sapiens.
 OS
 XX US2003068780-A1.
 PN
 XX 10-APR-2003.
 PD
 XX 16-SEP-2002; 2002US-00245143.
 PF
 XX 02-AUG-2000; 2000US-0222695P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENTH) GENENTECH INC.
 PA
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 DR WPI, 2003-625485/59.
 DR N-PDB; ADA01121.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 11, Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 XX
 XX Sequence 781 AA;
 SQ
 Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 MGVGLVRLILAMVIGMCGMGRLLAPARANAGSRHHPGALLTRRSVMNQFVIEEYAGP 60

DB 1 MGVGLVRLILAMVIGMCGMGRLLAPARANAGSRHHPGALLTRRSVMNQFVIEEYAGP 60
 QY 61 EGVLLIGKLSHSDVDRGEGRTRKYLITGEGAGTVFVIDEATGNITHTKSLDREKAQYVLLAQ 120
 DB 61 EGVLLIGKLSHSDVDRGEGRTRKYLITGEGAGTVFVIDEATGNITHTKSLDREKAQYVLLAQ 120
 QY 121 AVDRASNPPLRPPSEFIIKQDINDNPPIPLGPGYHATVPMSVNGTSVIOVTAHDDDP 180
 DB 121 AVDRASNPPLRPPSEFIIKQDINDNPPIPLGPGYHATVPMSVNGTSVIOVTAHDDDP 180
 QY 181 SYGNSAKLVYTVLDLPPEFSVPDPTGVVRTAIPNMDRETOEFLVVIQAKMGHMGSL 240
 DB 181 SYGNSAKLVYTVLDLPPEFSVPDPTGVVRTAIPNMDRETOEFLVVIQAKMGHMGSL 240
 QY 241 GSTTIVTVLSDVNDNPPKFPQSLVQSVETAGPPTLVGRLRADPDLDGNALMAYSLD 300
 DB 241 GSTTIVTVLSDVNDNPPKFPQSLVQSVETAGPPTLVGRLRADPDLDGNALMAYSLD 300
 QY 301 GEGSEAFSISTDLQGRDGLTVRKXLDPESSORSYFVEATNTLIDPAYLRGPFKVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLTVRKXLDPESSORSYFVEATNTLIDPAYLRGPFKVAS 360
 QY 361 VRVAVQDAPPEPPAFQAAVHLLTPENKAPGTLVQGISADIDSPASPIRVSILHSDPER 420
 DB 361 VRVAVQDAPPEPPAFQAAVHLLTPENKAPGTLVQGISADIDSPASPIRVSILHSDPER 420
 QY 421 CFSIQEGSGTHTAFLPREARAHNLTVLATELGMSWGPBPGWVPLVAEWSAPAPQ 480
 DB 421 CFSIQEGSGTHTAFLPREARAHNLTVLATELGMSWGPBPGWVPLVAEWSAPAPQ 480
 QY 481 RSPVGSAGVIGDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAPGQIIQYIRA 540
 DB 481 RSPVGSAGVIGDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAPGQIIQYIRA 540
 QY 541 LDRDVGNSHVSRFGCPIDPANFTVQDNRP-----LPA-----WF 576
 DB 541 LDRDVGNSHVSRFGCPIDPANFTVQDNRP-----LPA-----WF 576
 QY 503 LDRDVGNSHVSRFGCPIDPANFTVQDNRGASLILPSPAPPRHAPLVPTELMDWG 562
 DB 503 LDRDVGNSHVSRFGCPIDPANFTVQDNRGASLILPSPAPPRHAPLVPTELMDWG 562
 QY 577 HPLMASASWMLH-----WPPAERGNQAPASOG 603
 DB 577 HPLMASASWMLH-----WPPAERGNQAPASOG 603
 QY 563 QPALSTATVTVSVRCQPDGSVASCWPEAHLSAAGISTG 602
 DB 563 QPALSTATVTVSVRCQPDGSVASCWPEAHLSAAGISTG 602
 RESULT 12
 ID ADA43679
 ADAA3679; protein: 781 AA.
 AC
 XX ADAA3679;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 OS
 XX US2003073190-A1.
 PN
 XX 17-APR-2003.
 PD
 XX 09-SEP-2002; 2002US-00238283.
 PF
 XX 01-JUL-1998; 98US-0091358P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 20-JUL-1999; 99US-0144758P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 25-AUG-1999; 99US-00380137.
 PR

PR 30-MAR-2000; 2000OWO-US008439.
 PR 02-JUN-2000; 2000OWO-US015254.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI, 2003-585304/55.
 DR N-PSDB; ADA43678.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 11, Fig 98, 352pp; English.

XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO2133, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.

XX
 SQ Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MNGVRLLIAMGCMGCMGRLLAPARAWAGSRHGGPALLTRRGWVNOFFVIEVNGP 60
 DB 1 MNGVRLLIAMGCMGCMGRLLAPARAWAGSRHGGPALLTRRGWVNOFFVIEVNGP 60
 QY 61 EYVLIGKLSHSDVDRGEGRTKYLITGEGAGTVFIDEATGNIHTVSTLDRKCAQVLLAQ 120
 DB 61 EYVLIGKLSHSDVDRGEGRTKYLITGEGAGTVFIDEATGNIHTVSTLDRKCAQVLLAQ 120
 QY 121 AVDRASNRPLEPPSEFIKGDINDNPPFPLGPHYHATVPKSNVGSVIVQTADADDP 180
 DB 121 AVDRASNRPLEPPSEFIKGDINDNPPFPLGPHYHATVPKSNVGSVIVQTADADDP 180
 QY 121 AVDRASNRPLEPPSEFIKGDINDNPPFPLGPHYHATVPKSNVGSVIVQTADADDP 180
 DB 121 AVDRASNRPLEPPSEFIKGDINDNPPFPLGPHYHATVPKSNVGSVIVQTADADDP 180
 QY 181 SYGNSAKLYVTVLDGLPFPSSVDPTQGVVTAIPNNDRTOEFLVVIQAKMGHMGSL 240
 DB 181 SYGNSAKLYVTVLDGLPFPSSVDPTQGVVTAIPNNDRTOEFLVVIQAKMGHMGSL 240

DB 181 SYGNSAKLYVTVLDGLPFPSSVDPTQGVVTAIPNNDRTOEFLVVIQAKMGHMGSL 240
 QY 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVYETAGPTLVLRBAQDPDLGDNALMAVSLD 300
 DB 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVYETAGPTLVLRBAQDPDLGDNALMAVSLD 300
 QY 301 GEGSEAFSISTDLQGRDGLITVRKPLDFESQSSYSFRVATNTLIDPAYLRGPFQDVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDFESQSSYSFRVATNTLIDPAYLRGPFQDVAS 360
 QY 361 VRYAVODAPBPAPFPTAAAYHLTVPEKAKGTLVGQISADLDSFASPIYSLIPSHDPER 420
 DB 361 VRYAVODAPBPAPFPTAAAYHLTVPEKAKGTLVGQISADLDSFASPIYSLIPSHDPER 420
 QY 421 CFSIQPEEGTHTAPLIDREARAWNLTVLATELGMSWGPBGWYLLVAEWSAPAAPQ 480
 DB 421 CFSIQPEEGTHTAPLIDREARAWNLTVLATELGMSWGPBGWYLLVAEWSAPAAPQ 480
 QY 481 RSPVGSAGVLPDSSQASRRVQVATOTLDENNAIPQALPPTFVCDASAPGOLIQTIRA 540
 DB 481 RSPVGSAGVLPDSSQASRRVQVATOTLDENNAIPQALPPTFVCDASAPGOLIQTIRA 540
 QY 541 LDREYGNSSHVSFOGPIPLPDANFTVQDNRD-----LPA-----WF 576
 DB 503 LDREYGNSSHVSFOGPIPLPDANFTVQDNRDGASALLPSRAPPRHAYLVPIELMDWG 562
 QY 577 HPLMASASLWH-----WPPAERGNQPSASG 603
 DB 563 QPALSTATVTVVCRCPDGSVASCPPEAHLSAAGLSIG 602

RESULT 13

ADA06941
 ID ADA06941 standard; protein; 781 AA.

AC ADA06941;

XX 06-NOV-2003 (first entry)

DE Human PRO polypeptide #49.

XX Human, PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor- α ; TNF- α ; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW bone disorder; cartilage disorder; sports injury; proteoglycan;
 KW cartilage; sports-related joint problem; articular cartilage defect;
 KW osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder;
 KW thalassemia; immune system cell infiltration; cancer; vulnery;
 KW antianemic; osteopathic; antirheumatic; antiarthritic.

OS Homo sapiens.

FN US2003068781-A1.

PD 10-APR-2003.

PE 16-SEP-2002; 2002US-00245771.

XX 03-AUG-1999; 99US-0146843P.

PR 15-MAY-2000; 2000OWO-US013358.

PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GENTH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI, 2003-625486/59.
 DR N-PSDB; ADA06940.

PT Novel secreted and transmembrane polypeptides, PRO polypeptides useful
PT for stimulating proliferation or differentiation of chondrocyte cells and
PT inducing endothelial cell tube formation.

PS Claim 11; Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating various bone and/or cartilage disorders
CC such as sports injuries and arthritis. PRO polypeptides which stimulate
CC the release of proteoglycans from cartilage are useful for treating
CC sports-related joint problems, articular cartilage defects,
CC osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful
CC for treating various mammalian haemoglobin-associated disorders such as
CC various thalassemias and conditions which may benefit from enhanced
CC local immune system cell infiltration. This sequence represents a human
CC PRO polypeptide of the invention.

XX Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 MWGLVRLILAMTGGWCMGRLAAPARAWAGSREHPGALLRTRRSWTWNOFFVIEEYAGP 60
DB 1 MWGLVRLILAMTGGWCMGRLAAPARAWAGSREHPGALLRTRRSWTWNOFFVIEEYAGP 60
QY 61 EPTVIGKLHSDVDGEGRTKYLITGEGAGTFFVDEATGNHITKSLDREKQYVLLAQ 120
DB 61 EPTVIGKLHSDVDGEGRTKYLITGEGAGTFFVDEATGNHITKSLDREKQYVLLAQ 120
QY 121 AVDRASNRPLEPPEPFIITKQDINDNPPFPLGPHATVPKSNVGTSVIQTVAHADDP 180
DB 121 AVDRASNRPLEPPEPFIITKQDINDNPPFPLGPHATVPKSNVGTSVIQTVAHADDP 180
QY 181 SYGNSAKLVTVLGLPFESVDPQGVARTAIPIIMDEPQEEFLVYIQAQDMGSHGSL 240
DB 181 SYGNSAKLVTVLGLPFESVDPQGVARTAIPIIMDEPQEEFLVYIQAQDMGSHGSL 240
QY 241 GSTTAVTVLSDVNDNPKFPQSLYQFSVETAGGTLVGRRAQDDPLGDNALMAYSIID 300
DB 241 GSTTAVTVLSDVNDNPKFPQSLYQFSVETAGGTLVGRRAQDDPLGDNALMAYSIID 300
QY 301 GEGSEARISITDLOGRGDGLTVRKPLDPEESORSYSPFEVETNTLIPAYIRRGEPFQVAS 360
DB 301 GEGSEARISITDLOGRGDGLTVRKPLDPEESORSYSPFEVETNTLIPAYIRRGEPFQVAS 360
QY 361 VRVAVODAPPEPFAFQAHLTVPENKAPGTLVGOISADLDPSPASIRYSIIIPHSDDPR 420
DB 361 VRVAVODAPPEPFAFQAHLTVPENKAPGTLVGOISADLDPSPASIRYSIIIPHSDDPR 420
QY 421 CFSIQPEEGTHTAAPIIDREKRAMHNTTVLATELGMSWGPERGWPLVAVMSAPAAPQ 480
DB 421 CFSIQPEEGTHTAAPIIDREKRAMHNTTVLATELGMSWGPERGWPLVAVMSAPAAPQ 480
QY 481 RSPGASVGIPODSSAQASRVOVAIQTLDENDNAPQLAEPYDTFVCDSPAAGQLIQVIRA 540

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DB 455 -----DSSAQASRVOVAIQTLDENDNAPQLAEPYDTFVCDSPAAGQLIQVIRA 502
QY 541 LDRDEVGNSSHYVFCGPGPDANTVQDNRD-----LPA-----WF 576
DB 503 LDRDEVGNSSHYVFCGPGPDANTVQDNRDGASLLPSRPAPRHAIVLPILMDWG 562
QY 577 HPLMASASWLH-----WPAERGNQPA5QG 603
DB 563 GPALSTATVTVSVRCQPDGVSACWPEAHL5AAGLSTG 602

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RESULT 14

ADA08429
ID ADA08429 standard; protein; 781 AA.

AC ADA08429;

DT 06-NOV-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO34009.

XX osteopathic; antirheumatic; antiarthritic; gene therapy;

KW cell proliferation stimulator;

KW chondrocyte cell differentiation stimulator;

KW secreted and transmembrane protein; PRO human; PRO113; PRO20080;

KW PRO21383; human microvascular endothelial cell proliferation; PRO6071;

KW PRO4487; PRO6006; PRO2406; PRO2556; PRO698; PRO1002; PRO4316; tumour;

KW adrenal tumour; lung tumour; colon tumour; breast tumour;

KW prostate tumour; rectal tumour; cervical tumour; liver tumour;

KW sports-related joint problem; articular cartilage defect; osteoarthritis;

KW rheumatoid arthritis; tissue typing.

XX Homo sapiens.

XX US2003068783-A1.

XX 09-MAY-2001; 2001US-0290589P.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WL, Zhang Z,

XX Fong S;

XX WPI; 2003-625488/59.

XX N-P8DB; ADA08428.

XX Novel isolated PRO113, PRO20080 or PRO21383 polypeptide useful for

XX stimulating proliferation of human microvascular endothelial cells, and

XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte

XX cells.

PS Claim 11; Fig 98; 308pp; English.

CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (1). PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO113, PRO20080,
CC or PRO21383 polypeptide is useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487, or PRO6006
CC polypeptide is useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides such as PRO210, PRO256,
CC PRO698, PRO1002, PRO4316, etc., are useful for detecting the presence of
CC tumour in a mammal which involves comparing the level of expression of
CC the above mentioned polypeptides in a test sample of cells taken from the
CC mammal, and a control sample of normal cells of the same cell type, where
CC a higher level of expression of the PRO polypeptide in the test sample as

CC compared to the control sample is indicative of the presence of tumour in
 CC the mammary, the tumour being adrenal tumour, lung tumour, colon tumour,
 CC breast tumour, prostate tumour, rectal tumour, cervical tumour or liver
 CC tumour. PRO6018 polypeptide is useful for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis, or rheumatoid
 CC arthritis. PRO polypeptides are useful as molecular weight markers for
 CC protein electrophoresis. (I) is also useful for screening compounds to
 CC identify those that mimic the PRO polypeptide (agonists) or prevent the
 CC effect of the PRO polypeptide (antagonists). The polynucleotide (II)
 CC encoding (I) is useful as hybridisation probes, in chromosome and gene
 CC mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid
 CC is also useful for the preparation of PRO polypeptides. The full-
 CC length native sequence of PRO gene or its portions may be used as
 CC hybridisation probes for a cDNA library to isolate the full-length PRO
 CC cDNA or to isolate still other cDNAs. Nucleotide sequences encoding PRO
 CC can also be used to construct hybridisation probes for mapping the gene
 CC which encodes that PRO and for the genetic analysis of individuals with
 CC genetic disorders. (II) encoding (I) or its modified forms can also be
 CC used to generate either transgenic animals or knockout animals which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents. (II) encoding PRO polypeptides are also useful in gene
 CC therapy techniques to treat conditions associated with aberrant
 CC expression or activity of (I). The PRO polypeptides and nucleic acid
 CC molecules are useful for tissue typing. This is the amino acid sequence
 CC of a novel human secreted and transmembrane PRO polypeptide.

XX Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
 Best Local Similarity 84.8%; Pred. No. 1.8e-221;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MGVLRLLIAMIIGMGCGRILAAPARAWAGSRHHPGALLTRRSWNNQFVIEEYAGP 60
 DB 1 MGVLRLLIAMIIGMGCGRILAAPARAWAGSRHHPGALLTRRSWNNQFVIEEYAGP 60
 QY 61 EPLVIGKLSHSDVDGEGRTKTLTGEAGTVEIDEAGNIHVKRSIDREKKAQYVLLAQ 120
 DB 61 EPLVIGKLSHSDVDGEGRTKTLTGEAGTVEIDEAGNIHVKRSIDREKKAQYVLLAQ 120
 QY 121 AVDRASNPRLPEPSEFIKGGDINDNPPIFPLGPHATVPMSNVGTSVIQVTAHADDP 180
 DB 121 AVDRASNPRLPEPSEFIKGGDINDNPPIFPLGPHATVPMSNVGTSVIQVTAHADDP 180
 QY 121 AVDRASNPRLPEPSEFIKGGDINDNPPIFPLGPHATVPMSNVGTSVIQVTAHADDP 180
 DB 121 AVDRASNPRLPEPSEFIKGGDINDNPPIFPLGPHATVPMSNVGTSVIQVTAHADDP 180
 QY 181 SYGSAKIVTVLGLPFFSVDPOTGVVTRAIIPNNDRTOEELFVIOAKMGSHMGLS 240
 DB 181 SYGSAKIVTVLGLPFFSVDPOTGVVTRAIIPNNDRTOEELFVIOAKMGSHMGLS 240
 QY 241 GSTTIVTILSDVNDNPKFPQSLYQFSVETAGEGTLGRLRAADPDLGDNALMAYSLD 300
 DB 241 GSTTIVTILSDVNDNPKFPQSLYQFSVETAGEGTLGRLRAADPDLGDNALMAYSLD 300
 QY 301 GEGSARFISITDLQGRDGLTVRKPLDRESORSISFRFVATNTLIDPAYLRGPFKYAS 360
 DB 301 GEGSARFISITDLQGRDGLTVRKPLDRESORSISFRFVATNTLIDPAYLRGPFKYAS 360
 QY 301 GEGSARFISITDLQGRDGLTVRKPLDRESORSISFRFVATNTLIDPAYLRGPFKYAS 360
 DB 301 GEGSARFISITDLQGRDGLTVRKPLDRESORSISFRFVATNTLIDPAYLRGPFKYAS 360
 QY 361 VRVAVQDAPEPPAFQAAYHILTVPENKAPGLTVQGISADADSPASPRYSIILHSPER 420
 DB 361 VRVAVQDAPEPPAFQAAYHILTVPENKAPGLTVQGISADADSPASPRYSIILHSPER 420
 QY 421 CFSIQPEEGTHTAALPDRERAMENLTVALTEGMSWGPGRGWVPLIVAEWSAPAAPQ 480
 DB 421 CFSIQPEEGTHTAALPDRERAMENLTVALTEGMSWGPGRGWVPLIVAEWSAPAAPQ 480
 QY 481 RSPVSAVGIPODSSAQRVQVAIQTDENDNAPQLAEPDITFVCSAARFQILQYIRA 540
 DB 481 RSPVSAVGIPODSSAQRVQVAIQTDENDNAPQLAEPDITFVCSAARFQILQYIRA 540
 QY 545 -----DSSAQSRVQVAIQTDENDNAPQLAEPDITFVCSAARFQILQYIRA 502
 DB 545 -----DSSAQSRVQVAIQTDENDNAPQLAEPDITFVCSAARFQILQYIRA 502
 QY 541 LDRDEVGNSHVSFOGPIGPDPANFTVQDNRD-----LPA-----WF 576
 DB 541 LDRDEVGNSHVSFOGPIGPDPANFTVQDNRD-----LPA-----WF 576
 QY 503 LDRDEVGNSHVSFOGPIGPDPANFTVQDNRDGSAILLPSPAPPRFAPLVLPTELDWG 562
 DB 503 LDRDEVGNSHVSFOGPIGPDPANFTVQDNRDGSAILLPSPAPPRFAPLVLPTELDWG 562
 QY 577 HPLMASASSMHL-----WPAERKGNPAGSG 603
 DB 577 HPLMASASSMHL-----WPAERKGNPAGSG 603

DB 563 GPALSTATVTSVCRCPDPSVASCWPEAHLSAAGLSYG 602

RESULT 15

ID ADB99722 standard; protein; 781 AA.

XX ADB99722;

DT 04-DEC-2003 (first entry)

XX Human PRO polypeptide SEQ ID 98.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;

KM tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

KM adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;

KM microvascular endothelial cell; endothelial cell tube formation;

KM sports-related joint problem; articular cartilage defect; osteoarthritis;

XX rheumatoid arthritis; osteopathic; anti-rheumatic; antiarthritic.

OS Homo sapiens.

XX US2003082728-A1.

XX 01-MAY-2003.

XX 16-SEP-2002; 2002US-00245185.

XX 07-JUL-1998; 98US-0091878P.

XX 02-JUN-1999; 99WO-US012252.

XX 25-AUG-1999; 99US-00380137.

XX 29-AUG-2001; 2001WO-US027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GENTH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;

XX Fong S;

XX WPI; 2003-743898/70.

XX N-PSDB; ADB99721.

XX New isolated, secreted and transmembrane PRO polypeptides and nucleic

XX acids, useful for diagnosing, preventing and/or treating tumors, such as

XX lung, colon, breast, prostate, rectal, kidney or liver tumors.

XX Claim 11; Fig 98; 308pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and

XX transmembrane polypeptides) and the polynucleotides encoding them. The

XX invention also relates to an antibody which specifically binds to a PRO

XX polypeptide, a method for stimulating the release of tumour necrosis

XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the

XX proliferation or differentiation of chondrocyte cells and a method for

XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,

XX colon, breast, prostate, rectal, cervical and liver tumours). The

XX polynucleotides are useful in molecular biology, including uses as

XX hybridisation probes, in chromosome and gene mapping, in generating

XX antisense RNA and DNA and in gene therapy. The polynucleotides may also

XX be used in preparing PRO polypeptides by recombinant techniques and in

XX generating either transgenic animals or knock-out animals which are

XX useful in the development and screening of therapeutically useful

XX reagents. The PRO polypeptides or antibodies are used in preparing a

XX medicament for treating a condition responsive to the polypeptides or

XX antibodies, such as tumours, for stimulating and inhibiting proliferation

XX of human microvascular endothelial cells, for inducing endothelial cell

XX tube formation and for treating sports-related joint problems, articular

XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence

XX represents a human PRO polypeptide of the invention.

XX Sequence 781 AA;

Query Match 81.9%; Score 2746.5; DB 7; Length 781;
Best Local Similarity 84.8%; Pred. No. 1.8e-221;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILLANLGGWGCCKGRLAAPARAWAGSRHEHPGALLRTRRSWYWNQFFVIEEYAGP 60
DB 1 MMGLVRLILLANLGGWGCCKGRLAAPARAWAGSRHEHPGALLRTRRSWYWNQFFVIEEYAGP 60
QY 61 EPLVIGKLHSDVDKGEGRKTKYLITGEGAGTVFVIDEATGNHVTKSLDREKKAQYVLLAQ 120
DB 61 EPLVIGKLHSDVDKGEGRKTKYLITGEGAGTVFVIDEATGNHVTKSLDREKKAQYVLLAQ 120
QY 121 AVDRASNPPLPEPSEFIIKQDINDNPPIFPLGPHATVPMSNVGTSVIQVTAHADDDP 180
DB 121 AVDRASNPPLPEPSEFIIKQDINDNPPIFPLGPHATVPMSNVGTSVIQVTAHADDDP 180
QY 181 SYGNSAKLYTVTLGDLPEFSVDPOTGVVRTAIPMDRETOEELVVIQAKDMGSHGGLS 240
DB 181 SYGNSAKLYTVTLGDLPEFSVDPOTGVVRTAIPMDRETOEELVVIQAKDMGSHGGLS 240
QY 241 GSTTIVTVTLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSIID 300
DB 241 GSTTIVTVTLSDVNDNPPKFPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSIID 300
QY 301 GEGSEAFSISTDLQGRGLTVRRKPLDSEGRSYSFVEANTLIDPAYLRGPFKDYAS 360
DB 301 GEGSEAFSISTDLQGRGLTVRRKPLDSEGRSYSFVEANTLIDPAYLRGPFKDYAS 360
QY 361 VRVAVODAPBPAPFTQAAYHLTVPENKAPGTLVGCISADLDSFASPIRYSIILPHSDPER 420
DB 361 VRVAVODAPBPAPFTQAAYHLTVPENKAPGTLVGCISADLDSFASPIRYSIILPHSDPER 420
QY 421 CFSIQPEEGTIHTAAPLDREARAWHNLTVLATELGMSGPERGWPLLVAMNSAPAAPFQ 480
DB 421 CFSIQPEEGTIHTAAPLDREARAWHNLTVLATELGMSGPERGWPLLVAMNSAPAAPFQ 480
QY 481 RSPVGSAYGIPQDSSAQSRVQVAIQTLDENNDNAPOLABPYDFVCDSPAAPGQLIOYIRA 540
DB 481 RSPVGSAYGIPQDSSAQSRVQVAIQTLDENNDNAPOLABPYDFVCDSPAAPGQLIOYIRA 540
QY 455 -----DSSAQSRVQVAIQTLDENNDNAPOLABPYDTVCDSPAAPGQLIOYIRA 502
DB 455 -----DSSAQSRVQVAIQTLDENNDNAPOLABPYDTVCDSPAAPGQLIOYIRA 502
QY 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHVSFGPLGPDANFTVQDNRD-----LPA-----WF 576
QY 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGSASLLPSRPAPRHAPYLVPILMDWG 562
DB 503 LDRDEVGNSSHVSFGPLGPDANFTVQDNRDGSASLLPSRPAPRHAPYLVPILMDWG 562
QY 577 HPLMASASSWLH-----WPAERGNQZPASOG 603
DB 577 HPLMASASSWLH-----WPAERGNQZPASOG 603
QY 563 QPALSTRTVTVSVCRCPDGSVASCWPEZAHLSAAGLSTG 602
DB 563 QPALSTRTVTVSVCRCPDGSVASCWPEZAHLSAAGLSTG 602

Search completed: December 8, 2004, 10:13:02
Job time : 266.185 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 51.4357 Seconds

(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-4

Perfect score: 3354

Sequence: 1 MWGLVRLLLMLGSGMGCMGR.....LPSCQLPLGIPALGIVLCAS 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1602	47.8	796	2	A38992
2	1596	47.6	796	2	A53584
3	1593	47.5	796	2	148277
4	1593	47.5	796	2	149556
5	1529.5	45.6	793	2	D38992
6	1442	43.0	789	2	152701
7	1441	43.0	790	2	137016
8	1432.5	42.7	785	2	150180
9	1412.5	42.1	790	2	G02678
10	1400	41.7	790	2	150178
11	1389.5	41.4	790	2	151638
12	1368.5	40.8	794	2	159372
13	940.5	28.0	784	1	IJHUC5
14	604	18.0	913	1	IJHUCR
15	601	17.9	906	1	IJUSCN
16	594.5	17.7	906	1	IJHUC2
17	594	17.7	906	1	IJHUCN
18	592	17.7	877	1	IJHUCN
19	591	17.6	912	1	IJHUCN
20	589	17.6	913	1	A47543
21	586	17.5	887	1	IJHUC1
22	581	17.3	882	1	IJHUC2
23	581	17.3	905	1	IJHUC1
24	574.5	17.1	712	1	IJUSCT
25	574.5	17.1	717	2	I51206
26	567	16.9	916	2	B38992
27	563.5	16.8	713	2	G02878
28	553.5	16.5	814	2	G02878
29	535	16.0	2809	2	T30213

30	531	15.8	732	1	IJHUCB
31	531	15.8	783	2	I50116
32	524	15.6	884	1	IJUSCE
33	523.5	15.6	896	2	I45858
34	521	15.5	884	2	S34438
35	519	15.5	871	2	S47518
36	512	15.3	3034	2	T14119
37	510.5	15.2	826	2	B55363
38	510.5	15.2	896	2	A55363
39	507	15.1	732	1	IJUSCM
40	502.5	15.0	820	1	IJUSCP
41	502	15.0	829	1	IJHUCP
42	486	14.8	3097	2	T00021
43	491	14.6	840	2	I37281
44	491	14.6	894	2	I37282
45	487	14.5	770	2	B48910

ALIGNMENTS

RESULT 1		A38992		cadherin 11 precursor - human	
N;Alternate names: OB-cadherin, osteoblast		C;Species: Homo sapiens (man)		C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jul-2004	
C;Accession: A38992		R;Suzuki, S.; Sano, K.; Tanihara, H.		Cell Regul. 2, 261-270, 1991	
A;Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous		A;Reference number: S24305; PMID:91283540; PMID:2059658		A;Cross-references: UNIPROT:P55287; GB:L34056; NID:9506403; PIDN:AAA35622.1; PID:950640	
A;Accession: A38992		A;Status: Preliminary; translated from GB/EMBL/DBJ		A;Molecule type: mRNA	
A;Residues: 1-796 <SUZ>		A;Gene: GDB:CDH11; OB		A;Cross-references: GDB:512891; OMIM:600023	
A;Map position: 16q22.1-16q22.1		C;Superfamily: cadherin repeat homology		C;Keywords: calcium binding; cell adhesion; duplication	
F;56-159/Domain: cadherin repeat homology <CR1>		F;162-268/Domain: cadherin repeat homology <CR2>		F;271-383/Domain: cadherin repeat homology <CR3>	
F;386-488/Domain: cadherin repeat homology <CR4>		Query Match		Best local similarity 50.4%; Pred. No. 1.1e-98;	
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;		47.8%; Score 1602; DB 2; Length 796;		17 CWGRLA-----APAR-----AWAGSRE--HGGPALRRBSWVWVQFVIEFAGPEPV 63	
13 CLQMLCHSHAFAPERGGHLPSPFHGHEKGEQVLRSGKRWVWVQFVIEFAGPEPV 72		64 LICKLHSDVDGSGEGRKYLLTGEGAGTVFVIDEATGNIHVTKSLDREKAQVYLLAQAVD 123		73 LVERLHSDIDSGDGNIKYILSGGAGTIFVIDDKSGNIAHTKILDRBBAQYLLMAQAVD 132	
124 RASNRPLEPSPSEFIIIGQDINDNPPIFPLGPPYATAPPEMSNVGTSTVIOVTAHADDPSVG 183		133 RDNRRPLEPSPSEFIVKQDINDNPPEFLHETTYANPESNVGTSTVIOVTAHADDPSVG 192		184 NSAKLVYTVVDGLPFPFSDVPQGTGVATATPMDRETQEEFLVYIQAKMGHNGVLSGT 243	
193 NSAKLVYTVVDGLPFPFSDVPQGTGVATATPMDRETQEEFLVYIQAKMGHNGVLSGT 252		244 TVTTLTSDVNDNPPKPPQSIYQFSVETAGPGTLVGRLAQDPDLQDNALMAYSLIDGGG 303		253 KVTITLTDVNDNPPKPPQSIYQFSVETAGPGTLVGRLAQDPDLQDNALMAYSLIDGGG 312	
304 SEAFSTIDTQGDGLLTAVKKPLDPFSQRSYSPREVAETWTLIDPAVLRGGPFQVAVSV 363					

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Db      313 MESFETITDYTOEGLVILKKPVPDEFERAVSLKVEANVHIDPKFISNGPFCOTVTKI 372
Qy      364 AVQDAPEPPAFTQAAYHILTVPENKAPGTLVGQISAADLSPASPIRYSILPHSPERCF 423
Db      373 SVEDEBPMTFLASYSIHEVOENAAAGTVGRVAPKAPDPAANSPIRYSIDRHLDLDFFT 432
Qy      424 IQPEEGTIIHTAPLDREARAHNLTVLATBELGWSGWERGVNPLVAEWSAPAAPQORSP 483
Db      423 INPEDGFIXTKPLDREBTAWLNTITVFAAEI-----463
Qy      484 VGSANGIPQDSSAASRQVAILQTLDENDNAFQALPEYDTFVCS-----AARQOLIQVIR 539
Db      464 -----NHRHQAQVPAIRVLVDVNDNAPKFAAYEGFICSDQTKPLSNQPIVTIS 514
Qy      540 ALRDEVNSSSHVFGCP--LGPDAFTVQDNRLPA-----WPHPLM 581
Db      515 ADDKDDTANGPRFIFSLPEIINHNPFTVRNNTAGVYARRGFSRQKODLYLPIVI 574
Qy      582 ASASSWLHWPAAERGNQAPAGCKSSLP-CG-RUPGALPSC 620
Db      575 -----SDGIPMSSTNTLITKVCOCGVNGALLSC 604
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RESULT 2

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A53584
Cb-cadherin precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C.Accession: A53584
R.Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amano, E.
J. Biol. Chem. 269, 12092-12098, 1994
A.Title: Molecular cloning and characterization of Cb-cadherin, a new member of cadherin
A.Reference number: A53584; MUID:94216322; PMID:8163513
A.Accession: A53584
A.Status: preliminary
A.Molecule type: mRNA
A.Cross-references: UNIPROT:P55288; GB:D21253; NID:g994774; PID:BA04797.1; PID:g994775
C.Superfamily: cadherin, cadherin repeat homology
C.Keywords: transmembrane protein
F156-159/Domain: cadherin repeat homology <CR1>
F162-268/Domain: cadherin repeat homology <CR2>
F186-488/Domain: cadherin repeat homology <CR4>
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Query Match 47.6%; Score 1596; DB 2; Length 796;
Best Local Similarity 50.7%; Pred. No. 2.7e-98;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;

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Qy      31 SREHP-----GPALIRTRSWVWNOFVIEEYAGPEPVLIGKLSHDVDRGERT 79
Db      29 SHLPSFHGHKEKKEGOVLRSKRGWVWNOFVIEEYTGPDVLVGRLHSDIDSGDNI 88
Qy      80 KYLLTGAGATFVIDATGNIHTKSLDREKAQVYLLAQAVDRAANRPLEPSEFIK 139
Db      89 KYLLSGGAGTIFVIDKSGNIHATKTLDRERAAQYLLMAQAVDRDNRPLEPSEFIK 148
Qy      140 GQDINDNPPIPLPGYATVPEMSNVGTSVIQTAAHDADPSYGSNAKLYTVTLGDLPPF 199
Db      149 VQDINDNPPEFLHETIYANVPERSNVGTSVIQTASADDPITGNSAKLYVSLIEQPIF 208
Qy      200 SYDPQTGVATLPMNMRTOEELVYIQAKMGKHGSGSTTVTVLSDVNDNPPK 259
Db      209 SVEAQGTIRFALPMNMRKAEEHVYIQAKMGKHGSGSTTVTVLSDVNDNPPK 268
Qy      260 POSLYQSVSVETAGPTLVGRRAQDPLDGNALMAYSLIDGEGSAFISTDLQGRDL 319
Db      269 POSYQSVSVAAPGSEVGRVAKAPDIDENGIVTYNIIVDGDGILFEITTDYEQDV 328
Qy      320 LTVKRLDPEQSYSRVEATNTLIDPAVLRGPFKDVASVAVQDAPEPPAFTQAAY 379
Db      329 VKLKPVDPEFKRAVSLKIEANVHIDPKFISNGPFCOTVTKISVEDADEPMTAPSY 388
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Qy      380 HLTVENKAPGTLVGQISAADLSPASPIRYSILPHSPERCFISIOPEEGTIIHTAPLDR 439
Db      389 IHEVOENAAAGTVGRVAPKAPDPAANSPIRYSIDRHLDLDFFTINPEDGFIXTKPLDR 448
Qy      440 EAAAHNLTVLATBELGWSGWERGVNPLVAEWSAPAAPQORSPVGSANGIPQDSSAAS 499
Db      449 EETAWLNTISFAAEI-----NHRHQAET 470
Qy      500 RQVAVIQTLDENDNAFQALPEYDTFVCSAAP-----GQLIQVIRALDRDEVNSSSHVFO 555
Db      471 KYPVAIRVLVDVNDNAPKFAAYEGFICSDHPKALSNPIYTVGADODDITANGPRFIFS 530
Qy      556 GP--LGPDAFTVQDNRLPA-----WPHPLMASASSWLHWPAAERGN 597
Db      531 LPEIEMHNPNFTVRNNTAGVYARRGFSRQKODFYLLPIVI-----SDGII 579
Qy      598 OPASQKSSSLP-CG-RUPGALPSC 620
Db      580 PMSSTNTLITKVCOCGVNGALLSC 604
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RESULT 3

```
148277
cadherin-11 - mouse
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 148277
R.Hoffmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A.Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A.Reference number: 148277; MUID:95263886; PMID:7750649
A.Accession: 148277
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-796 <RES>
A.Cross-references: UNIPROT:P55288; EMBL:X77557; NID:G642796; PID:CAA54674.1; PID:G66666
C.Superfamily: cadherin, cadherin repeat homology
F156-159/Domain: cadherin repeat homology <CH>
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Query Match 47.5%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4.3e-98;
Matches 316; Conservative 98; Mismatches 127; Indels 84; Gaps 8;

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Qy      31 SREHP-----GPALIRTRSWVWNOFVIEEYAGPEPVLIGKLSHDVDRGERT 79
Db      29 SHLPSFHGHKEKKEGOVLRSKRGWVWNOFVIEEYTGPDVLVGRLHSDIDSGDNI 88
Qy      80 KYLLTGAGATFVIDATGNIHTKSLDREKAQVYLLAQAVDRAANRPLEPSEFIK 139
Db      89 KYLLSGGAGTIFVIDKSGNIHATKTLDRERAAQYLLMAQAVDRDNRPLEPSEFIK 148
Qy      140 GQDINDNPPIPLPGYATVPEMSNVGTSVIQTAAHDADPSYGSNAKLYTVTLGDLPPF 199
Db      149 VQDINDNPPEFLHETIYANVPERSNVGTSVIQTASADDPITGNSAKLYVSLIEQPIF 208
Qy      200 SYDPQTGVATLPMNMRTOEELVYIQAKMGKHGSGSTTVTVLSDVNDNPPK 259
Db      209 SVEAQGTIRFALPMNMRKAEEHVYIQAKMGKHGSGSTTVTVLSDVNDNPPK 268
Qy      260 POSLYQSVSVETAGPTLVGRRAQDPLDGNALMAYSLIDGEGSAFISTDLQGRDL 319
Db      269 POSYQSVSVAAPGSEVGRVAKAPDIDENGIVTYNIIVDGDGILFEITTDYEQDV 328
Qy      320 LTVKRLDPEQSYSRVEATNTLIDPAVLRGPFKDVASVAVQDAPEPPAFTQAAY 379
Db      329 VKLKPVDPEFKRAVSLKIEANVHIDPKFISNGPFCOTVTKISVEDADEPMTAPSY 388
Qy      380 HLTVENKAPGTLVGQISAADLSPASPIRYSILPHSPERCFISIOPEEGTIIHTAPLDR 439
Db      389 IHEVOENAAAGTVGRVAPKAPDPAANSPIRYSIDRHLDLDFFTINPEDGFIXTKPLDR 448
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QY 440 EAAKMHNLTVLATELGWKGPERGVPLVAEMSAAPAPQORVSGAVGIPQDSSAQAS 499
| : : : : :
DB 449 EETAMNLISVFAADI-----HNRHQT 470
QY 500 RVQVAIQTLDENDNAPOLAEPYDTVCDSAP-----GQLIQVIRALDRDEVGNSHVSFQ 555
| : : : : :
DB 471 KVPVAILVDVNDNAPKFAAPYEGFICESHPKALSNQPIVTVSADDDOTDANGPRIFIS 530
QY 556 GP--LGPDAFTVODNRLPA-----WFHPLMASASSWLHMPAERGN 597
| : : : : :
DB 531 LPPEIMHNPFTVADNNDNTAGVYARRGGSFROKQDFLPLIVL-----SDGGI 579
QY 598 QPASQKSSSLP-CG-RUPGALPSC 620
DB 580 PPMSTNTLITIKVCGCDVNGALLSC 604

RESULT 4

149556
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R/Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: 149556; MUID:95269887; PMID:7750650
A:Accession: 149556
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <RES>
A:Cross-references: UNIPROT:P55288; GB:D31963; NID:G974190; PIDN:BA06730.1; PID:G974191
F:56-159/Domain: cadherin repeat homology <CDH>

Query Match 47.5%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4.3e-98;
Matches 317; Conservative 95; Mismatches 128; Indels 86; Gaps 8;

QY 31 SREHP-----GPALTRRSWYWNQFVIEEYAGPEPVILGKLSHDVDRGEGRT 79
| : : : : :
DB 29 SHLPSFHGHHEKKEGVQLQSKRGWYNQFVIEETGPDVTVGRHSDIDSGGNT 88
QY 80 KYLLTSGAGTVFVIDEATGNIHTKSLDREKAQYVLLAQAVDRASNRPLEPSEFTIK 139
| : : : : :
DB 89 KYILSGEGAGTIFVIDKSGNIIHATKTLIDREEAQYTLMAQAVDRDTRPLEPSEFTIK 148
QY 140 GODINDNPPILPGYHATVPEMSVNGSVIQTVAHADDPSSYNSAKLVYTVVDGPGPF 199
| : : : : :
DB 149 VQDINDNPEPLHEIYHANVPERSNVGTISVQVNASDADDPYNSAKLVYSILEGQYF 208
QY 200 SVDPEGVVTAIPNMDRETOEBPLVVIQAQDMGSHGSLGSTTVTVTLSDVNDNPKF 259
| : : : : :
DB 209 SVEAQGTIIRTAIPNMDSEAKEEYHVVIQAQDMGSHGSLGSTTKVITLTDVANDNPKF 268
QY 260 POSLYQSFVETAGGTIVGRRLADDPDLGNALMAVILIDEGSEAFSTIDQGRGL 319
| : : : : :
DB 269 POSVQWQVSEAAVGEVGRKADPDIGENGALTVAIVDGDLELFTITDYETDQGV 328
QY 320 LTVKPLDPESQSYSPFVEATNTLIDPAYLRGPFKDVASVRAVQDAPPEPAFTQAY 379
| : : : : :
DB 329 VKLKPVPDEFKRAKSLIKIAANVAIDPKFISNGFKQTVVKISVEDADEPMEFLPSY 388
QY 380 HLTVPENKAPGLVQCIADIDSPASPIRYSILPHSPERCFSIQPEEGTIIHTAAFLDR 439
| : : : : :
DB 389 IHEVQENAAAGTVVGRVAKCPDANSPIRYSIDHTLDRFFITNPEDGFIKTKPLDR 448
QY 440 EAAKMHNLTVLATELGWKGPERGVPLVAEMSAAPAPQORVSGAVGIPQDSSAQAS 499
| : : : : :
DB 449 EETAMNLISVFAADI-----HNRHQT 470
QY 500 RVQVAIQTLDENDNAPOLAEPYDTVCDSAP-----GQLIQVIRALDRDEVGNSHVSFQ 555
| : : : : :
DB 500 RVQVAIQTLDENDNAPOLAEPYDTVCDSAP-----GQLIQVIRALDRDEVGNSHVSFQ 555

DB 471 KVPVAILVDVNDNAPKFAAPYEGFICESHPKALSNQPIVTVSADDDOTDANGPRIFIS 530
| : : : : :
QY 556 GP--LGPDAFTVODNRLPA-----WFHPLMASASSWLHMPAERGN 597
| : : : : :
DB 531 LPPEIMHNPFTVADNNDNTAGVYARRGGSFROKQDFLPLIVLSD-----GG 578
QY 598 QPASQKSSSLP--PCG-RUPGALPSC 620
DB 579 PPMSTNTLITIKVCGCDVNGALLSC 604

RESULT 5

D38992
C:Species: Homo sapiens (man)
C/Accession: D38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:L34060; NID:G506411; PIDN:AAA35628.1; PID:G506412
A:Gene: GDB:CDH8
A:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 45.6%; Score 1529.5; DB 2; Length 793;
Best Local Similarity 47.8%; Pred. No. 7.2e-94;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 39 LLETRRSWYWNQFVIEEYAGPEPVILGKLSHDVDRGEGRTKYLTLGEGAGTVFVIDEAT 98
| : : : : :
DB 49 LNSKRGWYWNQFVIEEFSGPEPILVGRHLDLPDGSKKIKYILSGDAGTIFQINDVT 108
QY 99 GNHVTKSLDREKAQYVLLAQAVDRASNRPLEPSEFTIKGODINDNPPILPGYHAT 158
| : : : : :
DB 109 GDHAIKRLDREKAETLTLAQAVDMETSKPLEPSEFTIKQDINDNAPFLNGLYHAT 168
QY 159 VPMSNVGTISVQVTAHADDPSSYNSAKLVYTVVDGLDFEFSVDQTVVTRTAIPNMDRE 218
| : : : : :
DB 169 VPMSILGTISYNTVATDADDPVYNSAKLVYSILEGQYFIEBETALIKTALPNMDRE 228
QY 219 TQEEPLVVIQAQDMGSHGSLGSTTVTVTLSDVNDNPKFPOSIXQSFVETAGGTV 278
| : : : : :
DB 229 AKEEYLVVIQAQDMGSHGSLGSTTLLVTLTDVNDNPKFKQSLHFSVPEDEVLTGI 288
QY 279 GRLLAODPDLGNALMAVILIDEGSEAFSTIDQGRDGLTVKRPDLDPESQSYSPFV 338
| : : : : :
DB 289 GRKANDQDQIGENAAQSYVIDDGTALFEISDAQAQGIIRLRKPLDPFETKSYTLKD 348
QY 339 EANTTILIDPAYLRGPFKDVASVRAVQDAPPEPATQAAHLLTVPENKAPGLVQCI 398
| : : : : :
DB 349 EAAVVAIDIRFSRGPFKQTVKIVVEDADEPVVFSSTYILEVHENALNSVIGQVTA 408
QY 399 ADIDSPASPIRYSILPHSPERCFSIQPEEGTIIHTAAPDREARAHNLTVLATELGW 458
| : : : : :
DB 409 RQDDITSSPIRFSIDHTLERQFINNADGKTLATPLDRLSVWHNTIITLATEL----- 464
QY 459 GPERGVPLVAEMSAAPAPQORVSGAVGIPQDSSAQASQVQVAILQILDENDNAPOLA 518
| : : : : :
DB 465 -----RNHSGISRPVAKIKVLDVNDNAPEDA 490
QY 519 EPYDTVCDSAPAGQLIQVIRALDRDEVGNSHVSFQGLPDP-----ANFTVQDND 571
| : : : : :
DB 491 SEYEAFLCENKRGQVITQVVSAMDKDPKNGH--FLYGLLBEMVNNRPFTIKKEDNLS 548

QY 572 -----LPAWHPLMASASWLMHPPA-----ENQNPASGCKSSSL-PCG-RLPGA 616
 Db 549 SILAKHNGFNROKOEYVLLPITL-----SDSGNPPLSTSTLTTRVCGCNDGV 597
 QY 617 LPSCQ-----LPLGI---PALGIYLC 634
 Db 598 VQSCVNEAYVLPFGISWGLALAILAC 623

RESULT 6

152701
 K-cadherin - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 152701
 R.Xing, Y.Y.; Tanaka, M.; Suzuki, M.; Teraishi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, Cancer Res. 54, 3034-3041, 1994
 A:Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer A:Reference number: 152701; MUID:94243827; PMID:8187093
 A:Accession: 152701
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-789 <RES>
 A:Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435461
 A:Gene: KCAD
 C:Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.0%; Score 1442; DB 2; Length 789;
 Best Local Similarity 43.7%; Pred. No. 4.8e-88;
 Matches 298; Conservative 118; Mismatches 160; Indels 106; Gaps 10;
 7 LLLMLG-----GWGCMRLAAPARAW---AGREHPGALLTRRSWV 48
 Db 8 LLLFWGQPYPTFSPNPLSKRTSGP-----PAKRRLLELSANRNE---LSRSKSWV 57
 QY 49 NQFVIEEYAGPEVLLIGKLSHDVDRGEGRTKYLTEGAGTVFVIDEATGNHTKSLD 108
 Db 58 NQFELIEYGSDDYQYVKLHSDDRGDSLKYLISGDGADLFIINENGDIOATRLDRE 117
 QY 109 REEAQYVLLAQAADRAASNRPLPEPSEFIKGGDINDNPPFLPGYHATVPEMSVGS 168
 Db 118 REEPVYILRAQAINRRTGPRVPESEFIKIHINDNEPIFKVDYATATVPEMAVGTF 177
 QY 169 VIQTADADDPYSYNSAKLYTVTLDELPEFSVDPTQGVRTAI PMNDETQSEFLVVIQ 228
 Db 178 VVQVATDADDPYTGNSAKVYVSILOQPYFVSSESGIITKTLALMDRENREGYVVIQ 237
 QY 229 AKMGGMGLSGSTTVTLSDVNDNPKFPOSIVQFSVETAGTGLVGRRAODPDL 288
 Db 238 AKMGGMGLSGSTTVTLSDVNDNPKFPOSIVQFSVETAGTGLVGRRAODPDL 297
 QY 289 GDNALMAYSLIDGSEAFSISTDLOGRDLITVRKPLDEESQSYSFVEATNTLIDPA 348
 Db 298 GENAEIYSTIDGSHMFDVITDQETQEGIIIVKKLDEPKKRVYTLKVEASNPHEER 357
 QY 349 YLRGPRKDVASRVAVQDAPEPPAFTQAAYHLTVENKAPGTLVQOISADIDSPASFI 408
 Db 358 FLVIGPRKDSATYRIIVDDVDEPPVFSKPAYIIQIREDQINTTISVAADPDAAARNV 417
 QY 409 RYSLIPSDPERCSIOPEEGTHTAAPLDREARAHNLTVLATELGMSGPERGVPL 468
 Db 418 KYSDRHTMDRIFFNIDSGSIFITSKLDRETLNHNITVATEI----- 463
 QY 469 VAEKSAAPAPPPQSPVGSAGVIGIPQDSSAQAQSRVQVAIQTLDENDNAPQALPEYDTFVCS 528
 Db 464 -----NNPKQSSRPVLYIKVLVDVNDNAPFAEFETVCEK 499
 QY 529 AAFGLIQTALDRDBEVGNSHVSFGPLGPDA-----NFTVQDND 571
 Db 500 AKDQIQTALHAVDKDDPYSGHQFSF--LAPPAAGSNFTIIONDKONTAGILTRNGVNR 557

QY 572 ---LPAWHPLMASASWLMHPPA-----ENQNPASGCKSSSL-PCGRLP 614
 Db 558 RHEMSTYLLPVLISND-----YVQSGTGTVTRVACDHHGNQSCHAEBALIHPTGLST 613
 QY 615 GALPSCQLPLGIYALGIYLCAS 636
 Db 614 GALVAILCLCTIVLLTVLVPFA 635

RESULT 7

137016
 cadherin-6 - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C:Accession: 137016
 R.Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitaajima, M.; Hirohashi, S. Cancer Res. 55, 2206-2211, 1995
 A:Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the A:Reference number: 137016; MUID:95262134; PMID:7743525
 A:Accession: 137016
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-790 <RES>
 A:Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185
 A:Gene: GDB:CDH6
 C:Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.0%; Score 1441; DB 2; Length 790;
 Best Local Similarity 43.3%; Pred. No. 5.6e-88;
 Matches 294; Conservative 124; Mismatches 161; Indels 100; Gaps 9;
 7 LLLMLG-----GWGCMRLAAPARAWAGREHPGALLTRRSWVNOF 51
 Db 8 LLLFWGQPYPTLSTPLSKRTSGFPAPKR---ALEISGNSKN--ELNSKSKSWVNOF 60
 QY 52 FVIEEYAGPEVLLIGKLSHDVDRGEGRTKYLTEGAGTVFVIDEATGNHTKSLDRE 111
 Db 61 FLIEEYGSDDYQYVKLHSDDRGDSLKYLISGDGADLFIINENGDIOATRLDRE 120
 QY 112 KAQVYLLAQAADRAASNRPLPEPSEFIKGGDINDNPPFLPGYHATVPEMSVGSVIO 171
 Db 121 KPVYILRAQAINRRTGPRVPESEFIKIHINDNEPIFKVEYATATVPEMSDVGTFVVO 180
 QY 172 VTADADDPYSYNSAKLYTVTLDELPEFSVDPTQGVRTAI PMNDETQSEFLVVIQAKD 231
 Db 181 VTATDADDPYTGNSAKVYVSILOQPYFVSSESGIITKTLALMDRENREGYVVIQAKD 240
 QY 232 MGHNGMGLSGSTTVTLSDVNDNPKFPOSIVQFSVETAGTGLVGRRAODPDLGN 291
 Db 241 MGGGMGLSGSTTVTLSDVNDNPKFPOSIVQFSVETAGTGLVGRRAODPDLGN 300
 QY 292 ALMAYSLIDGSEAFSISTDLOGRDLITVRKPLDEESQSYSFVEATNTLIDPAYLR 351
 Db 301 AEIYSTIDGSHMFDVITDQETQEGIIIVKKLDEPKKRVYTLKVEASNPVEPFLY 360
 QY 352 RGPEDVASRVAVQDAPEPPAFTQAAYHLTVENKAPGTLVQOISADIDSPASPIRYS 411
 Db 361 LGPRKDSATYRIIVDDVDEPPVFSKPAYIIQIREDQINTTISVATQDDAARNPKYS 420
 QY 412 ILHPSDPERCSIOPEEGTHTAAPLDREARAHNLTVLATELGMSGPERGVPLVIAE 471
 Db 421 VDRHTMDRIFFNIDSGSIFITSKLDRETLNHNITVATEI----- 463
 QY 472 WSAAPAPPPQSPVGSAGVIGIPQDSSAQAQSRVQVAIQTLDENDNAPQALPEYDTFVCS 531
 Db 464 -----NNPKQSSRPVLYIKVLVDVNDNAPFAEFETVCEK 502
 QY 532 GGLIQTALDRDBEVGNSHVSFGPLGPDA-----NFTVQDND 571
 Db 503 DQIQTALHAVDKDDPYSGHQFSF--LAPPAAGSNFTIIONDKONTAGILTRNGVNR 560

RESULT 10

150178
cadherin-6B - chicken
C/Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: 150178
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A/Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: 150178; MUID:9530915; PMID:7540531
A/Accession: 150178
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <NA>
A/Cross-references: UNIPROT:Q90762; GB:DA2149; NID:G9867998; PIDN:BA07720.1; PID:G9867998
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 41.7%; Score 1400; DB 2; Length 790;
Best Local Similarity 49.0%; Pred. No. 36-85;
Matches 263; Conservative 109; Mismatches 121; Indels 44; Gaps 3;
QY 39 LTRRRSWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRTKLLTGEAGTVFVIDEAT 98
DB 48 LSRKRSWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRTKLLTGEAGTVFVIDEAT 107
QY 99 GNIVHTSLDREKKAQVLLAQAVDRASNPPLPEPSEFIIKGGDINDNPIPLGPHAT 158
DB 108 GDIQATKLDREKKAQVLLAQAVDRASNPPLPEPSEFIIKGGDINDNPIPLGPHAT 167
QY 159 VPENSVGTSTVLTADADDPSSYGNASAKLVYTVLDGLPFSVPDPTGVVRAIPMDRE 218
DB 168 IPESDVGTSTVLTADADDPSSYGNASAKLVYTVLDGLPFSVPDPTGVVRAIPMDRE 227
QY 219 TQEFVLVIQAKMGGMGLSGSTTVTLSDVNNDPKPKPSIYQSVFVETAGGTLV 278
DB 228 NREQYVLIQAKMGGMGLSGSTTVTLSDVNNDPKPKPSIYQSVFVETAGGTLV 287
QY 279 GRLEAOPDLDGNALMAYSILDEGESEAFSISTDLQGRDGLTVRKPLDFESORSYSPV 338
DB 288 GRLEAOPDLDGNALMAYSILDEGESEAFSISTDLQGRDGLTVRKPLDFESORSYSPV 347
QY 339 EATVTLDPATVLRGPKDVASVAVQADAPPEPAFQAAYHLTVENKAPGLVQIQA 398
DB 348 EATVTLDPATVLRGPKDVASVAVQADAPPEPAFQAAYHLTVENKAPGLVQIQA 407
QY 399 ADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAPLDREARAHNLTVLATELGMSW 458
DB 408 QDPRAKNPVKYSVDRHTDMRVNINSNGSIFTSKTLDRFTLLMNTVIAAEI----- 463
QY 459 GPERGWVPLVAEWSAPAPQPSVGSVAVGIPQSSAQASRVQVAIQTLDENNAPOLA 518
DB 464 -----NNPKQSSRVPEFIKVLVDVNDNAPEFA 489
QY 519 EPYDFVCSAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDNND 571
DB 490 MFYDFVCSAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDNND 544

RESULT 11

151638
F-cadherin - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 151638; S55391
R:Espebeth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A/Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A/Reference number: 151638; MUID:9603953; PMID:7496627
A/Accession: 151638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-790 <ESP>

A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:G854634; PIDN:CAA59679.1; PID:G854634
C/Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 41.4%; Score 1389.5; DB 2; Length 790;
Best Local Similarity 45.9%; Pred. No. 1-58-84;
Matches 282; Conservative 107; Mismatches 164; Indels 61; Gaps 9;
QY 41 RTRRSWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRTKLLTGEAGTVFVIDEATGN 100
DB 49 RTRRSWNNQFVIEEYVAGPEPVLLIGKLSVDVDRGEGRTKLLTGEAGTVFVIDEATGN 108
QY 101 IHVHTSLDREKKAQVLLAQAVDRASNPPLPEPSEFIIKGGDINDNPIPLGPHATVP 160
DB 109 IHVHTSLDREKKAQVLLAQAVDRASNPPLPEPSEFIIKGGDINDNPIPLGPHATVP 168
QY 161 EMSNVGTSTVLTADADDPSSYGNASAKLVYTVLDGLPFSVPDPTGVVRAIPMDRETO 220
DB 169 EMSNVGTSTVLTADADDPSSYGNASAKLVYTVLDGLPFSVPDPTGVVRAIPMDRETO 228
QY 221 EEFVLVIQAKMGGMGLSGSTTVTLSDVNNDPKPKPSIYQSVFVETAGGTLVGR 280
DB 229 EEFVLVIQAKMGGMGLSGSTTVTLSDVNNDPKPKPSIYQSVFVETAGGTLVGR 288
QY 281 LRAOPDLDGNALMAYSILDEGESEAFSISTDLQGRDGLTVRKPLDFESORSYSPV 340
DB 289 LRAOPDLDGNALMAYSILDEGESEAFSISTDLQGRDGLTVRKPLDFESORSYSPV 348
QY 341 TNLTLDPATVLRGPKDVASVAVQADAPPEPAFQAAYHLTVENKAPGLVQIQAAD 400
DB 349 TNLTLDPATVLRGPKDVASVAVQADAPPEPAFQAAYHLTVENKAPGLVQIQAAD 408
QY 401 LDSPASPIRYSILPHSDPERCFSIQPEEGTHTAPLDREARAHNLTVLATELGMSW 460
DB 409 LDSPASPIRYSILPHSDPERCFSIQPEEGTHTAPLDREARAHNLTVLATELGMSW 468
QY 461 ERGWVPLVAEWSAPAPQPSVGSVAVGIPQSSAQASRVQVAIQTLDENNAPOLA 520
DB 463 -----NNPKQSSRVPEFIKVLVDVNDNAPEFA 490
QY 521 YDFVCSAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDNNDPAMF 576
DB 523 YDFVCSAAPGQLIOVIRALDRDEVGNSHVSFGGLGPA-----NFTVQDNNDPAMF 548
QY 577 --HPLMASASMLWLP--PAERGNOPASGKSSS--PCGRPLPALPSCQ-----LP 623
DB 549 LTRRGFKQSQSTFVYPLILSDGNPNRLSTGTTLTQVCSGDK-DGDIWSCNAEPYTL 607
QY 624 LGI---PALGIVLC 634
DB 608 ISLSRGALITLTC 621

RESULT 12

159372
cadherin 12 - human
N/Alternate names: Br-cadherin
C/Species: Homo sapiens (man)
C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C/Accession: 159372
R:Seilig, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.N.
Proc. Natl. Acad. Sci. U.S.A. 92, 3707-3706, 1995
A/Title: Expressed cadherin pseudogenes are localized to the critical region of the spli
A/Reference number: 159372; MUID:9524954; PMID:7731968
A/Accession: 159372
A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A/Molecule type: mRNA
A/Cross-references: UNIPROT:P55289; GB:L33477; NID:G793942; PIDN:AA848539.1; PID:G793942
A/Genes: GDB:CDH12
A/Cross-references: GDB:596324

A:Map position: 5p13-5p14
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:57-160/Domain: cadherin repeat homology <CR1>
F:163-269/Domain: cadherin repeat homology <CR2>
F:272-384/Domain: cadherin repeat homology <CR3>
F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <INT>

Query Match 44.8%; Score 1368.5; DB 2; Length 794;
Best Local Similarity 44.4%; Pred. No. 3.8e-83;
Matches 282; Conservative 114; Mismatches 154; Indels 65; Gaps 11;

30 GSREHPGALLTRRSVMNQFVIEYAGEPVLICKLHSDVDGSGRTKYLITGEAG 89
44 GQRSH---FORVKKRWVMNQFVIEYMGSEPPQYVKLSHSDLDKGGTAVYLSGDAG 99
90 TVFYDEATGNHTKSLDREKAQVYLAAVDRASNPPEPSEFIIKGQDINDNPI 149
100 TVFTIDETGDIHAIKSLDREKPPYTLRAQAVIEIRKPLEPSEFIIKQDINDNEPK 159
150 FPLGPRHATVEMSNVGTSLQVTAHDADPSYGNKAKLYTVLDELPPFSDPQTVR 209
160 FLDDGYATVPEMSPVGAIVYQVAKADADPTNGSARVYSILQGGPYFSDPKTVIR 219
210 TATNMDRETOEFLVLAQADNGHNGLSGTTVTYLSDVNDNPPKPOSIXQSYV 269
220 TALNMDREVEKQVQLQADMGQGGAGTIVITLTDVNDNPPREPKSIFHLKVP 279
270 ETAGGTGVRGLRAQDPGLGNALMAYSILDEGSEAFSISTDQGRDGLTVKRPDPE 329
280 ESSPGSAIGIRAVDPFGQNAIEKNTVPGDGNLFIDTDDEGVIKLKKPDPFE 339
330 SQRSYSPFEATNTLIDPAYLRGPPQVASVRAVQADAPPAPTAAYHLTVPENKAP 389
340 TKKAYTFKVDASNHLDRFHSAGPFKDTATKISLVDVBPFFSKPLTMEYEDTPV 399
390 GTUAGQSAADLSPASIRYSILPHSDPERCFISQPEEGTTHAAPLDEPARAHNLT 449
400 GTTGAVTAQDLDDGSSAVRYFLDKSDGDSYFTIDNGEITANELLIDREKTAQVPSI 459
450 LATELGMSWGPGRGVPLLVAEWSAPAPQPSVPSVAGVIGPOSSAQSARVQVATLD 509
460 IASKVS-----NPL-----TSKVNILINVL 481
510 ENDNAPQALAEPYDFVCSAAPQGLQVIRALDRDEVGNSSHVSFOGRLGPD-----NFT 565
482 VNEPPEISVPEYTAVCENAKPGQITQVSAADRLSPAGQGSFR--LSSEALIKRNPFT 539
566 VQNRNDLPA-----WFHPLIMASASWLMHPAERGNQAPSOQSSSLP 609
540 VRDFPNNTAGIETRANGYSRQQLYFLPVVIEDSSY-----PYQ-----SSNTMTIR 588
610 CGRL--PGALPSCQ-----LPLGTPA---LGIIVLC 634
589 VCRCDSDGTLISCNVEAIFLPVGLSTGALIALILLC 623

RESULT 13
13THUC5
cadherin 5 precursor - human
N:Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: S49893; S24305; A43418
R:Brevario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A:Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov
A:Reference number: S49893
A:Accession: S49893
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-784

A:Cross-references: UNIPROT:P3151; EMBL:X79981; NID:G559833; PIDN:CAA6306.1; PID:G5599
R:Guzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: S24305
A:Molecule type: mRNA
A:Residues: 5-516, '1', 518-784 <SUZ>
A:Cross-references: EMBL:X59796; NID:G639976; PIDN:CAA42468.1; PID:G29593
R:Lampugnani, M.G.; Resnati, M.; Ralteri, M.; Pigott, R.; Piscane, A.; Hosen, G.; Ruco
J. Cell Biol. 118, 1511-1522, 1992
A:Title: A novel endothelial-specific membrane protein is a marker of cell-cell contact:
A:Reference number: A43418; MUID:92394977; PMID:1522121
A:Accession: A43418
A:Molecule type: protein
A:Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254.
A:Note: sequence extracted from NCBI backbone (NCBI:P113040, NCBI:P113045, NCBI:P113047
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
C:Genetics: GDB:CDHS
A:Gene: GDB:CDHS
A:Cross-references: GDB:134230; OMIM:601120
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pr
F:1-25/Domain: signal sequence #status predicted <PRO>
F:26-47/Domain: propeptide #status predicted <PRO>
F:48-784/Product: cadherin 5 #status predicted <XMT>
F:48-593/Domain: extracellular #status predicted <EXT>
F:50-151/Domain: cadherin repeat homology <CR1>
F:154-258/Domain: cadherin repeat homology <CR2>
F:261-372/Domain: cadherin repeat homology <CR3>
F:375-479/Domain: cadherin repeat homology <CR4>
F:481-587/Domain: cadherin repeat homology <CR5>
F:591-620/Domain: transmembrane #status predicted <TM>
F:621-784/Domain: intracellular #status predicted <INT>
F:735-753/Region: serine-rich
F:61,112,157,362,442,523,535/Binding site: carboxylate (Asn) (covalent) #status predic

Query Match 28.0%; Score 940.5; DB 1; Length 784;
Best Local Similarity 39.5%; Pred. No. 1.1e-54;
Matches 227; Conservative 85; Mismatches 208; Indels 55; Gaps 12;

6 RLILAWLQGWGCGRLAPAPARAGSRHPPG-----FALLRTRRSVMNQFVIEBY 57
3 RLMLLATSGACIGLLAAVAAGA--NPAQRDTHSLPFRROKRDWINQMIDEK 60
58 ACEPPLIKGLSDVDGRGRTKYLITGSGACTVPIVDATGNHTKSLDREKAQVYL 117
61 NTSLPFHVKIKISSVR--KNAKYLLKGYVAKVRVDAETDVAIERLDENISEYHL 118
118 LAQAVDRASNPPEPSEFIIKGQDINDNPIFPICPYATVPEMNVGTSYQVTAHDA 177
119 TAYIVKQDGENLETSSFTIKHYVNDWPEFTHRLFNASVPSSAVGTSVISTAVADA 178
178 DDESYNKAQVYTVLDELPPFSDPQTVGVRVTAIPNMDRETOEFLVLAQADNGHNG 237
179 DDETVGDHASVMWQILKGEYFAID--NSGRITITIKSLDREKQARVEIVEARDAQG--LR 236
238 GLSGSTTVVTLSDVNDNPPKPOSIXQSYVETAGPGLVRLRAQDPDLGNALMAYS 297
237 GDSGLTAVTLTDINDNPPFTQIKYTVVPEDRVGVSGSLFPEDDDEQNRTKTS 296
298 ILDEGSEAFSISTDQGRDGLTVKRPDPESSQRSYSPFEATNTLIDPAYLRGPPFD 357
297 ILRGVQDAFTLETNANHEGIIKPKPLDYETIQQYSFIVEATPTIDLRVM--SPPAQN 355
358 VASVRVAQDAPPAPFTAAYHLTVPEN--KAPGLTVGQISAADSDPASPIRYSTLPS 416
356 RAQVITITVDDEPPLFQGPFFHFLKENQKP--LIGIVLAMPDPAAHSIGISIRRS 413

Qy 417 DPEECFSIQEEGTHTAAPLDRBARAHNLVLTATELGMSWGPBERGWLVAEMGAPA 476
Db 414 DKQGFPRV-TKKGITYNEKELDRREYEMNLTVAEKL-----450
Qy 477 APQPSVSAVGIPIQDSSAQSVOVAIQTLDDNDNAPQIAEYDTFVCDSPAAGQLIQ 536
Db 451 -----DSTGTP---TGKESIYQVHIEVLDDNDNAPFAKPYQKVCENAVHGLVL 498
Qy 537 VIRALDREVNSSHSVFCGLGPDANFTVQDND 571
Db 499 QISAIKDI--TPRWKFKFTLTNTENNFTLTNDH 531

RESULT 14

ICRHR
R-cadherin precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: J0424
R:Inuzuka, H.; Miyatani, S.; Takeichi, M.
Neuron 7, 69-79, 1991
A:Title: R-cadherin: a novel G22-dependent cell-cell adhesion molecule expressed in the
A:Reference number: J0424; MUID:91299341; PMID:1172604
A:Accession: J0424
A:Molecule type: mRNA
A:Residues: 1-913 <INU>
A:Cross-references: UNIPROT:P24503; GB:D14459; GB:D00849; NID:G222854; PIDN:BA03356.1;
A:Experimental source: retina
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; retina; transmem
F:127-166/Domain: signal sequence #status predicted <PRO>
F:167-913/Product: R-cadherin #status predicted <EXT>
F:167-913/Domain: extracellular #status predicted <EXT>
F:169-274/Domain: cadherin repeat homology <CR1>
F:244-249/Region: cadherin binding #status predicted
F:227-389/Domain: cadherin repeat homology <CR2>
F:392-504/Domain: cadherin repeat homology <CR3>
F:507-612/Domain: cadherin repeat homology <CR4>
F:613-721/Domain: cadherin repeat homology <CR5>
F:722-753/Domain: transmembrane #status predicted <TM>
F:754-913/Domain: intracellular #status predicted <INT>
F:870-885/Region: serine-rich
F:280,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 18.0%; Score 604; DB 1; Length 913;
Matches 195; Conservative 82; Mismatches 236; Indels 102; Gaps 23;

Qy 4 LVRLILAM-----IGGNGCM-----GRLAAP-----RAMGSR 32
Db 97 LILVLTAMDPTLGRMWAIVRFVGEKLQNGHKPKGRKSGPVDLAQOQSDTLPP--R 153
Qy 33 EH-EGPALLTRRSWMNQFFVIEYAGPEPVLIGKLSVDVDRGRTKYLITGEAG-- 89
Db 154 QHQAKGLRQGRKRWVPIPIVNPENSRGPPQQLVIRISKDK-EHIRYSITGVADDP 212
Qy 90 --TFVVIDEATGNIHVTKSLDREKAQYVLLAQAVDRASRPLPEPSEFIKQDINDP 147
Db 213 PMEFSDIPVSGRMVYVIRPMDREBRASVYLRARAVMNGRK-YENIDYIYVIDNDR 271
Qy 148 PIFPLGYHATVPMSVNGTSVICTPAHDADPSYGSALVTVVIGDP-----FFSV 201
Db 272 PEFINQVYNSVDEGSRGTYVTVIRANDADSTIAN-GVRRIRITYOTPOPSQMMFTI 330
Qy 202 DPQIGVVRPAIPNNDRTOEPLVLTIOAKMGHMG-GLSGSTTVTLSDVNDNPKFP 260
Db 331 NSEIGDITVAAGIDREKVOQYVIVQATMEGNLNGLSNTATAIITVDVNDNPEPT 390
Qy 261 QSLVQFVETAGGTIGRLRAQDPL--GDNALMAVSTLDEGESEASISIDQGRG 318
Db 391 TSTYSGVEPNR-VEVVVNLVTMDRDQPHSPYNNAIYRISGDSGHFTIRIDPVTEG 449

Qy 319 LITVKKPDLFESQRYSFVEATNTLIDPAVLRG---PFQDVASVYAVODAEPPAPT 375
Db 450 WTVVRAVDYENKRAFMLTWVSN---QALASGIONSFQSTAGVTISTVDVNEAPFP 505
Qy 376 QAAVHLTPENKAPFTLVGOISAADLDS-PASPIRYSILPSPDERCFSIQEEGTHTA 434
Db 506 TMHKLIRIEGVPSTVLTFSADVDPDFMQQAVRYSKL--SDPANMINIANTQILTA 563
Qy 435 APIDREARAHNLVLTATELGMSWGPBERGWLVAEMGAPAPQPSVSAVGIQDSS 494
Db 564 AVLDRESDYIKNNVYEA-----FLAANDGIPPA-----SGTGLQ-- 599
Qy 495 SAQASRGVVAIQTLDDNDNAPQIAEYDTFVCDSPAAGQLIQVIRALDREVNSSHSV 554
Db 600 -----IYLIDINDNABELL-PKNAQICER--PUNLVNITTAADADIDPVGPFV 646
Qy 555 QGPLGPD--NFTV 566
Db 647 ELPSVPSAVRKWMTI 661

RESULT 15

ICRSCN
N-cadherin precursor, neuronal - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A32759; A46163
R:Miyatani, S.; Shimamura, K.; Hatta, M.; Nagafuchi, A.; Nose, A.; Matsumaga, M.; Hatta,
Science 245, 631-635, 1999
A:Title: Neural cadherin: role in selective cell-cell adhesion.
A:Reference number: A32759; MUID:89346748; PMID:2762814
A:Accession: A32759
A:Molecule type: mRNA
A:Residues: 1-906 <MT>
A:Cross-references: UNIPROT:P15116; GB:M31131; NID:G192327; PIDN:AA37353.1; PID:G309122
R:Miyatani, S.; Copeland, N.G.; Gilbert, D.U.; Jenkins, N.A.; Takeichi, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 8443-8447, 1992
A:Title: Genomic structure and chromosomal mapping of the mouse N-cadherin gene.
A:Reference number: A46163; MUID:92409532; PMID:11528849
A:Accession: A46163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 839-906 <MT>
A:Cross-references: GB:S45011; NID:G256010; PIDN:AA823356.1; PID:G256011
A:Note: sequence extracted from NCBI backbone (NCBI:113759, NCBI:113760)
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F:127-166/Domain: signal sequence #status predicted <PRO>
F:169-274/Domain: cadherin repeat homology <CR1>
F:227-389/Domain: cadherin repeat homology <CR2>
F:392-504/Domain: cadherin repeat homology <CR3>
F:507-612/Domain: cadherin repeat homology <CR4>
F:613-721/Domain: cadherin repeat homology <CR5>
F:722-753/Domain: transmembrane #status predicted <TM>
F:754-913/Domain: intracellular #status predicted <INT>
F:870-885/Region: serine-rich
F:280,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 17.9%; Score 601; DB 1; Length 906;
Matches 190; Conservative 76; Mismatches 214; Indels 80; Gaps 21;

Qy 33 EHPGALLTRRSWMNQFFVIEYAGPEPVLIGKLSVDVDRGRTKYLITGEAGT-- 90
Db 149 KHSG-ALQGRKRWVPIPIVNPENSRGPPQQLVIRISDKNLS-LRYSVTGGAGQPP 206
Qy 91 --VFVIDEATGNIHVTKSLDREKAQYVLLAQAVDRASRPLPEPSEFIKQDINDP 148

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 254.926 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-4

Perfect score: 3354
Sequence: 1 MWGLVRLLLAMLGWGMGR.....LPSCQLPLGIPALGIVLCAS 636

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2992.5	89.2	819 1 CADO_HUMAN	Q86UPO homo sapien
2	2606	77.7	781 2 G6PFK6	Q6PFK6 mus musculu
3	2606	77.7	781 2 AAH57373	AAH57373 mus muscu
4	2386	71.1	493 2 Q96L07	Q96L07 homo sapien
5	1602	47.8	796 1 CADB_HUMAN	P55287 homo sapien
6	1601	47.7	796 1 Q96C29	Q96C29 homo sapien
7	1596	47.6	796 1 CADB_MOUSE	P55288 mus musculu
8	1595.5	47.6	796 2 Q8C706	Q8C706 mus musculu
9	1587.5	47.2	794 2 Q93264	Q93264 xenopus lae
10	1558	46.5	792 1 CADB_CHICK	Q93319 gallus gall
11	1536.5	45.8	716 2 Q8C449	Q8C449 mus musculu
12	1536.5	45.8	716 2 AAH57581	AAH57581 mus muscu
13	1536.5	45.8	799 1 CADB_HUMAN	P55286 homo sapien
14	1533.5	45.7	754 1 Q8BRK4	Q8BRK4 mus musculu
15	1530.5	45.6	799 1 CADB_RAT	Q54800 rattus norv
16	1528.5	45.6	799 1 CADB_MOUSE	P55289 mus musculu
17	1526.5	45.5	716 2 Q8C375	Q8C375 mus musculu
18	1486.5	43.3	370 2 Q86T00	Q86T00 homo sapien
19	1448.5	43.2	788 1 CADA_HUMAN	Q9Y68C homo sapien
20	1448	43.0	801 1 CADA_HUMAN	Q9Y68C homo sapien
21	1442.5	43.0	789 1 CADA_CHICK	P79995 gallus gall
22	1442	43.0	789 1 CADA_RAT	P55280 rattus norv
23	1441	43.0	790 1 CADA_HUMAN	P55285 homo sapien
24	1438.5	42.9	788 2 Q8Y168	Q8Y168 mus musculu
25	1437.5	42.9	788 2 Q8Y168	Q8Y168 mus musculu
26	1437.5	42.9	788 2 AAH62362	AAH62362 mus muscu
27	1432.5	42.7	785 1 CADD7_CHICK	Q90763 gallus gall
28	1428.5	42.6	801 2 Q920M3	Q920M3 mus musculu
29	1426.5	42.5	798 2 Q7ZYV7	Q7ZYV7 gallus gall
30	1426.5	42.5	798 2 Q80GH3	Q80GH3 gallus gall
31	1424	42.5	551 2 Q8AKW2	Q8AKW2 gallus gall

32	1420	42.3	789 1 CADD9_HUMAN	Q9A1B4 homo sapien
33	1415.5	42.2	785 1 CADD7_HUMAN	Q9A1B5 homo sapien
34	1413	42.1	790 1 CADD6_MOUSE	P97326 mus musculu
35	1412.5	42.1	790 1 CADD1_HUMAN	Q13634 homo sapien
36	1412	42.1	630 2 Q8Y178	Q8Y178 homo sapien
37	1408	42.0	785 2 Q8BM92	Q8BM92 mus musculu
38	1400	41.7	790 1 CADD6_CHICK	Q90762 gallus gall
39	1395.5	41.6	790 2 Q8N522	Q8N522 homo sapien
40	1389.5	41.4	790 2 Q91838	Q91838 xenopus lae
41	1372.5	40.9	508 2 Q6PAN4	Q6PAN4 mus musculu
42	1372.5	40.9	508 2 AAH60200	AAH60200 mus muscu
43	1372.5	40.9	794 2 Q86UD2	Q86UD2 homo sapien
44	1368.5	40.8	794 2 CADD_C_HUMAN	P55289 homo sapien
45	1347	40.2	813 1 CADD_MOUSE	Q9WCPS mus musculu

ALIGNMENTS

RESULT 1
CADO_HUMAN STANDARD: PRT; 819 AA.
ID Q86UPO; Q86UPL; Q9NT84;
AC Q86UPO; Q86UPL; Q9NT84; (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-UTL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (NM02834/PRO34009).
GN Name=CDH24; Synonyms=CDH11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP CATEININS.
RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA Katsifas B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
RT II cadherin.";
RL J. Biol. Chem. 278:27513-27519(2003).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bruch J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Barton D., Foster J., Grimaldi C., Gu O., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yanura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Testis;
RA Blum H., Bauerbach S., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. Cadherin-24 mediate strong
CC cell-cell adhesion.
CC - SUBUNIT: Associates with alpha-, beta- and delta-catenins.
CC - SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Long form;
CC Isoid=Q86UPO-1; Sequence=Displayed;
CC Name=2; Synonyms=Short form;

Db	161	SYGNASAKLVTYVLDGLPFPSVDPTQGVKRTAIPNMDEDETOEELVYIQAKDMGSHMGSL	240
Qy	241	GSTVTVTTVLTSDVNDNPKPKFQSLYQFSVETAGGTLVGRLRADPDLGNALMAYSILD	300
Db	241	GSTVTVTTVLTSDVNDNPKPKFQSLYQFSVETAGGTLVGRLRADPDLGNALMAYSILD	300
Qy	301	GGSGAFSISDTDLGGPGLTVRXPDLPEESORSRSPFEVATNTLIDPAYIRGPFKQVAS	360
Db	301	GGSGAFSISDTDLGGPGLTVRXPDLPEESORSRSPFEVATNTLIDPAYIRGPFKQVAS	360
Qy	361	VRAVODAPBPDPATQAAVHLTVENKAPAGTLVQOISAAIDLDPSPSIRYSILPHSDPER	420
Db	361	VRAVODAPBPDPATQAAVHLTVENKAPAGTLVQOISAAIDLDPSPSIRYSILPHSDPER	420
Qy	421	CFSTQPEEGTHTTAAPLDREKRAHNTLVATELGMSWGEBRGVPLLVAMWSAPAPQ	480
Db	421	CFSTQPEEGTHTTAAPLDREKRAHNTLVATELGMSWGEBRGVPLLVAMWSAPAPQ	480
Qy	481	RSPGSAVGLPQDSSAQSRYQVAIQTLDENDNAPQLAEYDFVFCSPAIPGOLIQYRA	540
Db	481	RSPGSAVGLPQDSSAQSRYQVAIQTLDENDNAPQLAEYDFVFCSPAIPGOLIQYRA	540
Qy	541	LDREVEGNSHVSQGLGPDANTTVODNRD-----LPA-----WF 576	
Db	541	LDREVEGNSHVSQGLGPDANTTVODNRDGSASLLPBRPAPPRHAPYLVEIEMDWG 600	
Qy	577	HPLMASASSWLH-----WPPAERGQAPSOG 603	
Db	601	QPALSTATVTVSVCRQCPDGSVASCPHEHLSAAGSTG 640	

RESULT 2

CEPFx6 ID Q6PFx6 PRELIMINARY; PRT; 781 AA.

AC Q6PFx6

DT 05-JUL-2004 (TREMBlrel_27, Created)

DT 05-JUL-2004 (TREMBlrel_27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel_27, Last annotation update)

DE Cadeherin-like 24.

GN Name=Cdh24;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stadleron M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange S., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J., Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.R., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzyzanski M.I., Skalska U., Smalusz D.E., Schmech A., Schein J.E., Jones S.U., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6; TISSUE=Brain;

RA Strausberg R.;

Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: BC057373; AAH57373.1; -
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00028; Cadherin_C; 5
DR Pfam: PF01049; Cadherin_C; 1
DR PRINTS: PRO0205; CADHERIN.
DR SMART: SM00112; CA; 4.
DR PROSITE: PS00232; CADHERIN_1; 2.
DR PROSITE: PS50268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 781 AA; 84104 MW; 1599606E6C985AA CRC64;

Query Match	77.7%;	Score 2606;	DB 2;	Length 781;
Best Local Similarity	79.1%;	Pred. No. 1.3e-153;		
Matches 518;	Conservative 24;	Mismatches 47;	Indels 66;	Gaps 7;

Qy	1	MMGLVRLILAMJGCMGCMGRLLAAPRAAAGSEHEHGPALLRRRSMWNQFVIEEYAGP	60
Db	1	MMGLVRLILAMJGCMGCMGRLLAAPRAAAGSRGHSGPTLLRRRSMWNQFVIEEYSGP	60
Qy	61	EPVLIGKHSVDVREEGRTKYLITBEGAGTVIVIDEATGNHVTSSLDREEAQVYLLAQ	120
Db	61	EPVLIGKHSVDVREEGRTKYLITBEGAGTVIVIDEATGNHVTSSLDREEAQVYLLAQ	120
Qy	121	AVDRASNPRLPEPSEFIIKQGDINNPRIFFPLGPHATVPENSNVGTSVLYQTAHADDP	180
Db	121	AVDRASNPRLPEPSEFIIKQGDINNPRIFFPLGPHATVPENSNVGTSTVLYTAHADDP	180
Qy	181	SYGNSAKIYTVYLDGLPEFSVDPOGVVATAPMMDREQEEELVIAQKMGHMGGS	240
Db	181	SYGNSAKIYTVYLDGLPEFSVDPOGVVATAPMMDREQEEELVIAQKMGHMGGS	240
Qy	241	GSTIVTVLSDVNDNPKEPFGSLYQFSVETAGPGLTVGLRLAOPDLDGNALMAYSILD	300
Db	241	GSTIVTVLSDVNDNPKEPFGSLYQFSVETAGPGLTVGLRLAOPDLDGNALMAYSILN	300
Qy	301	GECSAPFSISTDQGRDGLTVRKPLDPEFSQSSYSRRVATNTLLDPALRRGPFDVVS	360
Db	301	GECSAPFSISTDQGRDGLTVRKPLDPEFSQSSYSRRVATNTLLDPALRRGPFDVVS	360
Qy	361	VRAVQDAPEPPAFTOAAVHTLVENKAGTLVGQISAADLDSAPSPIRYSILPHSDPER	420
Db	361	VRAVQDAPEPPAFTOATHLAVPENKAPGLTVGQISAADLDSAPSPIRYSILPHSDPER	420
Qy	421	CFSIPOEECTHTAAPLDREARFAMNHLVYATLETGSMGSPERGWBLVAEWSAPAPAQ	480
Db	421	CFSIPEPBOTITATVRLDREARVMMHLLTILABEL	454
Qy	481	RSPVSGAVGIPODSSHQASRVQVAYIOTLDENDNAPOLAEPPYDTFVCDSSAAPQOLIOVIRA	540
Db	485	-----DSSHQASRVQVAYIOTLDENDNAPOLAEPPYDIFVCDSSAAPQOLKVIRA	502
Qy	541	LDRDEVGNSSHVSFOCPGLPDANFTVQDNKRDLPAMHPPLMASASSGMLHMPAER----	595
Db	503	LDRDEVGNSSQVSLGCPGVDPANFTVRDNRDGS-----SLILPSRA-----PPQAPVILP	555
Qy	556	-----GNQPASQKSS-----SLPCGRLPGALPBCQ-PLGIRA-----LGIVLC	634
Db	556	IELMDWGALSTATVTVSVCRCRPDGSMASCPAQSLPTGLSGALLAIVTC	610

RESULT 3		
AAH57373	PRELIMINARY;	PRT; 781 AA.
ID AAH57373		
AC AAH57373;		
DT 02-VAR-2004 (TREMblrel. 27, Created)		
DT 02-VAR-2004 (TREMblrel. 27, Last sequence update)		
DT 02-VAR-2004 (TREMblrel. 27, Last annotation update)		
DE Caderin-like 24.		

CN Mus musculus (Mouse) .
 OS Mus musculus (Mouse) .
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RN
 RP
 RE
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Palmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tothylki S., Cannini P., Prange C.,
 RA Rana S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.U., McKernan K.J., Malek J.A., Gamarate P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.U., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
 [2]
 RN
 RP
 RE
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strauberg R.L.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057373; AAHS7373.1; -
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;
 Query Match 77.7%; Score 2606; DB 2; Length 781;
 Best Local Similarity 79.1%; Pred. No. 1.3e-153;
 Matches 518; Conservative 24; Mismatches 47; Indels 66; Gaps 7
 QY 1 MWGIVRLLATLGGWCGMCGRGLAARAAAGSRHHGPTLLPRRRWYNNQPFVIEYAGP 60
 Db 1 MWGIVRLLATLGGWCGMCGRGLAARAAAGSRHHGPTLLPRRRWYNNQPFVIEYAGP 60

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Db      61  EPVLIGKHSVDNDSRGRTKXLLTGEGAGTVFVIDEATGNHVTKSLDREERAOYVLLAAQ  120
QY      121  AVDRASNPLEPPPSFFITKGODINDNPILFPLGPHALVVPKSNSTGYIQTATHADDP  180
Db      121  AVDRASNPLEPPPSFFITKGODINDNPVFPFGPHAVVPKSNSTGYIQTATHADDP  180
QY      161  SYGNASAKIVTYVLDLPFFSVDPQCTGVVRIAPNNDRRETOEBFLVVIQAKDMGHHGGLS  240
Db      161  SYGNASAKIVTYVLDLPFFSVDPQCTGVVRIAPNNDRRETOEBFLVVIQAKDMGHHGGLS  240
QY      241  GSTTYVTVLSDVNDNPKFPOSLOVSVETAGPGLTVGLRLAOPDPJDGNLMAYSITLD  300
Db      241  GSTTYVTVLSDVNDNPKFPOSLOVSVETAGPGLTVGLRLAOPDPJDGNLMAYSITLD  300
QY      301  GEGSRAFSISDLDGRDGLTVRKRLDPESSORSYSFRVEATNTLLDPAYLRGPFCDVAS  360
Db      301  GEGSRAFSISDLDGRDGLTVRKRLDPESSORSYSFRVEATNTLLDPAYLRGPFCDVAS  360
QY      361  VRVAVQDAPEBPAPFTQAAVHTLVPENKAPGLTVGGISADLSDSPASPIRYSILPHSDPER  420
Db      361  VRVAVQDAPEBPAPFTQAAVHTLVPENKAPGLTVGGISADLSDSPASPIRYSILPHSDPER  420
QY      421  CFSIQPEBSGTHITAPLDRERAGAHNNLVLTATELMSWGPBERGWVPLVAEMKSAAPAPQ  480
Db      421  CFSIQPEBSGTHITAPLDRERAGAHNNLVLTATELMSWGPBERGWVPLVAEMKSAAPAPQ  480

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QY 481 RSPGASGVIGIPQDSSAQAARVOYA IOTLDENDNA POLAEPYDPTVCDSAPGOLIOYIRA 540
Db 455 -----DSSAGSSRVQVAIQTLDENDNA PQLAEPDIFVCSPAAPGOLIKYIRA 502
QY 541 LDRDEVGNSSHSVSPQGLPGDPANFTVQDNRLPAMFPLIMASASSWIMHPER----- 595
Db 503 LDRDEVGNSSQVSLQGPVGPDPANFTVRDNRGSA---SLLPSPRA---PPQAPYLP 555
QY 596 -----GNQPAQSGSS-----SLPGRLPGLPSCQL-PLGIPA---LGYVC 634
Db 556 IELMDWGPALSTATVTVSVCRGCRPDGSMASCMPEAQLSPSTGLTGALLAIVTC 610

RESULT 4
Q96LQ7 PRELIMINARY; PRT; 493 AA.
ID Q96LQ7
AC Q96LQ7;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Nimomaya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanahara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 cadherin domains.
DR EMBL; AK057922; BAB1613.1; -.
DR HSSP; P12830; 1065.
DR Genew; HGNC:14265; CDH24.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR001216; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS0268; CADHERIN_2; 4.
DR KEGG; K04461; Calcium-binding.
KW Calcium-binding.
SQ
SEQUENCE 493 AA; 53618 MW; 33F10DF3AF09C1E CRC64;

Query Match 71.1%; Score 2386; DB 2; Length 493;
Best Local Similarity 93.5%; Pred. No. 3.3e-140;
Matches 462; Conservative 2; Mismatches 8; Indels 22; Gaps 2;

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Db 241 GSTTAVTSLDVNDNPPKPFQSLYQFSVETAGPGLVGRLRADDPDLGNALMAYSLD 300
QY 301 GEGSAFISITDLQGRDGLTVRKPLDESGRSYSFVREANTNLIIDPAYLRGPFKVAS 360
Db 301 GEGSAFISITDLQGRDGLTVRKPLDESGRSYSFVREANTNLIIDPAYLRGPFKVAS 360
QY 361 VRAVQDAPPEPAPFOAAYHLTVPENKAPGLVQGISADUDSPASPRISILHSPER 420
Db 361 VRAVQDAPPEPAPFOAAYHLTVPENKAPGLVQGISADUDSPASPRISILHSPER 420
QY 421 CESIQPEGTHTAFLDREARAHNLTVALTELQ-----NSWGPER 462
Db 421 CESIQPEGTHTAFLDREARAHNLTVALTELQ-----NSWGPER 462
QY 463 GWVPLVAMNSAPA 476
Db 477 GWRVLTALAPSPA 490

RESULT 5
CADB HUMAN STANDARD; PRT; 796 AA.
ID CADB HUMAN
AC P55287; Q15065; Q15066; Q9U093; Q9U094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (osteoblast-cadherin) (OB-cadherin) (OSF-4).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Taniguchi H., Sano K., Helmer R.L., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin."
RL Cell Adhes. Commun. 2:15-26 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Osteosarcoma;
RX MEDLINE=95073006; PubMed=7982033;
RX MEDLINE=94216322; PubMed=8163513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Teijimura A., Kudo A.,
RA Amano E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts."
RL J. Biol. Chem. 269:12092-12098 (1994).
RN [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Taniguchi H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RT nervous tissue."
RL Cell Regul. 2:261-270 (1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Kools P.F.J., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
RT molecules are detectable in both human cancer and normal cells."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=Displayed;

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CC      Name=2;
CC      Isoid=PS5287-2; Sequence=VSP 000640, VSP 000641;
CC      TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC      other tissues. Expressed in neuroblasts.
CC      -1- SIMILARITY: Contains 5 cadherin domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; J34056; AAA5622.1; -
DR      EMBL; D21254; BAA04798.1; -
DR      EMBL; D21255; BAA04799.1; -
DR      EMBL; AF060370; AAD27755.1; -
DR      EMBL; AF060369; AAD27755.1; JOINED.
DR      EMBL; AF060370; AAD27755.1; -
DR      EMBL; AF060369; AAD27755.1; JOINED.
DR      PIR; A38992; A38992.
DR      HSSP; P09803; 117W.
DR      Genem; HGNC:1750; CDH11.
DR      MIM; 600023; -
DR      GO; GO:0016021; C: integral to membrane; NAS.
DR      GO; GO:0007156; P: homophilic cell adhesion; NAS.
DR      GO; GO:0001503; P: ossification; NAS.
DR      InterPro; IPR002126; Cadherin.
DR      InterPro; IPR000233; Cadherin_C-term.
DR      Pfam; PF00028; Cadherin_5.
DR      Pfam; PF01049; Cadherin_C_1.
DR      PRINTS; PR00205; CADHERIN.
DR      SMART; SM00112; CA; 5.
DR      PROSITE; PS00232; CADHERIN_1; 3.
DR      PROSITE; PS00268; CADHERIN_2; 5.
KW      Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW      Repeat; Signal; Transmembrane.
FT      SIGNAL 1 22
FT      PROPEP 23 53
FT      CHAIN 54 796
FT      DOMAIN 54 617
FT      TRANSMEM 618 640
FT      DOMAIN 641 796
FT      DOMAIN 54 159
FT      DOMAIN 160 268
FT      DOMAIN 269 383
FT      DOMAIN 384 486
FT      DOMAIN 487 612
FT      CARBOHYD 455 455
FT      CARBOHYD 540 540
FT      VARSPLIC 632 693
FT      VARSPLIC 694 796
FT      VARSPLIC 796 796
FT      CONFLICT 271 272
FT      CONFLICT 275 275
FT      CONFLICT 340 340
FT      CONFLICT 373 373
FT      CONFLICT 471 471
FT      SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB2E CRC64;
Query Match 47.8%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 3.9e-91;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;
17 CWGRDA-----APAS-----AWAGSR--HGPALATRRSWWNOFVIEEYAGEPEV 63
DB 13 CUGMCHSHAFAPRERGHILRSPFHGHKKEGCVTLGSKGWVNGCFVIEETGDPV 72

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QY 64 LIGKHSVDVRGGRTRKYLITGEGATVEIDEATGNIHVTSKLDREKAYVLLAQAVD 123
DB 73 LVKRLHSDIDSQDGNKITLSGEGACTIFVIDKSGNIHATKTLDBREKAYVLLAQAVD 132
QY 124 RASNPRLPEPSEFIITKQDINDNPPIPIGPHATVPKSNVGTSTVQTADADDPSTG 183
DB 133 RDNRLPEPSEFIIVAQDINDNPPEFLHETHANVPKSNVGTSTVQTADADDPSTG 192
QY 184 NSAKVYVTLDDGPEPSVDPQGVVPTAIPNDRENOEFLVIAKMGHAGSGST 243
DB 193 NSAKVYVTLDDGPEPSVDPQGVVPTAIPNDRENOEFLVIAKMGHAGSGST 252
QY 244 TVVTVLSDVNDNPPEPQSLYQSVETAPGTLVGRRLAODPDLDGNALMAYSLDGE 303
DB 253 KVTITLTDVNDNPPEPQSLYQSVETAPGTLVGRRLAODPDLDGNALMAYSLDGE 312
QY 304 SEAFSISTDLQGRDGLITRKPLDESORSYFRVETATLTDPAVLRGPKDVAVYV 363
DB 313 MESFEITDYEIQEGVTKKRPVDETERAVSLKVAANVHIDPKISNGPKDVTYVYK 372
QY 364 AVQDAPEPPAFQAAYHTLVPEKKAFTLVQGISAADLDPASPTRYSTILPSPDERCPS 423
DB 373 SVEDADEPMPFLAPSVIHVGEMAAAGTVGVHAKDPDPAANSPIRYSIDRHTDDPFT 432
QY 424 IQPEEGTHTPAFLDREAPAMNLTVLATELGMSGPERGVPLVAEWSAPAAPQSP 483
DB 433 INEDPFIKTYTLPDEESTAMNITVFAEI ----- 463
QY 484 VGSAGVIGIPDSSAQASRVOVAIQTLDENMDAPOLAEPTVFCDS-----AARGLIQVR 539
DB 464 -----HNHQEQVVAIRVLDVNDMAKPAAPYGFICBSQTPLSNPVTIS 514
QY 540 ALDRDEVGNSHVSFGP--LGPDAFTVQNRDIPD-----WHPILM 581
DB 515 ADDKDDTANGPRFIFLPEIITHNPFTVDRNDNAGVYARGRGSRQDLYLPIVI 574
QY 582 ASASLWHPAPRGNQPSQKSSLP-CG-RIGALDSC 620
DB 575 -----SDGGIPVYSTNTVLTIKVGCDDVAGLASC 604
RESULT 6
Q96CZ9 PRELIMINARY; PRT; 796 AA.
AC Q96CZ9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cadherin 11, type 2, isoform 1 preproprotein.
GN Name=CDH11;
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Scheimen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan D.M., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mausina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hulton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

```

RA	Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Strausberg R.;
RL	Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC	-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins (By similarity).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-1- SIMILARITY: Contains 5 cadherin domains.
DR	EMBL; BC013609; AAH13609.1; -.
DR	HSSP; P09803; 117M.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005509; F:calcium ion binding; IEA.
DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR	InterPro; IPR002126; Cadherin.
DR	InterPro; IPR000233; Cadherin_C_term.
DR	InterPro; IPR01901; Secf.
DR	Pfam; PF00028; Cadherin; 5.
DR	Pfam; PF01049; Cadherin_C_1.
DR	PRINTS; PR00205; CADHERIN.
DR	SMART; SM00112; CA; 5.
DR	PROSITE; PS00232; CADHERIN_1; 3.
DR	PROSITE; PSS0268; CADHERIN_2; 5.
DR	PROSITE; PS01067; SECF_SFCD6; UNKNOWN 1.
DR	Calcium-binding; Cell adhesion; Transmembrane.
SO	SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64.
Query Match	47.7%; Score 1601; DB 2; Length 796;
Best Local Similarity	50.4%; Pred. No. 4,5e-91;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10	
QY	17 CMGRLA-----APAR-----AMASRE--HPGALLRTRSMWMOFYIEEYAGPEPV 63
DB	13 CLCLMLCHSHAFAPERGHLPSEFHHEKKKGEGVLRSSKGVMMQFVIEETPDVV 72
QY	64 LIQLKLSVDYRGEGRTKYLLTEGAGTGVDEATGNIHVTKSLDREKAQVTLAQAVD 123
DB	73 LVGRHSDDLDSGGNIKIYLLISEGAGTIFVIDSKSGNIHATKTLDRERQAQITLMAQAVD 132
QY	124 RASNRPLEPPSEFIITKQDINDNPETPLGPYHATVPBMNGVTSTVQTADHADDPSTG 183
DB	133 RDNRRLPEPSEIIVFDINDNPEEPFHETVHANVERSGVSTVQVVASPADPTVG 192
QY	184 NSAKLVYTALDGLPFPSVDPOTGVARTAI PMWDSETOEELFVVIQAKDMGHMGSGST 243
DB	193 NSAKLVYSILLEGQPIYSVAQGIGIRTLPMNDDEAEENHYVIAQKDGMHGMSIGTT 252
QY	244 TVTVTLSDVNNDPKFPQSGLVQFSVETAGTGTLVGRLARADDPLGDNALMAYSILDSEG 303
DB	253 KWIITLTVDNNDPKFPQSQVSOMSYSEAAYGEEVGRVKAKDPDIGENGIVTYNIIDGGG 312
QY	304 SEAFSTSTLOGRDGLITVRKPLEDESQRYSFVEATNTLLIPAYLRARPFCDVASYV 363
DB	313 MESFEITTYIEROEGIKLKRVDETRAAISLVKEANAHIDKFLSNQPFQDYVAKI 372
QY	364 AVODAEPAEPFACTOAAYHLVLENPKRPGTLVQGISAADLDSPASFIRYSILPHSDPERCS 423
DB	373 AYEDADEPMPFLAPSIVIEHQGNAAAGTVGVRHAHXOPDAANSPIRYSIDRHDLDRFT 432
QY	424 IQEBEGTIFTAAPLDREAAMNLTVLATELGWNGEGRGWPLVLAMNSAPAAPQRS 483
DB	433 INEDDFIKITKFLRREETAAMINTVFPAEI----- 463
QY	484 VGSAGVIPDSSKQASQVAIQTIDENDNAPOLAEPYDTFVCDSS---AAFQOLIQVIR 539
DB	464 -----HANHQEAQKVALARVLDVDVNDAPKRAAPYEAGTICSDQTKLSNQPIVITS 514
QY	540 ALDRDEVGNSSHVSFGQP--LGPDANFTVQDNRLPA-----WHFFPLIM 591

Db	515	ADDXDDTANGPRFIFGLPELIIHNPNFTVRDRNDNTAGVYARRGCFGRQKODYLLPIVI	574
Cy	582	ASASSWHLWHPAERGNQSPASQKSSLS-CG-RLPGLPSC	620
Db	575	-----SDGGIPMWSINTTLITIVCGCDVNGALLSC	604
RESULT 7			
CADB_MOUSE			
ID	CADB_MOUSE	STANDARD;	PRT; 796 AA.
AC	P55288;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Cadherin-11 precursor (osteoblast-cadherin) (OB-cadherin) (OSF-4).		
GN	Name=cdh11, Synonyms=Cad-11;		
OS	Mus musculus (mouse).		
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
NP	SEQUENCE FROM N.A.		
RP	MEDLINE=95259886; PubMed=7750649;		
RA	Hoffmann I.H., Balling R.;		
RT	"Cloning and expression analysis of a novel mesodermally expressed		
RT	cadherin.";		
RL	Dev. Biol. 169:337-346(1995).		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=95259887; PubMed=7750650;		
RA	Kimura Y., Matsumami H., Inoue T., Shimamura K., Uchida N., Ueno T.,		
RA	Miyazaki T., Takeichi M.;		
RT	"Cadherin-11 expressed in association with mesenchymal morphogenesis		
RT	in the head, somite, and limb bud of early mouse embryos.";		
RL	Dev. Biol. 169:347-358(1995).		
NP	SEQUENCE FROM N.A.		
RP	STRAIN=C57BL/6; TISSUE=Calvaria;		
RC	MEDLINE=94216322; PubMed=8163513;		
RA	Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,		
RA	Amano E.;		
RT	"Molecular cloning and characterization of OB-cadherin, a new member		
RT	of cadherin family expressed in osteoblaste.";		
RL	J. Biol. Chem. 269:12092-12098(1994).		
NP	SEQUENCE FROM N.A.		
RP	TISSUE=Olfactory epithelium;		
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,		
RA	Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Matsumura K., Farmer A.A., Rubin J.M., Hong L.,		
RA	Stepleten M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ushid T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loughran P.J., Peters G.J., Abramson R.D., Mulhany S.J.,		
RA	Bohak S.A., McMan P.J., McKernan K.T., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hults S.W.,		
RA	Villalón D.C., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,		
RA	Smetsch A., Schein J.E., Jones S.J.M., Matra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
NP	DEVELOPMENTAL STAGE.		
RC	STRAIN=C57BL/6; TISSUE=Testis;		
RC	MEDLINE=87033837; PubMed=8879495;		

RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RT fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction.";
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; X77557; CAAS4674.1; -;
 DR EMBL; D31963; BAA06730.1; -;
 DR EMBL; D21253; BAA04797.1; -;
 DR EMBL; BC046314; AAA46314.1; -;
 DR PIR; A53584; A53584;
 DR PIR; I48277; I48277;
 DR PIR; I49556; I49556;
 DR HSSP; P09803; I17W;
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CABOHD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHD 540 540 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> M (in Ref. 1).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D2461D529 CRC64;
 Query Match 47.6%; Score 1596; DB 1; Length 796;
 Best Local Similarity 50.7%; Pred. No. 9,1e-91;
 Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;
 31 SREH-----GPAALTRRSWVWQPFYIEEYAGEPVLIGLSDVVRSGRT 79

Db 29 SHLHPSFHGHEKKEGQVLAQRSKGWNNQPFVIEEYGPDPVLVGRLLHSDGDN 88
 QY KYLLTSEAGATFVDEATGNTHWTKSLDREKAQVLLAQVADBSNRPSPSEFTIK 139
 Db 89 KYLLTSEAGATTFLVDDKSGNTHAKTKLDRERAQYLLMAQVDDTNRPSPSEFTIK 148
 QY 140 GQDINDNPIPLGPHYATVPMNSVGTISVIQVTAHADDPDSYGNASAKLVYTVLDGLPFF 199
 Db 149 VQDINDNPEFLHEITHANVPERSNVGTISVIQVTAHADDPDSYGNASAKLVYTVLDGLPFF 208
 QY 200 SYDPQGVATRLPMMDETOEFLVIAQKMGHMGLSSTVTVTLSPVNNPPEF 259
 Db 209 SEAQGILRIALPNNDRAKEEHVAVIQAKMGHMGLSSTVTVTLSPVNNPPEF 268
 QY 260 PSQYQSVYETAGGTGLVRLAODPDLGNALMAYSLDGESEARSISTDLOGDGL 319
 Db 269 PSQYQSVYSEAAVGESEGVYKAKDPDIGNGLVTVNIVDDGTELEFETITDVEYQGV 328
 QY 320 LTRKRLDRESQSTSPREATNTLIDPAYLRGPFKVAASVAVQAPPEPATQAY 379
 Db 329 VTKRKVDDETRAVSLKLEANVHIDPFISNGPFKQTVKVISVEDADEPMLASYS 388
 QY 380 HLTVPENKAPGLVQGISAADLSDPASPIRSYIILPHSDPERCFSIQPEEGTHTAPLDR 439
 Db 389 IHEVGNAAGTVGVRVHAKDPAANSPIRSYIDRHTDLDREFTINPEDGFKITKPLDR 448
 QY 440 EAPAMNLTVALTELGSWSPERGVPPLVAEWSAPAPQPSVGSAGVLPDSSAQS 499
 Db 449 EETAMINISVFAEEL-----NHRHOET 470
 QY 500 RYQVATQTLDENDNAQLAEPYDFVCDSSAP-----GQIQTVALDDEVGSSHVSQ 555
 Db 471 KQVALRIVDNDNAPKFAPEGFCSDHFKALSNQPIVVSADDDDTNNGRPFIS 530
 QY 556 GP--LGPANFTVQDNRDLPA-----WEPPLMASASSWILWMPAERGN 597
 Db 531 LPPEIMENHNFIVRDBRDVTAQVYARGGFSRQKDFYLLPVI-----SDGDI 579
 QY 598 QPASQKSSSLP-CG-RLPGLPSC 620
 Db 580 PMSSTNTLTIRKCGDVNALLSC 604
 RESULT 8
 ID 08CT06 PRELIMINARY; PRT; 796 AA.
 AC 08CT06;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone:C530015F15 product:cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid:10090;
 RN [1] QUITRACD10090;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RX MEDLINE=9279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Spinal cord;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Spinal cord;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Spinal cord;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komno H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Irawa M., Ohara E., Wataniki M.,
 RA Koyada Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; Tissue=Spinal cord;
 RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kaoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sero H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK049652; BAC33860.1; -
 DR HSSP; P09803; 117W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF01049; Cadherin_5; 1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 796 AA; 88126 MW; 71963374B2E1B529 CRC64;
 SQ
 Query Match 47.6%; Score 1595.5; DB 2; Length 796;
 Best Local Similarity 51.6%; Pred. No. 9.8e-91;
 Matches 314; Conservative 97; Mismatches 125; Indels 73; Gaps 7;
 QY 36 GPALIRRRSVMNQFVIEBYAGPEPVLLIGKLHSDVDRGEGETTKYLLTGGAGTIVFVID 95
 DB 45 GQVLRKRRGWVWQFVIEBYTGPDLVGLRLHSDIDSDGNIKYLLSGGAGTIVFVID 104

QY 96 EATGNIHTKSLDREKAQYVLLAQVDRASNRELEPPSEFIIGGODINDNPFIPLGPY 155
 DB 105 DKSQNIHTKTLDRERAAQYTLMAQVDRDNRLEPPSEFIVKQDINDNPFELEHY 164
 QY 156 HATVPEMNGTGVQTAHADDPYSGNSAKVYTVLDGPFPSVPCQGVATAPM 215
 DB 165 HANVPERSNVGTSVQVATSPADDPYSGNSAKVYTVLDGPFPSVPCQGVATAPM 224
 QY 216 DRETOEBFLVYVIAQDMGNGHGLSGSTTVTLVSDVNDNPKRPPQSLYQSVVETAGPQ 275
 DB 225 DREAEEHVYVIAQDMGNGHGLSGSTTVTLVSDVNDNPKRPPQSVQSVGEAAVPG 284
 QY 276 TLVGLRAQDPDLGNALMAVSIIDGESSEAFSITDLOGRDGLYTRKPLDPSQSSYS 335
 DB 285 BEVGKVKAKDPDIGNGLVTVNIVDGDILFETITTYEQDGVKKKPPDEFETKAYS 344
 QY 336 FREVATNTLIDPAYRRPFQDVASVRAVADAEPPFQAHLTVPENKAGTIVGQ 395
 DB 345 LKIEAANHIDPKFTSNPFQDTYTKVSVADAEPPFQALSTVHVGQENAAAGTVGR 404
 QY 396 ISADLDSPASPIRYSILPHSDPERCSTIOEEGTHTAPLDREARAHNTVLALELG 455
 DB 405 VHAQDPDANSPIRYSIDRHTDLRPFINDEDFIKTKPLDREETAMNIVFAAEI- 463
 QY 456 MSWGERGWVPLVLAEMGAPAPAPQPSVGAVGIPQSSAQASRVQVAIOTLDENDNAP 515
 DB 464 -----HNKQETKVAIRVLDVNDNAP 486
 QY 516 QLAEPYDFVCDAAAP-----GQLIQVIRALDRDEVGNSSHVSFGCP--LGPDANFTVDN 569
 DB 487 KFAAPYEGFICSDHPKXLSNQPIVTSADQDDDTANGPFIPLPEIMHNPFTVRDN 546
 QY 570 RDLPK-----WFHPLMASASSLHMPAERGNQPSQGSSTLP-CG- 611
 DB 547 RDNTGVTARRGGSGRQKQDFLLPIVY-----SDGSLPMSNTVTLTKVCGC 595
 QY 612 RLPGALPSC 620
 DB 596 DYNGLALSC 604
 RESULT 9
 ID 093264 PRELIMINARY; PRT; 794 AA.
 AC 093264;
 DT 01-NOV-1998 (TREMBLrel. 08. Created)
 DT 01-NOV-1998 (TREMBLrel. 09. Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26. Last annotation update)
 DE Cadherin precursor.
 GN Name=Xcad-11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Zygote;
 RX MEDLINE=98202517; PubMed=9533956;
 RA Hadelball B., Borchers A., Medlich D.;
 RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Mnt
 RT signal."
 RL Mech. Dev. 72:101-113 (1998).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AF002983; AAC28073.1; -
 DR HSSP; P09803; 117W.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; P:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 potential.
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEFA719DB CRC64;
 Query Match 47.2%; Score 1582.5; DB 2; Length 794;
 Best Local Similarity 50.4%; Pred. No. 6,36-90;
 Matches 310; Conservative 97; Mismatches 133; Indels 75; Gaps 5;
 QY 36 GPALLRTRRSWVWNOQFVIEEYAGPEPVILGKHSVDVDRGGRKYLITGEGATVVID 95
 DB 45 GQVLRHSKRGWVWNOQFVIEEYTPDPVLGRLHSDVDSGWKIKYILSGGATITVID 104
 QY 96 EATGNIHVTKSLDREKKAQYVLLAQAVDRASNRPLEPSEETIKGODINDPPIFPLGPY 155
 DB 105 DKSNGIHAKTLDREERAGYTLMAQAVDRETNKLPEPSEETIVQDINDPPEFLHENY 164
 QY 156 HATVPENSVNGTSVIOVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 215
 DB 165 HANVPENSVNGTSVIOVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 224
 QY 216 DRETOEEFLVVIQAKDMGGMGSLSGSTTVTVLSDVNDNPKRPSQYQSVVETAGPG 275
 DB 225 DRAKEEYHVVIOAKDMGGMGSLSGSTTKVITLTDVNDNPKRPSQYQSVVETAGPG 284
 QY 276 TLVGRLLRAQDDPLGDNALMAYSILDEGSEAFSISTDLQGRDGLLTVRKPLDPESQSYS 335
 DB 285 EEVGRIRAKDPDIGNGLIKYRILEGDAEWEITADVTQEGVAKLKVDVETKKEYS 344
 QY 336 FRVATNTLIDPAVYLRGSPFQDVASVRYAVODAPPEPFAQAAHLVPEKKAAGTLVQ 395
 DB 345 MKVEAVNVHIDPRFSRPPDYATVTKISVEDPEPFLERSLILEYENAPSDTVVGR 404
 QY 396 ISAADLDSPASPIRYSILPHSDPERCFISQPEEGTIHTAPLDREARAHNLTVLATELG 455
 DB 405 VHAQDPDANSPIRISIDRHTDLDRFSINPEDGVIKTKGLDREESPMHNISITATEV- 463
 QY 456 MSWGERGWPVLLVAEMSAAPAAPPORBSVSAVGIPODSSAQARVOYALITLDENNAP 515
 DB 464 -----HNRIHETRVPAALIKVDKNAP 486
 QY 516 QLABRYDTFVCDASAPGQLIQVIRALDRDEVGNSSHVSGQP---LGDANFTQDNRDL 572
 DB 487 EFAPRYEAFVCEMNAPIINOFELITRAVDCDITANGIRLFRSPPELIVAPNPFITIDKDN 546
 QY 573 PA-----WFHPLMASASSWLWMPAER-----GNOPASQ 602
 DB 547 TASIRVGRGVFSRQKQDLYLVIVISDGS---PPMSTNTLTSVRICSCNSDQSQSCN 602
 QY 603 GKSSSLPGGRLLPGAL 617
 DB 603 AEPQSLNAGLSTGAL 617
 RESULT 10
 CADA_CHICK STANDARD; PRT; 792 AA.
 AC 093319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.
 CC NCBI_TaxID=9031;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=White Leghorn;
 CC Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thierry J.P.,
 CC Koteliansky V., Maesky M.W.;
 CC Molecular cloning of chick cadherin 11 and its expression during
 CC smooth muscle differentiation and formation of the tunica media.";
 CC Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC - FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC - SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC - SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AF053342; AAC3675.1; -.
 CC HESP: P09803; 117W.
 CC InterPro: IPR002126; Cadherin.
 CC InterPro: IPR000233; Cadherin_C_term.
 CC Pfam: PF00028; Cadherin_5.
 CC Pfam: PF01049; Cadherin_C_1.
 CC PRINTS: PR00205; CADHERIN.
 CC SMART: SM00112; CA; 5.
 CC PROSITE: PS00232; CADHERIN_1; 3.
 CC PROSITE: PS0268; CADHERIN_2; 5.
 CC Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 CC Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53 potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSMEM 614 634 Cytoplasmic (Potential).
 FT DOMAIN 635 792
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3486C6866731AB CRC64;
 Query Match 46.5%; Score 1558; DB 1; Length 792;
 Best Local Similarity 55.0%; Pred. No. 2,1e-88;
 Matches 296; Conservative 86; Mismatches 116; Indels 40; Gaps 2;
 QY 36 GPALLRTRRSWVWNOQFVIEEYAGPEPVILGKHSVDVDRGGRKYLITGEGATVVID 95
 DB 45 GQVLRHSKRGWVWNOQFVIEEYTPDPVLGRLHSDVDSGWKIKYILSGGATITVID 104
 QY 96 EATGNIHVTKSLDREKKAQYVLLAQAVDRASNRPLEPSEETIKGODINDPPIFPLGPY 155
 DB 105 DKSNGIHAKTLDREERAGYTLMAQAVDRETNKLPEPSEETIVQDINDPPEFLHENY 164
 QY 156 HATVPENSVNGTSVIOVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 215
 DB 165 HANVPENSVNGTSVIOVTAHDADDPBSYNSAKLYTVLDGLPFRSVDPQGVVTAIPNM 224
 QY 216 DRETOEEFLVVIQAKDMGGMGSLSGSTTVTVLSDVNDNPKRPSQYQSVVETAGPG 275
 DB 225 DRAKEEYHVVIOAKDMGGMGSLSGSTTKVITLTDVNDNPKRPSQYQSVVETAGPG 284

QY 276 TLVGRRAQDPDLDNLMAYSLIDEGSEAFSTLDLQGRDGLTLVRKPLDFESQSY 335
DB 285 EEWGVKXAKDDPIENGLVAYSLIDGDMFELTDTYEQEGVVKLKLKVLDEETKSY 344
QY 336 FRVETWTLIPAVLRGPFCDVASVRVADAPFPFQAAVHLVPEVKNKPGTLVQ 395
DB 345 LKVEANVHIDPKXISNPFMDITVTKITVEDADEPVFLKPSITFEVQNAASGIVVK 404
QY 396 ISAADLDSAPSPIRYSILPHSDPERCSIOPEBGTITTAAPLDREARAWNLTVLTEL 455
DB 405 VHAKDPDANSAIRYSIDRHTDLERYFTLNADDGINKIKALDREETAMNISVFAVEV 463
QY 456 WSWPERGWPVLLVAEWSAPAPQSRPSGAVOIPDSSAQSRVQVATQTLDEMDNA 515
DB 464 -----HKQHQEKVFAIKVADVNDNA 486
QY 516 QLAPEYDTFVCDNAPGQLICVIRALDRDEVGNSSHVSGPFG--LGEFANFTVQDRD 571
DB 487 KFAAAVEAFVCEMARNRNOQFITTISADKXDSANGPRIFSLPPIINRPFSLRDNRD 544
RESULT 11
Q8C449 PRELIMINARY; PRT; 716 AA.
AC Q8C449;
DT 01-MAR-2003 (Tremblrel. 23. Created)
DT 01-MAR-2003 (Tremblrel. 23. Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28. Last annotation update)
DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
DE library, clone:6530002D14 product:cadherin 8, full insert sequence
DE (Cdh8 protein).
GN Name=Cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "High efficiency full-length cDNA cloning";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashitume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RT Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalske U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Strausberg R.,
RT Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC EMBL: AK083092; BAC38758.1; -.
CC EMBL: BC057581; AAH57581.1; -.
CC DR HSSP: P15116; INCT.
CC DR MGD: MGI:107434; Cdh8.
CC DR GO: GO:0016020; C:membrane; IEA.
CC DR GO: GO:0005509; P:homophilic cell adhesion; IEA.
CC DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
CC DR InterPro: IPR002126; Cadherin.
CC DR InterPro: IPR00233; Cadherin_C term.
CC DR Pfam: PF01049; Cadherin_5.
CC DR PRINTS: PR00205; CADHERIN.
CC DR PROSITE: PS00232; CADHERIN_1; 3.
CC DR PROSITE: PS0268; CADHERIN_2; 5.
CC DR Calcium-binding; Cell adhesion; Transmembrane.
CC KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
CC SEQUENCE 716 AA; 79145 MW; 976FSD45F938BD CRC64;
Query Match 45.8%; Score 1536.5; DB 2; Length 716;

Best Local Similarity 48.1%, Pred. No. 4e-87;
Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;

QY 39 LLRTSRWVWVNFVIEEYAGEPEVILIGKLSVDVDRGEGRTKYLITGEGATVFIIDEAT 98
DB 56 LSRSGKGVWVWVNFVIEEYAGEPEVILIGKLSVDVDRGEGRTKYLITGEGATVFIIDEAT 115
QY 99 GNHYTKSLDREKAKQVYLLAQAVDRASNRLEPPESEFIITKQDINDNPPFLGPYHAT 158
DB 116 GDHAIKRLDREKAEYLLTAQAVDFETNKEPPESEFIITKQDINDNPPFLGPYHAT 175
QY 159 VPENSVGTSTVIOYTAHDADPSYNSAKLYVTLGDLFFSVDPOTGVATAPNDRE 218
DB 176 VPENSVGTSTVIOYTAHDADPSYNSAKLYVTLGDLFFSVDPOTGVATAPNDRE 235
QY 219 TOEEFLVVIQAKMGHMGSLGSGTITVTLSDVNDNPKFQSLYQSVETAGPGLV 278
DB 236 AKEEYLVVVIQAKMGHMGSLGSGTITVTLSDVNDNPKFQSLYQSVETAGPGLV 295
QY 279 GRLEADDPDLGDMALMAYSLIDGSGEAFSISTDLOGRGLITVRKPLDFESQSYSPRY 338
DB 296 GRVKNDDOIGENAGSYDIIIDGGTALFEITSDAQDGVIRKRPDLDFETKKSITLV 355
QY 339 EATNTLIDPAYLRGPFQDVASVAVADAPPAFTQAAYHLYTPENKAPGLVQGIS 398
DB 356 EAAHNIHIDPRFSRGPFDOTATKIVEDADEPVPFSEPTLYLLEVENALNSVIGQVTA 415
QY 399 ADLDSAPPIRYSILPHSDPERCESTOPEEGTHTAPLDREBARAHNTLVATELGWSM 458
DB 416 RDPDITSSPFRSDRHTDLERQFINADGKITLAPLDRSLVSWHNTITITATEI 471
QY 459 GPERGWVPLVAEWSAPAPAPQSPVGSAGVIGPOSSAQSARVOVAIQTLDENDAPOLA 518
DB 472 -----RHSQISRPVPAIKVLDVNDNAPFA 497
QY 519 EPYDTFVCDASAPGQLIYIRALDRDEVGNSSHVSGQGLGPD-----ANFTVQDNRD 571
DB 498 SEYEAFLECNKFGQVITQVSAVDKDPKNGHF--FLYSLLPEWVNNPFTIKKEDNSL 555
QY 572 -----LPAWFPPLMLASASWLMHPAERGNOQASQKSSSL-PCG-RLPGA 616
DB 556 SILAKHNGFRKQKQEVYLLPIVI-----SDSGNPPLSSTLTITIRVCGGSDGV 604
QY 617 LPSCQ-----LPLGI--PALGIYLC 634
DB 605 VQSCNVEAYVLPILGSMGALITAILAC 630

RESULT 12
AAH57581 PRELIMINARY; PRT; 716 AA.

AC AAH57581;
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.U., Maier M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.,
RL Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC057581; AAH57581.1;
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 45.8%; Score 1536.5; DB 2; Length 716;

Best Local Similarity 48.1%, Pred. No. 4e-87;
Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;

QY 39 LLRTSRWVWVNFVIEEYAGEPEVILIGKLSVDVDRGEGRTKYLITGEGATVFIIDEAT 98
DB 56 LSRSGKGVWVWVNFVIEEYAGEPEVILIGKLSVDVDRGEGRTKYLITGEGATVFIIDEAT 115
QY 99 GNHYTKSLDREKAKQVYLLAQAVDRASNRLEPPESEFIITKQDINDNPPFLGPYHAT 158
DB 116 GDHAIKRLDREKAEYLLTAQAVDFETNKEPPESEFIITKQDINDNPPFLGPYHAT 175
QY 159 VPENSVGTSTVIOYTAHDADPSYNSAKLYVTLGDLFFSVDPOTGVATAPNDRE 218
DB 176 VPENSVGTSTVIOYTAHDADPSYNSAKLYVTLGDLFFSVDPOTGVATAPNDRE 235
QY 219 TOEEFLVVIQAKMGHMGSLGSGTITVTLSDVNDNPKFQSLYQSVETAGPGLV 278
DB 236 AKEEYLVVVIQAKMGHMGSLGSGTITVTLSDVNDNPKFQSLYQSVETAGPGLV 295
QY 279 GRLEADDPDLGDMALMAYSLIDGSGEAFSISTDLOGRGLITVRKPLDFESQSYSPRY 338
DB 296 GRVKNDDOIGENAGSYDIIIDGGTALFEITSDAQDGVIRKRPDLDFETKKSITLV 355
QY 339 EATNTLIDPAYLRGPFQDVASVAVADAPPAFTQAAYHLYTPENKAPGLVQGIS 398
DB 356 EAAHNIHIDPRFSRGPFDOTATKIVEDADEPVPFSEPTLYLLEVENALNSVIGQVTA 415
QY 399 ADLDSAPPIRYSILPHSDPERCESTOPEEGTHTAPLDREBARAHNTLVATELGWSM 458
DB 416 RDPDITSSPFRSDRHTDLERQFINADGKITLAPLDRSLVSWHNTITITATEI 471
QY 459 GPERGWVPLVAEWSAPAPAPQSPVGSAGVIGPOSSAQSARVOVAIQTLDENDAPOLA 518
DB 472 -----RHSQISRPVPAIKVLDVNDNAPFA 497
QY 519 EPYDTFVCDASAPGQLIYIRALDRDEVGNSSHVSGQGLGPD-----ANFTVQDNRD 571
DB 498 SEYEAFLECNKFGQVITQVSAVDKDPKNGHF--FLYSLLPEWVNNPFTIKKEDNSL 555
QY 572 -----LPAWFPPLMLASASWLMHPAERGNOQASQKSSSL-PCG-RLPGA 616
DB 556 SILAKHNGFRKQKQEVYLLPIVI-----SDSGNPPLSSTLTITIRVCGGSDGV 604
QY 617 LPSCQ-----LPLGI--PALGIYLC 634
DB 605 VQSCNVEAYVLPILGSMGALITAILAC 630

RESULT 13
CADD_HUMAN STANDARD; PRT; 799 AA.
ID CADD_HUMAN
AC P5286; Q9UB2;
DT 01-OCT-1996 (Rel. 34, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 CN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.,
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins."
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Helmark R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.,
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue."
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Vainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB035305; BA87419.1; -
 DR EMBL; U34060; AAA35628.1; ALT_INT.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:1767; CDH8.
 DR MIM; 603008; -
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR0205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00233; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 KM SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 30 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).

FT DOMAIN 62 167 Cadherin 1.
 FT 168 276 Cadherin 2.
 FT 277 391 Cadherin 3.
 FT 392 494 Cadherin 4.
 FT 495 616 Cadherin 5.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT 355 355 V -> D (in Ref. 2 and 3).
 FT 647 647 H -> HQ (in Ref. 2 and 3).
 SQ SEQUENCE 799 AA; 88253 MW; 9B119B86039C6A0A CRC64;
 Query Match 45.8%; Score 1536.5; DB 1; Length 799;
 Best Local Similarity 47.9%; Pred. No. 4.6e-87;
 Matches 300; Conservative 111; Mismatches 194; Indels 81; Gaps 9;
 QY 39 ILRTSRWVWVNPFIYIEYAGPEPYLIGKHSVDVDSRGRTKYLITGEGATVFVIDEAT 98
 DB 56 LNRSRGWVWVWVNPFIYIEYAGPEPYLIGKHSVDVDSRGRTKYLITGEGATVFVIDEAT 115
 QY 99 GNHHTKSLDPEERKQVYLAQAVDRASNRLEPPESEITIKGQDINNPPFIPGPHAT 158
 DB 116 GDHAIKRLDREERKAEVLTQAQVDETSKLEPPSSFTIKVQDINNAPFINGPHAT 175
 QY 159 VPENSVGTSVIQTADHDADPSYNSAKLYVTYLDGLPFPSVDPQTGVRTAIPNDRE 218
 DB 176 VPENSLGTSTVNTATDADDPVGNASKLYVSTLEQPVSIIEPTAIIKTLAPNDRE 235
 QY 219 TOEPLVITQAKNGKNGKGLSSSTVYVTLSDVNDNPKPKPSLYQPSVETKPGETLV 278
 DB 236 AKEEVLVITQAKNGKNGKGLSSSTVYVTLSDVNDNPKPKPSLYQPSVETKPGETLV 295
 QY 279 GLRQADPDLDNALMAYSIDGSEAFSISTDQGRDGLTVRKPLDFESQSYGFRV 338
 DB 296 GRVANDPDIDENNAOSSYDIIIDGGTALFELTSQAQDGIIRKRLDDETKSYLKV 355
 QY 339 EATNTLDIPAYLRGPFKDVASVRVAVODAPPAFTQAAVHLTVPENKAPGLVGOISA 398
 DB 356 EAAVNHIPRPSGSGPFQDTATVKIVVEDDEPVSFPLYLLEVHNAALNSYIGQVTA 415
 QY 399 ADLSPASPIRYSILPHSDPERCSIQPEESTHTTAPLIDREARAWNTLVLTAEGLMSW 458
 DB 416 RDPDTSSPIRFSIDRHLDERQINADSKITLAPLDELSVWNTITITATET 471
 QY 459 GPERGWVPLVAEWSAPAPAPQSPVSAVGIPODSSAQASRVQVAIQTIDENDAPOLA 518
 DB 472 -----RNHSQISRVVAIKVLDVNDNADEFA 497
 QY 519 EPIPTFVCDASAPQGLIOVITALDRDEVGNSHVSFOGPIGPD-----ANFTVQDNRD 571
 DB 498 SEYEAFLENGKPGQVITQVSAMKDPKNGHY--FYSLPDEVVNNPNPFIKKNEDNSL 555
 QY 572 -----LPAMFPLMASASGSLTHMPAERKGNOPASGKSSSL-PCG-RLPGA 616
 DB 556 SILAKHNGFNKKQKEVILPILI-----SDSGNPPLSTSLTLTRVCGCSNDGV 604
 QY 617 LPSCQ-----LPGLI---PALGIYLC 634
 DB 605 VQSCVNEAVYVLPILGSMGALITAIAC 630
 RESULT 14
 QGBRK4 ID QGBRK4 PRELIMINARY; PRT; 754 AA.
 AC QGBRK4;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Mus musculus (10 days neonate cortex cDNA, RIKEN full-length enriched
 library, clone:A830083f13 product:cadherin 8, full insert


```

OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=98190518; PubMed=5521872;
RA Kido M., Obata S., Tanahara H., Rochelle J.M., Seldin M.F.,
RT Taketani S., Suzuki S.T.;
RL "Molecular properties and chromosomal location of cadherin-8.";
RT Genomics 48:186-194(1998).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O54800-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O54800-2; Sequence=VSP_000638, VSP_000639;
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB010436; BAA24452.1; -
DR EMBL; AB010437; BAA24453.1; -
DR HSSP; P09803; 117M.
DR RGD; 69286; Cdh8.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR002333; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA_5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 61 Potential.
FT CHAIN 62 799 Extracellular (Potential).
FT DOMAIN 62 621 Extracellular (Potential).
FT TRANSMEM 622 642 Potential.
FT DOMAIN 643 799 Cytoplasmic (Potential).
FT DOMAIN 168 276 Cadherin 1.
FT DOMAIN 168 276 Cadherin 2.
FT DOMAIN 277 391 Cadherin 3.
FT DOMAIN 392 494 Cadherin 4.
FT DOMAIN 495 616 Cadherin 5.
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 514 532 IGVTSAMDSDPKXGHFL -> NISMLILANFVNCFLV
FT N (in isoform 2).
FT FTId=VSP_000638.
FT VARSPLIC 533 799 Missing (in isoform 2).
FT FTId=VSP_000639.
SQ SEQUENCE 799 AA; 88332 MW; F01D145A80966CB6 CRC64;

Query Match 45.6%; Score 1530.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 1.1e-86;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;
QY 39 LRTTRSVWVWQFVIEBAPBPVLTKGLHSDVDRGEGRTKYLITGEGAGTVFVIDEAT 98
DB 56 LNRKRGVWVWQFVIEBAPBPVLTKGLHSDVDRGEGRTKYLITGEGAGTVFVIDEAT 98

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QY 99 GNHYTKSLDREKAQVYLLAQAADVDRASNRPLEPSPSEFIKQDINDNPPIFLPGPYAT 158
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QY 159 VPEMANVTSVLTQTAAHADDPVSGNSAKLYVTYLDGLPFPSVDPQGVATAPMNDRE 218
DB 176 VPEMILTSVTVNVTATADDPVGSNSAKLYVSLIEGQPYSLPEFTALITAPMNDRE 235
QY 219 TQEEFLVYIQAQDMGSHGSGSTTVTLTSDVNDNPKPQSLYQSVVETAGPGLV 278
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QY 279 GRLAQPDPGLNMAVSIIDGESSEAFSISTDLQGRDGLITRKPLDFESQSSYSFRV 338
DB 296 GRVKANDDQIGEMNAOSSYDIIDGGTALFEITSDAQADGVITRKPLDFETKSYTLKV 355
QY 339 EATNTLIDPAYLRSGPFKDVASVRVAQDAPEPAFTQAAVHLYPENKAPGTLVQISA 398
DB 356 EAMNTHIDPRSGRPFQDTATVKI VEDDAPEPVFSPTVLLVHENAALNSVIGVTA 415
QY 399 ADLSPASPIRYSILPHSDPERCTSIQPEBGTHTAPLDRBAMHNLVTLATELQSW 458
DB 416 RPDITSSPIRFSIDRHTDLEROFINADDDKITLAPLDELTVWHNISIAIEI 471
QY 459 GPERGVPLVLAEMSAAPAPQRPSPVSAVGIPODSSAQASRYOVAIQTLDENAPOLA 518
DB 472 -----RHSQISRVVAILKVDVNDNABEFA 497
QY 519 EPHYTFVCDASAPGQLIGVIRALDRDEVGNSHVSFOGFLGPD-----ANFTVDNRD 571
DB 498 SEYEAFLCENGKPGVIGTVASAMDKDPKGNH--FLYSLLPEWNNPNFTIKKQDNSTL 555
QY 572 -----LPAMFHPILMASASSMHWPAAERGNQPAQSGKSSL-PCG-RLPGA 616
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QY 617 LPSCQ-----LPLGI---PALGIYLC 634
DB 605 VQSCNVEPYVPIGSMGALTAIILAC 630

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Search completed: December 8, 2004, 10:24:33
 Job time : 257.926 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 649.891 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-4
Perfect score: 3354
Sequence: 1 MNGIVRLILAWIGWGMGR.....LPSCQLPIGIPALGIYLCAS 636

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3354	100.0	636	10 US-09-788-051-4	Sequence 4, App1
2	3259	97.2	620	10 US-09-788-051-7	Sequence 7, App1
3	2746.5	81.9	781	9 US-09-860-868-2	Sequence 2, App1
4	2746.5	81.9	781	14 US-10-245-752-98	Sequence 98, App1
5	2746.5	81.9	781	14 US-10-245-859-98	Sequence 98, App1
6	2746.5	81.9	781	14 US-10-245-103-98	Sequence 98, App1
7	2746.5	81.9	781	14 US-10-245-107-98	Sequence 98, App1
8	2746.5	81.9	781	14 US-10-245-143-98	Sequence 98, App1
9	2746.5	81.9	781	14 US-10-245-771-98	Sequence 98, App1
10	2746.5	81.9	781	14 US-10-245-851-98	Sequence 98, App1
11	2746.5	81.9	781	14 US-10-245-883-98	Sequence 98, App1
12	2746.5	81.9	781	14 US-10-237-535-98	Sequence 98, App1
13	2746.5	81.9	781	14 US-10-238-163-98	Sequence 98, App1

14	2746.5	81.9	781	14	US-10-238-283-98	Sequence 98, App1
15	2746.5	81.9	781	14	US-10-238-370-98	Sequence 98, App1
16	2746.5	81.9	781	14	US-10-245-055-98	Sequence 98, App1
17	2746.5	81.9	781	14	US-10-245-147-98	Sequence 98, App1
18	2746.5	81.9	781	14	US-10-245-730-98	Sequence 98, App1
19	2746.5	81.9	781	14	US-10-245-739-98	Sequence 98, App1
20	2746.5	81.9	781	14	US-10-246-210-98	Sequence 98, App1
21	2746.5	81.9	781	14	US-10-239-196-98	Sequence 98, App1
22	2746.5	81.9	781	14	US-10-243-024-98	Sequence 98, App1
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25	2746.5	81.9	781	14	US-10-245-880-98	Sequence 98, App1
26	2746.5	81.9	781	14	US-10-245-033-98	Sequence 98, App1
27	2746.5	81.9	781	14	US-10-243-095-98	Sequence 98, App1
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29	2746.5	81.9	781	14	US-10-245-427-98	Sequence 98, App1
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33	2746.5	81.9	781	14	US-10-246-976-98	Sequence 98, App1
34	2746.5	81.9	781	14	US-10-243-320-98	Sequence 98, App1
35	2746.5	81.9	781	14	US-10-162-435-13	Sequence 13, App1
36	2746.5	81.9	781	14	US-10-242-743-98	Sequence 98, App1
37	2746.5	81.9	781	14	US-10-242-845-98	Sequence 98, App1
38	2746.5	81.9	781	14	US-10-237-636-98	Sequence 98, App1
39	2746.5	81.9	781	14	US-10-238-345-98	Sequence 98, App1
40	2746.5	81.9	781	14	US-10-238-346-98	Sequence 98, App1
41	2746.5	81.9	781	14	US-10-238-411-98	Sequence 98, App1
42	2746.5	81.9	781	14	US-10-243-124-98	Sequence 98, App1
43	2746.5	81.9	781	14	US-10-243-425-98	Sequence 98, App1
44	2746.5	81.9	781	14	US-10-243-446-98	Sequence 98, App1
45	2746.5	81.9	781	14	US-10-245-874-98	Sequence 98, App1

ALIGNMENTS

RESULT 1
US-09-788-051-4
Sequence 4, Application US/09788051
Publication No. US2003014491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dymac, Rodolfe T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-4
Query Match 100.0%; Score 3354; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 9.1e-242;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNGIVRLILAWIGWGMGRILAPARAMGRREHPALLRTSRVWVWVFFIEEYAGP 60

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Db      1  MMGLVRLLLAMLGCMGKRLAARPARMAGSREHPGALLTRRSWNNQFFVIEEYAGP 60
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Db      61  EPVLIGKLHSVDNREGRTKYLITGEGAGTVFIDEATGNHVTKSJDRREKAQYVLLAQ 120
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Db      181  SYGNSAKLVYTVLDGLPEFVSVDPTGVYRTAIPMDRETOEELVVIQAADMGGHGGLS 240
Qy      241  GSTTATLSDVNNPPEFPOSILYQFSVETAGGTLVGRRAQDDPLGDMALMAYSIID 300
Db      241  GSTTATLSDVNNPPEFPOSILYQFSVETAGGTLVGRRAQDDPLGDMALMAYSIID 300
Qy      301  GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
Db      301  GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
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Db      601  SQGKSSLPCCRLPGALPSCQLPLGIPALGIVLCAS 636

RESULT 2
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radjoe T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

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Query Match      97.2%; Score 3259; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1,1e-234;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61  EPVLIGKLHSVDNREGRTKYLITGEGAGTVFIDEATGNHVTKSJDRREKAQYVLLAQ 120
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Db      121  AVDRASNRPLEPSEFFIKGQDINDNPPIFPLGYNHATVPMSNVGTSVQVTAHDDDP 180
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Db      181  SYGNSAKLVYTVLDGLPEFVSVDPTGVYRTAIPMDRETOEELVVIQAADMGGHGGLS 240
Qy      241  GSTTATLSDVNNPPEFPOSILYQFSVETAGGTLVGRRAQDDPLGDMALMAYSIID 300
Db      241  GSTTATLSDVNNPPEFPOSILYQFSVETAGGTLVGRRAQDDPLGDMALMAYSIID 300
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Db      301  GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
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RESULT 3
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; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A J
; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-860-868-2

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Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

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DB      61 EPLVIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREBEKAQYVLLAQ 120
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DB      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVETAI PMNDRETOEEFLVVIQAKDMGGMGLS 240
QY      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSILD 300
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DB      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQRSYFVEATNTLIDPAYLRGPFKDVAS 360
QY      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGOISADLDSPASIRYSILPHSDPER 420
DB      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGOISADLDSPASIRYSILPHSDPER 420
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DB      421 CFSIQPEEGTHTAFLDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
QY      481 RSPVGSAGVIGPQDSSAQSARVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 540
DB      481 RSPVGSAGVIGPQDSSAQSARVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 540
QY      455 -----DSQAQSRVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 502
DB      455 -----DSQAQSRVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 502
QY      541 LDRDEVGNSSHVSGPGLPDANFTVQDNRD-----LPA-----WF 576
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QY      503 LDRDEVGNSSHVSGPGLPDANFTVQDNRDGASALLPSRAPPRHAPYLVPIELMDWG 562
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DB      577 HPLMASASWLH-----WPAERGNQASOG 603

RESULT 4
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, V. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephen, Jean-Phillippe
; APPLICANT: Macdonald, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P36301C66
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 10/17942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046

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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-245-752-98

Query Match      81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

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DB      1 MMGLVRLLLAMVLSGCMGCMRLAARAPAMAGSREHGPALLTRRSWVMNQFVIEYACP 60
QY      61 EPLVIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREBEKAQYVLLAQ 120
DB      61 EPLVIGKLSVDVDRGEGRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREBEKAQYVLLAQ 120
QY      121 AVDASNRPLEPPESEFIKQDINDNPPFPLGPGYHATVPMSVNGTSVQVTAHADDP 180
DB      121 AVDASNRPLEPPESEFIKQDINDNPPFPLGPGYHATVPMSVNGTSVQVTAHADDP 180
QY      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVETAI PMNDRETOEEFLVVIQAKDMGGMGLS 240
DB      181 SYGNSAKLVYTVLDGLPEFSVDPQTGVVETAI PMNDRETOEEFLVVIQAKDMGGMGLS 240
QY      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSILD 300
DB      241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRRAODPDLDGNALMAYSILD 300
QY      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQRSYFVEATNTLIDPAYLRGPFKDVAS 360
DB      301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQRSYFVEATNTLIDPAYLRGPFKDVAS 360
QY      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGOISADLDSPASIRYSILPHSDPER 420
DB      361 VRVAVQADPEPPATQAAVHLTVPEKAPGTLVGOISADLDSPASIRYSILPHSDPER 420
QY      421 CFSIQPEEGTHTAFLDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
DB      421 CFSIQPEEGTHTAFLDREARAHNLTVLATELGMSWGPGRGWPLVAEWSAPAAPQ 480
QY      481 RSPVGSAGVIGPQDSSAQSARVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 540
DB      481 RSPVGSAGVIGPQDSSAQSARVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 540
QY      455 -----DSQAQSRVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 502
DB      455 -----DSQAQSRVOVAIQTLDENNDAPQALAEPYDTVCDSAAFGQLIQVIRA 502
QY      541 LDRDEVGNSSHVSGPGLPDANFTVQDNRD-----LPA-----WF 576
DB      541 LDRDEVGNSSHVSGPGLPDANFTVQDNRD-----LPA-----WF 576
QY      503 LDRDEVGNSSHVSGPGLPDANFTVQDNRDGASALLPSRAPPRHAPYLVPIELMDWG 562
DB      503 LDRDEVGNSSHVSGPGLPDANFTVQDNRDGASALLPSRAPPRHAPYLVPIELMDWG 562
QY      577 HPLMASASWLH-----WPAERGNQASOG 603
DB      577 HPLMASASWLH-----WPAERGNQASOG 603
QY      563 QPALSTATVTVSVCRQPDGVSASCPPEAHLSAAGLSTG 602
DB      563 QPALSTATVTVSVCRQPDGVSASCPPEAHLSAAGLSTG 602

RESULT 5

```

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US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US2003006447A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C12
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match      81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAMLGWGMGRLAARAWAGSRHPPGALLRTSRVWVNOFFVIEYAP 60
DB 1 MMGLVRLLLAMLGWGMGRLAARAWAGSRHPPGALLRTSRVWVNOFFVIEYAP 60
QY 61 EPLLGLKLSHDVDRGEGRTYLLTGEGAGTVFVIDENTGNHVTXSLDSEKQAYLLAQ 120
DB 61 EPLLGLKLSHDVDRGEGRTYLLTGEGAGTVFVIDENTGNHVTXSLDSEKQAYLLAQ 120
QY 121 AVPRASRPLEPPEPFLIKQDINDNPPILPGLPYATVPEMNVGTSVYQVTAHDADP 180
DB 121 AVPRASRPLEPPEPFLIKQDINDNPPILPGLPYATVPEMNVGTSVYQVTAHDADP 180
QY 181 SYGSAKLVTYTLGDLFFFSVDVDTGVTATINMDRETOEFLVYIOAKDMGHGGLS 240
DB 181 SYGSAKLVTYTLGDLFFFSVDVDTGVTATINMDRETOEFLVYIOAKDMGHGGLS 240
QY 241 GSTTIVTTLSDVNDNPKFPQSLYQSFVETAGPGLVGLRAQDDPLDGNALMAYSIID 300
DB 241 GSTTIVTTLSDVNDNPKFPQSLYQSFVETAGPGLVGLRAQDDPLDGNALMAYSIID 300
```

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QY 301 GEGSEAFSISTDLQGRDGLTVRKLPDESORSYSFRVEATNTLLIDPAYLRGPFKVAS 360
DB 301 GEGSEAFSISTDLQGRDGLTVRKLPDESORSYSFRVEATNTLLIDPAYLRGPFKVAS 360
QY 361 VRVAQDAPEPPAFQAAVHITVPEBKAPGLTVQGISAAADDSPASPIRYSILPHSDP 420
DB 361 VRVAQDAPEPPAFQAAVHITVPEBKAPGLTVQGISAAADDSPASPIRYSILPHSDP 420
QY 421 CFSIQPEEGTHTAFLDREARAHNLTVLATELGWSGPERGWPLVWMSAPAAPQ 480
DB 421 CFSIQPEEGTHTAFLDREARAHNLTVLATELGWSGPERGWPLVWMSAPAAPQ 480
QY 481 RSPVGSANGITQDSSAQAQRQVAIQTLIDENDNAPQLAEPYDTVCDSAAAGQIQVIRA 540
DB 481 RSPVGSANGITQDSSAQAQRQVAIQTLIDENDNAPQLAEPYDTVCDSAAAGQIQVIRA 540
QY 541 LDRDEVGNSSHYVFCGPGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHYVFCGPGPDANFTVQDNRD-----LPA-----WF 576
QY 503 LDRDEVGNSSHYVFCGPGPDANFTVQDNRGASALLPSPAPPRHAPYIVPELWDWG 562
DB 503 LDRDEVGNSSHYVFCGPGPDANFTVQDNRGASALLPSPAPPRHAPYIVPELWDWG 562
QY 577 HPLMASASSWLH-----WPPAERGNQAPASQG 603
DB 577 HPLMASASSWLH-----WPPAERGNQAPASQG 603
QY 583 QPALSTATVTVSVCRCPDGSVASCPPEAHLISAAGLSTG 602
DB 583 QPALSTATVTVSVCRCPDGSVASCPPEAHLISAAGLSTG 602

RESULT 6
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C12
; CURRENT FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
```

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us-09-788-051-4.rapb

Page 5

US-10-245-103-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 38-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```
QY 1 MMGLVRLILAMLGWCMGCMRLAAPARAWAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
DB 1 MMGLVRLILAMLGWCMGCMRLAAPARAWAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
QY 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKQAYVLLAQ 120
DB 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKQAYVLLAQ 120
QY 121 AVDRASNRPLEPPESEFIKGGDINDNPPFPLGPHYATVPEMSNVGTSVIQYTAHDADP 180
DB 121 AVDRASNRPLEPPESEFIKGGDINDNPPFPLGPHYATVPEMSNVGTSVIQYTAHDADP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGSL 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGSL 240
QY 241 GSTTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRADPDLGDNALMAYSLD 300
DB 241 GSTTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRADPDLGDNALMAYSLD 300
QY 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVODAPPEPPAFTOAAHYHLTVPEKAPGTLVGOISADLDSASPISYILPHSDPER 420
DB 361 VRVAVODAPPEPPAFTOAAHYHLTVPEKAPGTLVGOISADLDSASPISYILPHSDPER 420
QY 421 CFSIOPEEGTHTTAAPLDREARAHNLTIVLATELGMSWGPGRGWVPLVAEMSAAPAPQ 480
DB 421 CFSIOPEEGTHTTAAPLDREARAHNLTIVLATELGMSWGPGRGWVPLVAEMSAAPAPQ 480
QY 481 RSPVGSAGVIGPODSSAQSRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIOVIRA 540
DB 481 RSPVGSAGVIGPODSSAQSRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIOVIRA 540
QY 541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
QY 577 HPLMASASSWLH-----WPAERGNQAPASQ 603
DB 577 HPLMASASSWLH-----WPAERGNQAPASQ 603
QY 563 QPALSTATVTVSVCRQCPDGSVASCWBEAHLSAAGISTG 602
DB 563 QPALSTATVTVSVCRQCPDGSVASCWBEAHLSAAGISTG 602
```

RESULT 7
US-10-245-107-98
Sequence 98, Application US/10245107
Publication No. US2003006879A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bacon, Dan
APPLICANT: Filvarsoff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, D. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16

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QY 1 MMGLVRLILAMLGWCMGCMRLAAPARAWAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
DB 1 MMGLVRLILAMLGWCMGCMRLAAPARAWAGSREHPGALLRTRRSWMNQFVIEEYAGP 60
QY 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKQAYVLLAQ 120
DB 61 EPLVIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTSLDREKQAYVLLAQ 120
QY 121 AVDRASNRPLEPPESEFIKGGDINDNPPFPLGPHYATVPEMSNVGTSVIQYTAHDADP 180
DB 121 AVDRASNRPLEPPESEFIKGGDINDNPPFPLGPHYATVPEMSNVGTSVIQYTAHDADP 180
QY 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGSL 240
DB 181 SYGNSAKLVYTVLDGLPFPSVDPQTGVVRTAIPNMDRETOEEFLVVIQAKDMGGMGSL 240
QY 241 GSTTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRADPDLGDNALMAYSLD 300
DB 241 GSTTVTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRADPDLGDNALMAYSLD 300
QY 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLITVRKPLDPESQSYSPFEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVODAPPEPPAFTOAAHYHLTVPEKAPGTLVGOISADLDSASPISYILPHSDPER 420
DB 361 VRVAVODAPPEPPAFTOAAHYHLTVPEKAPGTLVGOISADLDSASPISYILPHSDPER 420
QY 421 CFSIOPEEGTHTTAAPLDREARAHNLTIVLATELGMSWGPGRGWVPLVAEMSAAPAPQ 480
DB 421 CFSIOPEEGTHTTAAPLDREARAHNLTIVLATELGMSWGPGRGWVPLVAEMSAAPAPQ 480
QY 481 RSPVGSAGVIGPODSSAQSRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIOVIRA 540
DB 481 RSPVGSAGVIGPODSSAQSRVQVAIQTLDENDNAPQALAEPYDTFVCDSPAAGQLIOVIRA 540
QY 541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVGNSSHVSGQPLGPDANFTVQDNRD-----LPA-----WF 576
QY 577 HPLMASASSWLH-----WPAERGNQAPASQ 603
DB 577 HPLMASASSWLH-----WPAERGNQAPASQ 603
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98
Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 38-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Db 563 QPALSTXTVTVSVCRCQPDGVSASCPMEALHLSAAGLSTG 602

RESULT 8

US-10-245-143-98

Sequence 98, Application US/10245143

Publication No. US20030068780A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gunney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Wacande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C90

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 98

LENGTH: 781

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-143-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;

Best Local Similarity 84.8%; Pred. No. 3e-196;

Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MGGVIRLLMLGCGMGRLAARAAAGSREHPGRLIRTSRWMNQFVIEBYAP 60

Db 1 MGGVIRLLMLGCGMGRLAARAAAGSREHPGRLIRTSRWMNQFVIEBYAP 60

QY 61 EPTVIGLHSDVDVGRGERTKYLITGSGATVFVIDATGNIHTKSLDDEERAKQVYLLAQ 120

Db 61 EPTVIGLHSDVDVGRGERTKYLITGSGATVFVIDATGNIHTKSLDDEERAKQVYLLAQ 120

QY 121 AVDRASRPLPPESEFIIKQDINDNPFIPLGPHYATVPKMSNVGTSVYQVTAHDADP 180

Db 121 AVDRASRPLPPESEFIIKQDINDNPFIPLGPHYATVPKMSNVGTSVYQVTAHDADP 180

QY 181 SYGNSAKLVYTVLDGGLFFSVDPQTGVVTRTAIPNMDRETOEEFLVVIQAKDWGSHMGIS 240

Db 181 SYGNSAKLVYTVLDGGLFFSVDPQTGVVTRTAIPNMDRETOEEFLVVIQAKDWGSHMGIS 240

QY 241 GSTTIVTLSDVNDNPPKFPQSLYQFSVETAGFGLVGRIRADDPDLGDNALMAYSILD 300

Db 241 GSTTIVTLSDVNDNPPKFPQSLYQFSVETAGFGLVGRIRADDPDLGDNALMAYSILD 300

QY 301 GEGSEAFSISTDLOCRDGLTVRKPLDDESGRSYFVEATNTLIDPAYLRGPFKQVAS 360

Db 301 GEGSEAFSISTDLOCRDGLTVRKPLDDESGRSYFVEATNTLIDPAYLRGPFKQVAS 360

QY 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISADIDSASPISILHSDPER 420

Db 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISADIDSASPISILHSDPER 420

QY 421 CESTOPEEGTHTTAPLIDREARAHNLTVALTELGWKGPRGVPPLLVEMSPAPAPQ 480

Db 421 CESTOPEEGTHTTAPLIDREARAHNLTVALTELGWKGPRGVPPLLVEMSPAPAPQ 480

QY 481 RSPVSAVGIPDQSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIQVIRA 540

Db 481 RSPVSAVGIPDQSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIQVIRA 540

QY 455 -----DSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIQVIRA 502

Db 455 -----DSSAQSRVQVAIQTLDENDNAPOLAEPYDTFCDSAPAGQLIQVIRA 502

QY 541 LDRDEVGNSSHVSGPGLGPDANTVQDNRP-----LPA-----WF 576

Db 541 LDRDEVGNSSHVSGPGLGPDANTVQDNRP-----LPA-----WF 576

QY 503 LDRDEVGNSSHVSGPGLGPDANTVQDNRP-----LPA-----WF 576

Db 503 LDRDEVGNSSHVSGPGLGPDANTVQDNRP-----LPA-----WF 576

QY 577 HPLMASASWLM-----WPAERGRQPASOG 603

Db 577 HPLMASASWLM-----WPAERGRQPASOG 603

QY 563 QPALSTXTVTVSVCRCQPDGVSASCPMEALHLSAAGLSTG 602

Db 563 QPALSTXTVTVSVCRCQPDGVSASCPMEALHLSAAGLSTG 602

RESULT 9

US-10-245-771-98

Sequence 98, Application US/10245771

Publication No. US20030068781A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gunney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Wacande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C98

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 98
 LENGTH: 781
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-245-771-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
 Best Local Similarity 84.8%; Pred. No. 3e-196;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILAMVIGMGMCMGRLAAPARAWAGSREHPALLRTRRSWMNQFVIEEYAGP 60
 DB 1 MMGLVRLILAMVIGMGMCMGRLAAPARAWAGSREHPALLRTRRSWMNQFVIEEYAGP 60
 QY 61 EPLVIGKIHSDVDREGRTKYLITGEGAGTVFVIDEATGNHVTSLDREERAOYVLLAQ 120
 DB 61 EPLVIGKIHSDVDREGRTKYLITGEGAGTVFVIDEATGNHVTSLDREERAOYVLLAQ 120
 QY 121 AVDRASNRPLEPPESEFIKQDINDNPIFPLGPHATVPMSVNGSVIQTADHADDP 180
 DB 121 AVDRASNRPLEPPESEFIKQDINDNPIFPLGPHATVPMSVNGSVIQTADHADDP 180
 QY 181 SYGNSAKLVYTVLDGLPFPSVDPOTGVVRTAIPNMDRETOEFLVVIQAKDMGGMGGLS 240
 DB 181 SYGNSAKLVYTVLDGLPFPSVDPOTGVVRTAIPNMDRETOEFLVVIQAKDMGGMGGLS 240
 QY 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAOPDPLGDMALMAYSLD 300
 DB 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAOPDPLGDMALMAYSLD 300
 QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
 QY 361 VRVAVQDAPPEPPAFQAAHYHLTVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
 DB 361 VRVAVQDAPPEPPAFQAAHYHLTVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
 QY 421 CFSIQPEEGTHTTAAPLREARAWHNLTVLATELGMSWGPGRGWPLLVAEWSAPAPAPQ 480
 DB 421 CFSIQPEEGTHTTAAPLREARAWHNLTVLATELGMSWGPGRGWPLLVAEWSAPAPAPQ 480
 QY 481 RSPVGSAGVIGPQSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 540
 DB 481 RSPVGSAGVIGPQSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 540
 QY 545 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 502
 DB 545 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 502
 QY 577 HPLMASASWMLH-----WPPAERGNQAPASQ 603
 DB 577 HPLMASASWMLH-----WPPAERGNQAPASQ 603
 QY 563 QPALSTATVTVSVCRQCPDGSVASCWPEAHLSAAGISTG 602
 DB 563 QPALSTATVTVSVCRQCPDGSVASCWPEAHLSAAGISTG 602

RESULT 10

US-10-245-851-98
 Sequence 98, Application US/10245851
 Publication No. US20030068782A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Bacon, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, V. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Matembe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3630R1C93
 CURRENT APPLICATION NUMBER: US/10/245,851
 PRIOR FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/065027
 PRIOR FILING DATE: 1997-11-10
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/086478
 PRIOR FILING DATE: 1998-05-22
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090689
 PRIOR FILING DATE: 1998-06-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 116
 SEQ ID NO 98
 LENGTH: 781
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-245-851-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
 Best Local Similarity 84.8%; Pred. No. 3e-196;
 Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLILAMVIGMGMCMGRLAAPARAWAGSREHPALLRTRRSWMNQFVIEEYAGP 60
 DB 1 MMGLVRLILAMVIGMGMCMGRLAAPARAWAGSREHPALLRTRRSWMNQFVIEEYAGP 60
 QY 61 EPLVIGKIHSDVDREGRTKYLITGEGAGTVFVIDEATGNHVTSLDREERAOYVLLAQ 120
 DB 61 EPLVIGKIHSDVDREGRTKYLITGEGAGTVFVIDEATGNHVTSLDREERAOYVLLAQ 120
 QY 121 AVDRASNRPLEPPESEFIKQDINDNPIFPLGPHATVPMSVNGSVIQTADHADDP 180
 DB 121 AVDRASNRPLEPPESEFIKQDINDNPIFPLGPHATVPMSVNGSVIQTADHADDP 180
 QY 181 SYGNSAKLVYTVLDGLPFPSVDPOTGVVRTAIPNMDRETOEFLVVIQAKDMGGMGGLS 240
 DB 181 SYGNSAKLVYTVLDGLPFPSVDPOTGVVRTAIPNMDRETOEFLVVIQAKDMGGMGGLS 240
 QY 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAOPDPLGDMALMAYSLD 300
 DB 241 GSTTVTVTLSDVNDNPKFPQSLYQFSVETAGPGLVGRLAOPDPLGDMALMAYSLD 300
 QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
 DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVAS 360
 QY 361 VRVAVQDAPPEPPAFQAAHYHLTVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
 DB 361 VRVAVQDAPPEPPAFQAAHYHLTVPENKAPGTLVQGISADLDSPASPIRYSILPHSDPER 420
 QY 421 CFSIQPEEGTHTTAAPLREARAWHNLTVLATELGMSWGPGRGWPLLVAEWSAPAPAPQ 480
 DB 421 CFSIQPEEGTHTTAAPLREARAWHNLTVLATELGMSWGPGRGWPLLVAEWSAPAPAPQ 480
 QY 481 RSPVGSAGVIGPQSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 540
 DB 481 RSPVGSAGVIGPQSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 540
 QY 455 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 502
 DB 455 -----DSSAQASRVQVAIQTLIDENDNAPQALAPYDTFVCDASAPGQLIQVIRA 502

QY 541 LDRDEVNSSHVSPFGPLGPDANFTVODNRD-----LPA-----WF 576
DB 503 LDRDEVGNSSHVSPFGPLGPDANFTVODNRDGSASLLPSRPAPRPAPVPIELMDWG 562
QY 577 HPLMASASWLH-----WPPARGNQPSAQ 603
DB 563 QPALSSTATVTVSVCRCPDGSVASCPWEAHLASAAGLSTG 602

RESULT 11

US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245,883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 36-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAVLWGMCGRLLAARARAGSREHPGALRTSRSMWNOFVIEBYAGP 60
DB 1 MMGLVRLLLAVLWGMCGRLLAARARAGSREHPGALRTSRSMWNOFVIEBYAGP 60
QY 61 EPLVIGKLSVDVSGEGRITKYLITGEGAGTVFVIDEATGNIHTKSLDREKKAQVYLLAQ 120
DB 61 EPLVIGKLSVDVSGEGRITKYLITGEGAGTVFVIDEATGNIHTKSLDREKKAQVYLLAQ 120
QY 121 AVDASNRPLPEPSEFIITKODINDNRPFLPGYHATVEMNGSVQYTAHADDP 180

DB 121 AVDASNRPLPEPSEFIITKODINDNRPFLPGYHATVEMNGSVQYTAHADDP 180
QY 181 SYGNSAKIYTVLGLPFFSVDPQGVVTKTIIPMMDSETOEEELVYLQAKDMGGMGLS 240
DB 181 SYGNSAKIYTVLGLPFFSVDPQGVVTKTIIPMMDSETOEEELVYLQAKDMGGMGLS 240
QY 241 GSTTVTLVLSVDNNDPPEFPOSILYQSVETAGGTIVGRRAADPDLGDMALAAVYILD 300
DB 241 GSTTVTLVLSVDNNDPPEFPOSILYQSVETAGGTIVGRRAADPDLGDMALAAVYILD 300
QY 301 GEGSEAFSISTDLOGRDLITVRKPLDFESGRSISFVEATNTLIDAYLRGFKVYAS 360
DB 301 GEGSEAFSISTDLOGRDLITVRKPLDFESGRSISFVEATNTLIDAYLRGFKVYAS 360
QY 361 VRVAVQDAPPEPFAFTQAAVYHLLTVPENKAPGTLVQCIISAADUSPASPISILPHSPER 420
DB 361 VRVAVQDAPPEPFAFTQAAVYHLLTVPENKAPGTLVQCIISAADUSPASPISILPHSPER 420
QY 421 CFSIQPEEGTHTTAAPLDRERAMHNTLVLTATBELGMSGMPERGVPVLVWKSAPAAPQ 480
DB 421 CFSIQPEEGTHTTAAPLDRERAMHNTLVLTATBELGMSGMPERGVPVLVWKSAPAAPQ 480
QY 481 RSPVGSAGVIGIPQDSSAQSRYOVAIOTLDEVDNAPOLAEPYDTVCDSAPAGOLIIVIRA 540
DB 481 RSPVGSAGVIGIPQDSSAQSRYOVAIOTLDEVDNAPOLAEPYDTVCDSAPAGOLIIVIRA 540
QY 455 -----DSSAQASRYOVAIOTLDEVDNAPOLAEPYDTVCDSAPAGOLIIVIRA 502
DB 455 -----DSSAQASRYOVAIOTLDEVDNAPOLAEPYDTVCDSAPAGOLIIVIRA 502
QY 541 LDRDEVGNSSHVSPFGPLGPDANFTVODNRD-----LPA-----WF 576
DB 503 LDRDEVGNSSHVSPFGPLGPDANFTVODNRDGSASLLPSRPAPRPAPVPIELMDWG 562
QY 577 HPLMASASWLH-----WPPARGNQPSAQ 603
DB 563 QPALSSTATVTVSVCRCPDGSVASCPWEAHLASAAGLSTG 602

RESULT 12

US-10-237-535-98
; Sequence 98, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C3
; CURRENT APPLICATION NUMBER: US/10/237,535
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18

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Page 9

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PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-03-11
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PRIOR FILING DATE: 1999-04-01
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PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
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PRIOR FILING DATE: 2001-02-02
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PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
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PRIOR FILING DATE: 1998-11-19
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PRIOR FILING DATE: 1999-03-12
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PRIOR FILING DATE: 1999-10-18
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/872035
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PRIOR FILING DATE: 2001-08-06
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;; PRIOR APPLICATION NUMBER: 09/927796
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;; PRIOR FILING DATE: 2001-08-13
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;; PRIOR FILING DATE: 2001-08-16
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;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 10/081056
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: 10/119480
;; PRIOR FILING DATE: 2002-04-09

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MWGLVRLILAWLGWGMCGRLAPAPAMAGSREHGPALLTRRSWVMNQFVIEEYAGP 60
DB 1 MWGLVRLILAWLGWGMCGRLAPAPAMAGSREHGPALLTRRSWVMNQFVIEEYAGP 60
QY 61 EPLVIGKLSHVDGEGRTKYLITGEGAGTVFVDEATGNINHTKSLDREKQYVLLAQ 120
DB 61 EPLVIGKLSHVDGEGRTKYLITGEGAGTVFVDEATGNINHTKSLDREKQYVLLAQ 120
QY 121 AVDRASNRPLEPSEFIIKGGDINDNPPIPLGPHATVEMSNVGSVIVQVTAHADDP 180
DB 121 AVDRASNRPLEPSEFIIKGGDINDNPPIPLGPHATVEMSNVGSVIVQVTAHADDP 180
QY 181 SYGSATLKYTVVDGLTFFSVDPOTGVYRTAIPMDTEDEEPLVYIQAADMGGHGGLS 240
DB 181 SYGSATLKYTVVDGLTFFSVDPOTGVYRTAIPMDTEDEEPLVYIQAADMGGHGGLS 240
QY 241 GSTVTVTLSDVNDNPKFPQSLYQFSVETAGGTLVGLRAODPDLGNALMAYSLD 300
DB 241 GSTVTVTLSDVNDNPKFPQSLYQFSVETAGGTLVGLRAODPDLGNALMAYSLD 300
QY 301 GEGEAPASISTDLOGRGLLTVKRPDLFESQSYSPFAVETNTLIDPAYRRGPFDVVS 360
DB 301 GEGEAPASISTDLOGRGLLTVKRPDLFESQSYSPFAVETNTLIDPAYRRGPFDVVS 360
QY 361 VRVAVOAPPEPATTOAYHLTVPENKAPGTLVGOISAAALDPSAPIRYSILPHSDPER 420
DB 361 VRVAVOAPPEPATTOAYHLTVPENKAPGTLVGOISAAALDPSAPIRYSILPHSDPER 420
QY 421 CFSIQPEEGTHTAPLDRKARAHNTLVATELGMSWGERGWPVLVAEMGAPAPQ 480
DB 421 CFSIQPEEGTHTAPLDRKARAHNTLVATELGMSWGERGWPVLVAEMGAPAPQ 480
QY 481 RSPVGSANGIPQDSSAASRVQVAIOTLDENDNAPOLAEYDTEVDCSAPQOLIQVIRA 540
DB 481 RSPVGSANGIPQDSSAASRVQVAIOTLDENDNAPOLAEYDTEVDCSAPQOLIQVIRA 540
QY 455 -----DSSAASRVQVAIOTLDENDNAPOLAEYDTEVDCSAPQOLIQVIRA 502
DB 455 -----DSSAASRVQVAIOTLDENDNAPOLAEYDTEVDCSAPQOLIQVIRA 502
QY 541 LDRDEVANGSSHSFQGLPDPANFTVQDNRD-----LPA-----WF 576
DB 541 LDRDEVANGSSHSFQGLPDPANFTVQDNRD-----LPA-----WF 576
QY 503 LDRDEVANGSSHSFQGLPDPANFTVQDNRDGSASLLPFRPAPRPHAPVYIETLMDWG 562
DB 503 LDRDEVANGSSHSFQGLPDPANFTVQDNRDGSASLLPFRPAPRPHAPVYIETLMDWG 562
QY 577 HPLMASASSWTH-----WPPAREGNQPPASQ 603
DB 577 HPLMASASSWTH-----WPPAREGNQPPASQ 603
QY 563 QPALSTATVTVSVCRQPDGVSACWPEAHLAAGLSTG 602
DB 563 QPALSTATVTVSVCRQPDGVSACWPEAHLAAGLSTG 602

RESULT 13
US-10-238-183-98
; Sequence 98. Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin
;; APPLICANT: Eaton, Dan
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stephan, Jean-Philippe
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; APPLICANT: Fong, Sherman
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3630R1C11
;; CURRENT FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: 10/197942
;; PRIOR FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/059114
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/065027
;; PRIOR FILING DATE: 1997-11-10
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;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
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;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/106932
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119342
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: 60/123957
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;; PRIOR APPLICATION NUMBER: 60/123972
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PRIOR FILING DATE:	1999-07-20
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PRIOR APPLICATION NUMBER:	60/145698
PRIOR FILING DATE:	1999-07-26
PRIOR APPLICATION NUMBER:	60/146222
PRIOR FILING DATE:	1999-07-28
PRIOR APPLICATION NUMBER:	60/146833
PRIOR FILING DATE:	1999-08-03
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PRIOR FILING DATE:	1999-08-10
PRIOR APPLICATION NUMBER:	60/148513
PRIOR FILING DATE:	1999-08-12
PRIOR APPLICATION NUMBER:	60/149327
PRIOR FILING DATE:	1999-08-17
PRIOR APPLICATION NUMBER:	60/149395
PRIOR FILING DATE:	1999-08-31
PRIOR APPLICATION NUMBER:	60/150114
PRIOR FILING DATE:	1999-08-20
PRIOR APPLICATION NUMBER:	60/151700
PRIOR FILING DATE:	1999-08-31
PRIOR APPLICATION NUMBER:	60/151794
PRIOR FILING DATE:	1999-08-31
PRIOR APPLICATION NUMBER:	60/162506
PRIOR FILING DATE:	1999-10-23
PRIOR APPLICATION NUMBER:	60/170262
PRIOR FILING DATE:	1999-12-09
PRIOR APPLICATION NUMBER:	60/171718
PRIOR FILING DATE:	2000-01-20
PRIOR APPLICATION NUMBER:	60/179851
PRIOR FILING DATE:	2000-02-02
PRIOR APPLICATION NUMBER:	60/180921
PRIOR FILING DATE:	2000-02-08
PRIOR APPLICATION NUMBER:	60/187202
PRIOR FILING DATE:	2000-03-03
PRIOR APPLICATION NUMBER:	60/198587
PRIOR FILING DATE:	2000-04-18
PRIOR APPLICATION NUMBER:	60/199614
PRIOR FILING DATE:	2000-04-25
PRIOR APPLICATION NUMBER:	60/206330
PRIOR FILING DATE:	2000-05-23
PRIOR APPLICATION NUMBER:	60/206368
PRIOR FILING DATE:	2000-05-23
PRIOR APPLICATION NUMBER:	60/209832
PRIOR FILING DATE:	2000-06-05
PRIOR APPLICATION NUMBER:	60/218371
PRIOR FILING DATE:	2000-07-13
PRIOR APPLICATION NUMBER:	60/222695
PRIOR FILING DATE:	2000-08-02
PRIOR APPLICATION NUMBER:	60/229896
PRIOR FILING DATE:	2000-09-01
PRIOR APPLICATION NUMBER:	60/230621
PRIOR FILING DATE:	2000-09-05
PRIOR APPLICATION NUMBER:	60/232887
PRIOR FILING DATE:	2000-09-15
PRIOR APPLICATION NUMBER:	60/235177
PRIOR FILING DATE:	2000-09-22
PRIOR APPLICATION NUMBER:	60/261878
PRIOR FILING DATE:	2001-01-12
PRIOR APPLICATION NUMBER:	60/261910
PRIOR FILING DATE:	2001-01-16
PRIOR APPLICATION NUMBER:	60/261939
PRIOR FILING DATE:	2001-01-16
PRIOR APPLICATION NUMBER:	60/262150
PRIOR FILING DATE:	2001-01-16
PRIOR APPLICATION NUMBER:	60/264399
PRIOR FILING DATE:	2001-01-25
PRIOR APPLICATION NUMBER:	60/266422
PRIOR FILING DATE:	2001-02-02
PRIOR APPLICATION NUMBER:	60/267623

	Query Match	81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity	84.8%; Pred. No. 3e-196;	
Matches 543; Conservative	5; Mismatches 17; Indels 75; Gaps 4	
QY	1 MNGVLRLLAMVIGMGCMCGRLAAPARMAASRHHPGALLRTRRSWVWQOFVIEEYAP 60	
DB	1 MNGVLRLLAMVIGMGCMCGRLAAPARMAASRHHPGALLRTRRSWVWQOFVIEEYAP 60	
QY	61 EYVLGKSLHSVDYDRBEGTKYLLTGEASGTVFVIDEATGNVHTKSLDREERKQAYVLLAQ 120	
DB	61 EYVLGKSLHSVDYDRBEGTKYLLTGEASGTVFVIDEATGNVHTKSLDREERKQAYVLLAQ 120	
QY	121 AVDRASNPPLPEPSEFIIKGGDINDNPPIFELGPHYATVPEKSNVGTSVIQTVAHDADDP 180	
DB	121 AVDRASNPPLPEPSEFIIKGGDINDNPPIFELGPHYATVPEKSNVGTSVIQTVAHDADDP 180	
QY	181 SVGNASAKTVVTVLGLPSEFSDPDTGGVARTAINMDREIQEEFLVYIQAKMDGHHGGLS 240	
DB	181 SVGNASAKTVVTVLGLPSEFSDPDTGGVARTAINMDREIQEEFLVYIQAKMDGHHGGLS 240	
QY	241 GSTTATVTLSDVNNDNPKRFOSIVQFSVETAGBGLVGRLAQRADDELGDNALMAVSLID 300	

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Db 241 GSTTATVTLSDVNDNPKFPOSILYQFSVETAGGTLVGRADDPDLGNALMAYSLD 300
Qy 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSRYSFVEATNTLIDPAVLRGPFKDVAS 360
Db 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSRYSFVEATNTLIDPAVLRGPFKDVAS 360
Qy 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISAADLDPASPIRYSILPHSDPER 420
Db 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISAADLDPASPIRYSILPHSDPER 420
Qy 421 CFSIQPEBGTHTAAPLDREARAHNTLVLTATELGMSGPERGWPVLVAMGSAAPAPQ 480
Db 421 CFSIQPEBGTHTAAPLDREARAHNTLVLTATELGMSGPERGWPVLVAMGSAAPAPQ 480
Qy 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 540
Db 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 540
Qy 455 -----DSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 502
Db 455 -----DSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 502
Qy 541 LDRDEVGNSHVSGFQGLPDANFTVQDNRD-----LPA-----WF 576
Db 541 LDRDEVGNSHVSGFQGLPDANFTVQDNRD-----LPA-----WF 576
Qy 503 LDRDEVGNSHVSGFQGLPDANFTVQDNRDGASLLPSRPAPRRAPVLPVIELMDWG 562
Db 503 LDRDEVGNSHVSGFQGLPDANFTVQDNRDGASLLPSRPAPRRAPVLPVIELMDWG 562
Qy 577 HPLMASASWLH-----WPPARGNQOPASOG 603
Db 577 HPLMASASWLH-----WPPARGNQOPASOG 603
Qy 563 QPALSTATVTVSVRCQCPDGSVASCPWEALHLSAAGLSTG 602
Db 563 QPALSTATVTVSVRCQCPDGSVASCPWEALHLSAAGLSTG 602

RESULT 14
US-10-238-283-98
; Sequence 98, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238, 283
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98

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; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-238-283-98
Query Match
Best Local Similarity 81.8%; Score 2746.5; DB 14; Length 781;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Qy 1 MGLVRLILANLGGCGMGRILAPARAWASREHPGALLTRTSWMNOFFVEEYAGP 60
Db 1 MGLVRLILANLGGCGMGRILAPARAWASREHPGALLTRTSWMNOFFVEEYAGP 60
Qy 61 EFWLIGKLSHSDVDREGRTKYLITGEGAGTFVIDEATGNHVTXSLDREKQAYVLLAQ 120
Db 61 EFWLIGKLSHSDVDREGRTKYLITGEGAGTFVIDEATGNHVTXSLDREKQAYVLLAQ 120
Qy 121 AYDRASNPPLPPSPFFITKQDINDNPIPLFGSYHATVPMSVNGSVIQTADHDDP 180
Db 121 AYDRASNPPLPPSPFFITKQDINDNPIPLFGSYHATVPMSVNGSVIQTADHDDP 180
Qy 181 SYGNASAKLYTVDGLPFFSVDPQTGVYRTAIPNMDETQBEFLVVIQAKDMGSMGLS 240
Db 181 SYGNASAKLYTVDGLPFFSVDPQTGVYRTAIPNMDETQBEFLVVIQAKDMGSMGLS 240
Qy 241 GSTTATVTLSDVNDNPKFPOSILYQFSVETAGGTLVGRADDPDLGNALMAYSLD 300
Db 241 GSTTATVTLSDVNDNPKFPOSILYQFSVETAGGTLVGRADDPDLGNALMAYSLD 300
Qy 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSRYSFVEATNTLIDPAVLRGPFKDVAS 360
Db 301 GEGSEAFSISTDLQGRDGLTVRRKPLDFESQSRYSFVEATNTLIDPAVLRGPFKDVAS 360
Qy 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISAADLDPASPIRYSILPHSDPER 420
Db 361 VRVAVQDAPPEPPAFTQAAVHLTVPENKAPGTLVQGISAADLDPASPIRYSILPHSDPER 420
Qy 421 CFSIQPEBGTHTAAPLDREARAHNTLVLTATELGMSGPERGWPVLVAMGSAAPAPQ 480
Db 421 CFSIQPEBGTHTAAPLDREARAHNTLVLTATELGMSGPERGWPVLVAMGSAAPAPQ 480
Qy 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 540
Db 481 RSPVGSAGVIRQDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 540
Qy 455 -----DSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 502
Db 455 -----DSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCSAAGQLIQVIRA 502
Qy 541 LDRDEVGNSHVSGFQGLPDANFTVQDNRD-----LPA-----WF 576
Db 541 LDRDEVGNSHVSGFQGLPDANFTVQDNRD-----LPA-----WF 576
Qy 503 LDRDEVGNSHVSGFQGLPDANFTVQDNRDGASLLPSRPAPRRAPVLPVIELMDWG 562
Db 503 LDRDEVGNSHVSGFQGLPDANFTVQDNRDGASLLPSRPAPRRAPVLPVIELMDWG 562
Qy 577 HPLMASASWLH-----WPPARGNQOPASOG 603
Db 577 HPLMASASWLH-----WPPARGNQOPASOG 603
Qy 563 QPALSTATVTVSVRCQCPDGSVASCPWEALHLSAAGLSTG 602
Db 563 QPALSTATVTVSVRCQCPDGSVASCPWEALHLSAAGLSTG 602

RESULT 15
US-10-238-370-98
; Sequence 98, Application US/10238370
; Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME

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FILE REFERENCE: P3630R1C10
CURRENT APPLICATION NUMBER: US/10/238,370
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-238-370-98

Query Match 81.9%; Score 2746.5; DB 14; Length 781;
Best Local Similarity 84.8%; Pred. No. 3e-196;
Matches 543; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 MMGLVRLLLAWLGGWCMGRLLAAPARAWAGSRHFGPALLTRRSWVWVNFVIEEYAGP 60
DB 1 MMGLVRLLLAWLGGWCMGRLLAAPARAWAGSRHFGPALLTRRSWVWVNFVIEEYAGP 60
QY 61 EPLVIGKLSHSDVDREGEKTKYLLTGEAGTVFVIDEATGNHVTKSLDREKKAQVLLAQ 120
DB 61 EPLVIGKLSHSDVDREGEKTKYLLTGEAGTVFVIDEATGNHVTKSLDREKKAQVLLAQ 120
QY 121 AYDRASNRPLEPPSEFFIKGODINDNPPIPLGPHATVPMSNVGTSVIQVTAHDDP 180
DB 121 AYDRASNRPLEPPSEFFIKGODINDNPPIPLGPHATVPMSNVGTSVIQVTAHDDP 180
QY 181 SYGNSAKLVYTVLDGLPFFSVDPQTGVVTAIPMDRETOEEPLVVIQAKMGGMGGLS 240
DB 181 SYGNSAKLVYTVLDGLPFFSVDPQTGVVTAIPMDRETOEEPLVVIQAKMGGMGGLS 240
QY 241 GSTTVTVLSDVNDNPKFPQSLQSVETAGPGLVGRLAQDPDLGDNALMAYSLD 300
DB 241 GSTTVTVLSDVNDNPKFPQSLQSVETAGPGLVGRLAQDPDLGDNALMAYSLD 300
QY 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESORSYSFVEATNTLIDPAYLRGPFKDVAS 360
DB 301 GEGSEAFSISTDLQGRDGLTVRKPLDFESORSYSFVEATNTLIDPAYLRGPFKDVAS 360
QY 361 VRVAVQDAPEPPAFQAAVHITVPENKAPGTLVNGQISADLDDSPASPRYSILPHSDPER 420
DB 361 VRVAVQDAPEPPAFQAAVHITVPENKAPGTLVNGQISADLDDSPASPRYSILPHSDPER 420
QY 421 CFSIOPEEGTHTAAPLDREARAWNTLVATELGMSWGPBGRGWPLLVAEWSAPAAPQ 480
DB 421 CFSIOPEEGTHTAAPLDREARAWNTLVATELGMSWGPBGRGWPLLVAEWSAPAAPQ 480
QY 481 RSPVGSANGIPODSSAQSARVQVAICTLDENDNAPQLAEPYDTFVCD\$AAPGQILQVIRA 540
DB 481 RSPVGSANGIPODSSAQSARVQVAICTLDENDNAPQLAEPYDTFVCD\$AAPGQILQVIRA 540
QY 541 LDRDEVGN\$HVSFGQPLGPDANFTVQDNRD\$ASILL\$SRPAPRHAAYLVPIELMDWG 562
DB 541 LDRDEVGN\$HVSFGQPLGPDANFTVQDNRD\$ASILL\$SRPAPRHAAYLVPIELMDWG 562

Db 503 LDRDEVGN\$HVSFGQPLGPDANFTVQDNRD\$ASILL\$SRPAPRHAAYLVPIELMDWG 562
QY 577 HPLLMASASSWLH-----WPPAERGNQPASOG 603
Db 563 QPAL\$TATVTV\$VCRCQPDG\$VASC\$PBAHLSAAGL\$TG 602

Search completed: December 8, 2004, 11:34:26
Job time : 651.891 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 75.8394 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-4
Perfect score: 3354
Sequence: 1 MWGLVLLLMWLGSMGCMGR.....LPSCQLPGLPALGIYLCAS 636

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1607	47.9	693	2	US-08-738-349-6
2	1607	47.9	693	4	US-09-918-457-55
3	1607	47.9	796	2	US-08-738-349-4
4	1602	47.8	796	1	US-08-188-228-58
5	1602	47.8	796	1	US-08-332-643-52
6	1602	47.8	796	1	US-08-332-643-52
7	1602	47.8	796	4	US-09-654-328-2
8	1596	47.6	796	2	US-08-738-349-2
9	1530.5	45.6	799	1	US-08-188-228-42
10	1530.5	45.6	799	1	US-08-332-638-42
11	1529.5	45.6	793	1	US-08-188-228-54
12	1529.5	45.6	793	1	US-08-332-643-48
13	1529.5	45.6	793	1	US-08-332-638-54
14	1493	44.5	615	2	US-08-738-349-12
15	1468	43.8	532	1	US-08-188-228-44
16	1468	43.8	532	1	US-08-332-638-44
17	1365.5	40.7	794	1	US-08-188-228-60
18	1365.5	40.7	794	1	US-08-332-643-54
19	1365.5	40.7	794	1	US-08-332-638-60
20	1136.5	33.9	653	1	US-08-188-228-46
21	1136.5	33.9	653	1	US-08-332-638-46
22	938.5	28.0	780	1	US-08-188-228-50
23	938.5	28.0	780	1	US-08-332-643-44
24	938.5	28.0	780	1	US-08-332-638-50
25	596	17.8	906	4	US-09-417-039-11
26	591	17.6	913	2	US-08-474-067-6
27	591	17.6	913	2	US-08-474-068A-6

28	591	17.6	913	2	US-08-472-481-5	Sequence 5, Appli
29	586	17.5	837	2	US-08-474-067-7	Sequence 7, Appli
30	586	17.5	837	2	US-08-474-068A-7	Sequence 7, Appli
31	586	17.5	837	2	US-08-472-481-6	Sequence 6, Appli
32	580.5	17.3	555	2	US-08-453-702A-98	Sequence 98, Appli
33	576	17.2	556	1	US-07-998-003A-98	Sequence 98, Appli
34	576	17.2	556	1	US-08-453-274B-98	Sequence 98, Appli
35	576	17.2	556	1	US-08-453-274B-98	Sequence 98, Appli
36	576	17.2	556	1	US-08-268-161A-98	Sequence 98, Appli
37	576	17.2	556	3	US-09-099-639-98	Sequence 98, Appli
38	574.5	17.1	712	2	US-08-474-067-2	Sequence 2, Appli
39	574.5	17.1	712	2	US-08-474-067-5	Sequence 2, Appli
40	574.5	17.1	712	2	US-08-474-068A-2	Sequence 2, Appli
41	574.5	17.1	712	2	US-08-474-068A-5	Sequence 2, Appli
42	574.5	17.1	712	2	US-08-472-481-2	Sequence 2, Appli
43	574.5	17.1	717	2	US-08-474-067-4	Sequence 4, Appli
44	574.5	17.1	717	2	US-08-474-068A-4	Sequence 4, Appli
45	574.5	17.1	717	2	US-08-472-481-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 47.9%; Score 1607; DB 2; Length 693;
 Best Local Similarity 50.5%; Pred. No. 1.9e-134;
 Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

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QY 17 CMGSLA-----APAR-----AMAGSRB--HFGALLIRTRRSWVWNOFVIEEYAGEPEV 63
DB 13 CIGMLCHSHAPAPERRGHLRPSFGHHEKGEQGVLRQSKRGWVWNOFVIEEYTGDDPV 72
QY 64 LIGKLSHVDNDEGERTKYLITGEGAGTVFVIDEATGNHTKSLDREBKQVYLLAQAVD 123
DB 73 LVGLHSDIDSGDGNIKYILSGEGAGTIFVDDSGNHAHTKTLIDREERQYLLMAQAVD 132
QY 124 RASNPLEPPSEFFIKQDINDNPPILPGPYHATVEMSNVGTSVIQVTAHDADDPSYG 183
DB 133 RDTNRPLEPPSEFFIKQDINDNPPILPGPYHATVEMSNVGTSVIQVTAHDADDPSYG 192
QY 184 NSAKLVYTVLDGLPEFSVDPOQGVVRAIPMDRETOEFLVVIQAQDMGSHMGSLSGST 243
DB 193 NSAKLVYTVLDGLPEFSVDPOQGVVRAIPMDRETOEFLVVIQAQDMGSHMGSLSGST 252
QY 244 TVTVLSDVNDNPPKPFQSLVQFSVETAGGTLVGLRAODDPLGNALMAYSLIDGEG 303
DB 253 KVTITLTVNDNPPKPFQSLVQFSVETAGGTLVGLRAODDPLGNALMAYSLIDGEG 312
QY 304 SEAFSISTDLOGRDLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVASVRY 363
DB 313 MESFEITTDYETQEGVILKPKVPDEFETKRAVSLKVEANVHIDPKFISNGPFKDTVTVKI 372
QY 364 AVQDAPPEPAPTAQAHLTVPENKAPGLVQGISAADLSPASIRYSILPHSDPERCS 423
DB 373 AVEADDEPMPPLASVYHEVGENAAGTVGVRAKPDANSPIRYSIDRHDTLDRFT 432
QY 424 IOPEEGTHTAPLDREARAWHNTLVLTATELGMSWGERGVVPLVEMSAAPAPQSRP 483
DB 433 INPEGFIKTTPLDREBTALNITVPAEL----- 463
QY 484 VGSAGVIGPQSSAQSRYOVAIQTLDENDNAPOLAEFYDTFVDS---AAPGLIQVIR 539
DB 464 -----NHRHOEAKVPVAIRVLDVNDNAPKPAAYEGFICSDQTKPLSNQPIYIS 514
QY 540 ALDRDEVGNSSHVSFGQP--LGPDAFTVQDNRLPA-----WPHLLM 581
DB 515 ADDKDDTANGRRPFFSLPELIIHNPFTVRNDRNTAGVYARRGFSRQKODLYLPIVI 574
QY 582 ASASSWLHMPPEARGNOPASQKSSLP-CG-RLPGALPSC 620
DB 575 -----SDGIGPPMSSTNTLTITKVCQDVNGLLSC 604

```

RESULT 2
 US-09-919-497-55
 / Sequence 55, Application US/09919497
 / Patent No. 6773883
 / GENERAL INFORMATION:
 / APPLICANT: Muller, George L.
 / TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
 / FILE REFERENCE: B0801/7225
 / CURRENT APPLICATION NUMBER: US/09/919,497
 / PRIOR FILING DATE: 2001-07-31
 / PRIOR APPLICATION NUMBER: US 60/221,735
 / NUMBER OF SEQ ID NOS: 100
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 55
 / LENGTH: 693
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-919-497-55

Query Match 47.9%; Score 1607; DB 4; Length 693;
 Best Local Similarity 50.5%; Pred. No. 1.9e-134;
 Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

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QY 17 CMGSLA-----APAR-----AMAGSRB--HFGALLIRTRRSWVWNOFVIEEYAGEPEV 63
DB 13 CIGMLCHSHAPAPERRGHLRPSFGHHEKGEQGVLRQSKRGWVWNOFVIEEYTGDDPV 72
QY 64 LIGKLSHVDNDEGERTKYLITGEGAGTVFVIDEATGNHTKSLDREBKQVYLLAQAVD 123
DB 73 LVGLHSDIDSGDGNIKYILSGEGAGTIFVDDSGNHAHTKTLIDREERQYLLMAQAVD 132
QY 124 RASNPLEPPSEFFIKQDINDNPPILPGPYHATVEMSNVGTSVIQVTAHDADDPSYG 183
DB 133 RDTNRPLEPPSEFFIKQDINDNPPILPGPYHATVEMSNVGTSVIQVTAHDADDPSYG 192
QY 184 NSAKLVYTVLDGLPEFSVDPOQGVVRAIPMDRETOEFLVVIQAQDMGSHMGSLSGST 243
DB 193 NSAKLVYTVLDGLPEFSVDPOQGVVRAIPMDRETOEFLVVIQAQDMGSHMGSLSGST 252
QY 244 TVTVLSDVNDNPPKPFQSLVQFSVETAGGTLVGLRAODDPLGNALMAYSLIDGEG 303
DB 253 KVTITLTVNDNPPKPFQSLVQFSVETAGGTLVGLRAODDPLGNALMAYSLIDGEG 312
QY 304 SEAFSISTDLOGRDLTVRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVASVRY 363
DB 313 MESFEITTDYETQEGVILKPKVPDEFETKRAVSLKVEANVHIDPKFISNGPFKDTVTVKI 372
QY 364 AVQDAPPEPAPTAQAHLTVPENKAPGLVQGISAADLSPASIRYSILPHSDPERCS 423
DB 373 AVEADDEPMPPLASVYHEVGENAAGTVGVRAKPDANSPIRYSIDRHDTLDRFT 432
QY 424 IOPEEGTHTAPLDREARAWHNTLVLTATELGMSWGERGVVPLVEMSAAPAPQSRP 483
DB 433 INPEGFIKTTPLDREBTALNITVPAEL----- 463
QY 484 VGSAGVIGPQSSAQSRYOVAIQTLDENDNAPOLAEFYDTFVDS---AAPGLIQVIR 539
DB 464 -----NHRHOEAKVPVAIRVLDVNDNAPKPAAYEGFICSDQTKPLSNQPIYIS 514
QY 540 ALDRDEVGNSSHVSFGQP--LGPDAFTVQDNRLPA-----WPHLLM 581
DB 515 ADDKDDTANGRRPFFSLPELIIHNPFTVRNDRNTAGVYARRGFSRQKODLYLPIVI 574
QY 582 ASASSWLHMPPEARGNOPASQKSSLP-CG-RLPGALPSC 620
DB 575 -----SDGIGPPMSSTNTLTITKVCQDVNGLLSC 604

```

RESULT 3
 US-08-738-349-4
 / Sequence 4, Application US/08738349
 / Patent No. 5869638
 / GENERAL INFORMATION:
 / APPLICANT: Takeshita, Sunao
 / APPLICANT: Okazaki, Makoto
 / APPLICANT: Kawai, Shinji
 / APPLICANT: Tsujimura, Atsushi
 / APPLICANT: Amano, Egon
 / TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
 / TITLE OF INVENTION: Process for Its Production
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 / ADDRESSSEE: Dunner
 / STREET: 1300 I Street, N.W.
 / CITY: Washington
 / STATE: D.C.
 / COUNTRY: USA
 / ZIP: 20005-3315
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/738,349

Wed Dec 8 11:46:29 2004

us-09-788-051-4.rai

Page 3

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,435
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.123-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 47.9%; Score 1607; DB 2; Length 796;
Best Local Similarity 50.5%; Pred. No. 2,4e-134;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

17 CMGRLA-----APAR-----AMAGSRE--HGPALLRTRRSWVWVQFVIEEYAGPEPV 63
13 CLGMLCHSHAFAPRRGHLPSPFHGHEKKEQVQLQSKRGWVWVQFVIEEYAGPEPV 72
64 LIGLHSHVDSGEGRTKYLITGEGAGTVFIDEATNGNIHVTKSLDREKAQVYLLAAVD 123
73 LVGRHSHDIDSGDNKIKYILSGGAGTIFVIDKSGNIHATKTLDEEKAQVYLLAAVD 132
124 RASNRPLEPSEPFITIKGODINDNPIPLGPHYATVEMSNVGTSVIQTAAHDADPSYG 183
133 RDTNRPLEPSEPFITIKGODINDNPIPLGPHYATVEMSNVGTSVIQTAAHDADPSYG 192
184 NSAKLYTVVLDGLPFPSVDPQTGVVRLIENMDRETOEFLVYIQAKDGMGNGSLGSGT 243
193 NSAKLYVSLIEGQPYFVEAQTVGIRLALPMDRAKEEYHVYIQAKDGMGNGSLGSGT 252
244 TVVTLSDVNDNPPKPFPOSIVYFVETAGPGLVGRLLRADPDLDGNALMAVSIIDGEG 303
253 KVTITLTDVNDNPPKPFPOSIVYFVETAGPGLVGRLLRADPDLDGNALMAVSIIDGEG 312
304 SEAFSISTDLQGRDGLTVRKPLDFESQSYSFVEATNTLIDPAYLRGPFQVAVSYRV 363
313 MESFEITTDYETOEGVILKKKVPDEFETKRAVSLKYEANVHIDPFISNGPFQVAVSYRV 372
364 AVQDAPEPPAFQQAAYHLTVPENKAPGLVGOISAADLSPASPIRYSIILHSPERCS 423
373 AVEADDEBPWFAPSYIHEVQENAAAGTVGRVNAKDDAANSPRIYSIDHTDLDRFT 432
424 IQPEEGITHYAPLDRERAMNLTVLATELGMSWGPGRVPLLVAMSAAPAPQSRP 483
433 INPEDGFIKTKPLDREFTAMNITVFAAEI----- 463
464 VASAVGISTQDSSAQSRVQVALQITIDENDMAFQALPEYDTFYCDS---AAPGOLIQVIR 539
464 HNHQAKVPAVALRVLDVNDNAKFAAPAYEGFLCESDQTKPLSNQPIVITIS 514
540 ALDRBEGNSSHVSFGP--LGPDAFTVQDNRLPA-----MFPLLM 581
515 ADDKODTANGPRFISLPEIILHNPNFTVRDNRDTAGVYARAGGFSROKQDLYLLPIVI 574
582 ASASSWLHPAPABRGVQAPASQGSLLP--CG--RLTGALPSC 620
575 -----SDGGIPFMSSTNTLTIKVCGDVGALLSC 604

RESULT 4
US-08-188-228-58

Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Seare Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 47.8%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 6,6e-134;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

17 CMGRLA-----APAR-----AMAGSRE--HGPALLRTRRSWVWVQFVIEEYAGPEPV 63
13 CLGMLCHSHAFAPRRGHLPSPFHGHEKKEQVQLQSKRGWVWVQFVIEEYAGPEPV 72
64 LIGLHSHVDSGEGRTKYLITGEGAGTVFIDEATNGNIHVTKSLDREKAQVYLLAAVD 123
73 LVGRHSHDIDSGDNKIKYILSGGAGTIFVIDKSGNIHATKTLDEEKAQVYLLAAVD 132
124 RASNRPLEPSEPFITIKGODINDNPIPLGPHYATVEMSNVGTSVIQTAAHDADPSYG 183
133 RDTNRPLEPSEPFITIKGODINDNPIPLGPHYATVEMSNVGTSVIQTAAHDADPSYG 192
184 NSAKLYTVVLDGLPFPSVDPQTGVVRLIENMDRETOEFLVYIQAKDGMGNGSLGSGT 243
193 NSAKLYVSLIEGQPYFVEAQTVGIRLALPMDRAKEEYHVYIQAKDGMGNGSLGSGT 252
244 TVVTLSDVNDNPPKPFPOSIVYFVETAGPGLVGRLLRADPDLDGNALMAVSIIDGEG 303
253 KVTITLTDVNDNPPKPFPOSIVYFVETAGPGLVGRLLRADPDLDGNALMAVSIIDGEG 312
304 SEAFSISTDLQGRDGLTVRKPLDFESQSYSFVEATNTLIDPAYLRGPFQVAVSYRV 363
313 MESFEITTDYETOEGVILKKKVPDEFETKRAVSLKYEANVHIDPFISNGPFQVAVSYRV 372

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QY 364 AVODAPPEPATQAAHYLTVPEKKAAGTVGOISAAIDLSPASPRYSILTHSPDECFS 4223
Db 373 SVEDADEPMLASLYIHEVOEAAAGTVGKVHADPDANSPLRYSIDHHTLDNFT 4322
QY 424 IQPEEGITHAPLDREARAHNLTVLATELGMSWGPKEGWVPLVAEWSAPAPQORSP 483
Db 433 INPEDEGFIKTKPLDREETAMLNITVFAAEI ----- 463
QY 484 VGSANVG:POSSASASRYCAIOTLDENNAQLAEPYDTFYCDS-----AARQLIYIR 539
Db 484 -----HNRHOAQVPVAIRVLVDNNAPFAFPABYBGFICSDQTKPLSNPIVTIS 514
QY 540 ALRDEWGNSSHVSFOGP--LGPDANFTVQDNRLPA-----WFHDLML 581
Db 545 ADDXDDTANGRRFIFSLPEPIIHNPFTYRDNRDVTAGVYARGGFSNQXDLILVI 574
QY 582 ASASWMLWPEARNGNPASQGSSSLP-CG-RLGALPSC 620
Db 575 -----SDGGLPMSNTNLTITKVGCDVNGALLSC 604

RESULT 5
US-08-332-643-52
/ Sequence 52 Application US/08332643
/ Patent No.5639634
/ GENERAL INFORMATION:
/ APPLICANT: Suzuki, Shintaro
/ TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
/ NUMBER OF SEQUENCES: 56
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/352,643
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/872,643
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5639634and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/30795
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ. ID NO: 52:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 796 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-332-643-52

Query Match 47.8%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No.6.6e-134;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

17 CMGRLA-----APAR-----AWAGSRG--HGGPALLRTSRWVWVNOFFVTEBYAGPEPV 63
Db 13 CIGMLTCHSHAFPERGRGHLPSPFHGHHKKGEGVLORSKRGWVWNOFFVTEBYTGDDPV 72

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QY      64  LIGLHSDVDRGSGRRKTYLLTGGGAGTVYDAEANGNHHWTKSLIDREBKQVYLLAAVD  123
       73  LVGLHSDIDISGQGNKTYLLSGGAGTTFYDDSGNTHAKTYLLDREBRAGTYLLMAQAVD  122
QY      124  FASNRPLEPPESEFIIRKODINDNPFLPGLGFHATVPEMSVNGSVIOWTNAHADDBSYG  163
       133  RDTNRPLEPPESEFIVKODINDNPFFLHETVHAVPERSNVGTSVIOVTASDADDPYTG  192
QY      184  NSALVYTVYDGLPFPSVDPOTVYRTRAPMNDRETOEEFLVYIOADMGGHCGISGST  243
       193  NSALVYVSIIEGPPYSVEAQGTIRTAIPMNDRAKEHYVYIOADMGGHCGISGTT  252
QY      244  TVTVYVTSVDNNDPKFPQSLYQFSVYETAGPGLVGRUAPDPLDGNALMAVSYILDGEG  303
       253  KVTITLTDVNDNPKFPQRLYQMSVSEAAVPGEEVGRVKAKDPIDGENGLVTVYVNDGCG  312
QY      304  SEAFSISTDLQGGDGLLTVTRKPLDEESQASVSRFHEATNTLIDPAYLRGPFQDVASYRV  363
       313  MSESLEITDETDEOEGYIKKKKPVDETEBAVSLKVEANVHIDKFTISNGPFDOTVYVKI  372
QY      364  AVODAPEPAFPTOAAHYLTVPENKAPGTLVQIOISAADLDSPASPIRYSILPHSDPERCFG  423
       373  SVEADDEPFWFLAPSYIHEVGENAAAGTVYGRVHAKDPDANSPIRYSIDRHTDLDRFFY  432
QY      424  IOPEEGITHTAALDEEAAMNLTVLTATLGMSGMBGRGVPLLVAMSAAPAPQORS  483
       433  INPDGKITKTKPLDEETAMTNTVFAAEI----- 463
QY      484  VGSAVGIPODSSAQSARVQVAIQTDENDNAPOLAEPYDTFVCDSS---AAPQLIQVIR  539
       464  -----HNRIQEAQVVALRVLDVNDMAPKFAAPYEGTICSSDOTKRLSNQIVTIS  514
QY      540  ALRDEYGVSSSHVSPGCP--LQPDANFTVQDNRLPA-----WHPILKM  581
       515  ADKCDJTAGPREFITSLPEEIIHNNTFRNRNNTNGVYARRGFSROKODLYLLPIVI  574
QY      582  ASASSWLMHPPARERGQNPASQGSSSLP-CG-RLPGALPSC  620
       575  -----SDGGIPMSSNTTLTIRVCCGVNGALLSC  604

RESULT 6
US-08-332-638-58
; Sequence 58, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```


APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match 47.6%; Score 1596; DB 2; Length 796;
Best Local Similarity 50.7%; Pred. No. 2.3e-133;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;

31 SREHP-----GPAIIKTRRSWVNOFVIEEYAGPEVLLGKLSHDVDRGGRKT 79
29 SHLPSPFHGHEKKEQVLOKSSRGVWVNOFVIEEYGPDPVLGRLHSDIDSGDNI 88
80 KYLLTGEAGTVEVIDEATGNIHYTKSLDREKAQYVLLAQAVDRASNPLEPSPFFIK 139
89 KYLSGEGAGTIFVIDKSGNIHATKTLDBEREAQYTLMAQAVDRDTRNRLPEPSPFFIK 148
140 GQDINDNPPIFLPGPHATVPEMSNVGTSVIQTADADDPSSGNSAKLYTVLDELPPF 199
149 VQDINDNPPEFLHEIYANPERSNVGTSVIQTASDADPTGNSAKLYVSIIEQPYF 208
200 SVDPQGTGVRITAIENMDRETOEEFLVYIAKMGKMGSGSTTVTLTSDVNDPPKF 259
209 SVENQGTGITITALEPMOREAKEEYHYIAKMGKMGSGSTTKTITLTDVNDPPKF 268
260 POSTLYQPSVETAGPGLVLRRAQDDPLGDNALMAVSIIDGSGSAFSITDLOGRDL 319
269 POSTYQMSVSEBAAPGEVEGRVAKCPDIDENGILVYNIYIDGSGIILFEITDYEYQDGV 328
320 LTYAKPLDPSQSSYSFRVEATNTLLIDPAVLRGPFDDVASVAVQADAPPEPAFQAAV 379
329 VKLKKPVDFTKRAYSIKIPAAVHIDPKFISNGPKDITVYKISVEDADEPMTLAPSY 388
380 HLTVPENKAPGTLVGQISAADLSPASPIRYSILPSPDPCPSIQPEGTHITAAFLDR 439
389 IHEVOENAAAGTAVGVHAPDPAANSPIRYSIDRHTDLDRPFTINPEDEGFIKTKPLDR 448

440 EAWAHNLTVALTELQMSWGPBGRWVPLVAEMSAFAPQPSVGAIGIPDSSAQAS 499
445 EETAMLNISVPAEL-----HNRQET 470
500 RVOVALIQLDENDNAPQIAEPYDFVCSAAP---GQLIYIRALDRDEVGSSHWSEQ 555
471 KVPVIRVLDVNDNAPKPAAPYEGFICSDHPKALSNQPIYVADDDDTANGRFIFS 530
556 GP--LGPDPANFTVQDNRLLPA-----WFHPLMASASWHLWPAEIGN 597
531 LPPEIMHNPFTVRNDRNTAGVARRGGFBRKODFVLDIVL-----SDGI 579
598 QPASQKSSSLP-CG-RLPGALPSC 620
580 PMSSTNLTITIKVCCGVNALLSC 604

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 45.6%; Score 1530.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 1.6e-127;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;

33 LLRTRSWVNOFVIEEYAGPEVLLGKLSHDVDRGGRKTYLLTGEAGTVEVIDEAT 98
56 LNRSGRGVWVNOFVLEFSGPPIIVGRHTDLPSSKKIKYLSGAGTIFINDIT 115
99 GNHYTKSLDREKAQYVLLAQAVDRASNPLEPSPFFIIKQDINDNPPIFLPGPHAT 158

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Db 116 GDHAIKRLDREKAEYTLTQAQVDMETNKELEPSEFIITKQVDDINDNAPEFLNGPHAT 175
QY 159 VPEMSNVGTSVYQVTAHDADDPSSYNSAKLYVTVLDGLPEFSVDPQGTGVRTAIPNMORE 218
Db 176 VPEMSILGTSVNTATADDDPVYNSAKLYVSILEGQYFSEIPEETAIKTALPNMDRE 235
QY 219 TQEEFLVYVIAQKMGHNGSGSTVYTVLSDVNDNPKPEPQSLYQFSVETAGPQTV 278
Db 236 AKEEYLVVIAQKMGHSGSGSLGTTTLVTLVDVNDNPKFAQSLYHFSVPEDEVLTGTAI 295
QY 279 GRLEADPDLGDNALMAYSIIDGEGSEAFSISTDLQGRDGLTVRKPLDFESQSYSPRV 338
Db 296 GRVANDQDIGNAOSYDIIIDGDTALFEITSDAQADGVIRLRKPLDEFETKSYTLKV 355
QY 339 EATNTLIDPAYLRGPFEDVASVAVANQDAPPEPAFTQAAYHLTVPENKAPGLTVQISA 398
Db 356 EAANHIDIPRFGSGRPFEDTATVKIYVEDADEPEVFSPTYLEHENAALNSYIGQVTA 415
QY 399 ADLSPASPIRYSILPHSDPERCFISOEEGTHTAAPLDREARAHNLTVLATELGMSW 458
Db 416 RDPDITSSPIRFSIDRHTDLERQFNINADGKITLATPLDRELSSWHNISIATETL 471
QY 459 GPERGWVPLVAVMSAPAPQSPVGSVAVGIPODSSAQASRYQVAIQTLDENNDAPOLA 518
Db 472 -----LPMWFLPLMASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 518
QY 519 ERYDTFVCDASAPGQLIOVIRALDRDEVGNSSHVSGPLGPD-----ANFTVQDNRD 571
Db 498 SEYEAFLECNKPGQVITQVSAMDKDPKNGHP--FLYSLLPEVNNPNFTIKKEDNLS 555
QY 572 -----LPMWFLPLMASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 616
Db 556 SIKXNGFNROKQOEYVLLPIV-----SDSGNPPLSTSTLTIRVCGCSNDGV 604
QY 617 LPSCQ-----LPLGT---PALGIYVC 634
Db 605 VQSCNVEAYVLPGLSMGALIALIAC 630

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RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302

```

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REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42
Query Match 45.6%; Score 1530.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 1.6e-127;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;
QY 39 LIRTRSWVWVNFVYIEYVAGPEVYLGKLSVDVDRGEGRTKYLITGBAGTVFVYIDAT 98
Db 56 LIRSKKGWVWVNFVYIEYVAGPEVYLGKLSVDVDRGEGRTKYLITGBAGTVFVYIDAT 115
QY 99 GNHVTKSLDREKAEYTLTQAQVDMETNKELEPSEFIITKQVDDINDNAPEFLNGPHAT 158
Db 116 GDHAIKRLDREKAEYTLTQAQVDMETNKELEPSEFIITKQVDDINDNAPEFLNGPHAT 175
QY 159 VPEMSNVGTSVYQVTAHDADDPSSYNSAKLYVTVLDGLPEFSVDPQGTGVRTAIPNMORE 218
Db 176 VPEMSILGTSVNTATADDDPVYNSAKLYVSILEGQYFSEIPEETAIKTALPNMDRE 235
QY 219 TQEEFLVYVIAQKMGHNGSGSTVYTVLSDVNDNPKPEPQSLYQFSVETAGPQTV 278
Db 236 AKEEYLVVIAQKMGHSGSGSLGTTTLVTLVDVNDNPKFAQSLYHFSVPEDEVLTGTAI 295
QY 279 GRLEADPDLGDNALMAYSIIDGEGSEAFSISTDLQGRDGLTVRKPLDFESQSYSPRV 338
Db 296 GRVANDQDIGNAOSYDIIIDGDTALFEITSDAQADGVIRLRKPLDEFETKSYTLKV 355
QY 339 EATNTLIDPAYLRGPFEDVASVAVANQDAPPEPAFTQAAYHLTVPENKAPGLTVQISA 398
Db 356 EAANHIDIPRFGSGRPFEDTATVKIYVEDADEPEVFSPTYLEHENAALNSYIGQVTA 415
QY 399 ADLSPASPIRYSILPHSDPERCFISOEEGTHTAAPLDREARAHNLTVLATELGMSW 458
Db 416 RDPDITSSPIRFSIDRHTDLERQFNINADGKITLATPLDRELSSWHNISIATETL 471
QY 459 GPERGWVPLVAVMSAPAPQSPVGSVAVGIPODSSAQASRYQVAIQTLDENNDAPOLA 518
Db 472 -----LPMWFLPLMASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 518
QY 519 ERYDTFVCDASAPGQLIOVIRALDRDEVGNSSHVSGPLGPD-----ANFTVQDNRD 571
Db 498 SEYEAFLECNKPGQVITQVSAMDKDPKNGHP--FLYSLLPEVNNPNFTIKKEDNLS 555
QY 572 -----LPMWFLPLMASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 616
Db 556 SIKXNGFNROKQOEYVLLPIV-----SDSGNPPLSTSTLTIRVCGCSNDGV 604
QY 617 LPSCQ-----LPLGT---PALGIYVC 634
Db 605 VQSCNVEAYVLPGLSMGALIALIAC 630

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RESULT 11
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
Borun

```

```

/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/188,228
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/049,460
/ FILING DATE: 19 APR 1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/872,643
/ FILING DATE: 17 APR 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 559725and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31340
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 793 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-188-228-54

```

```

Query Match 45.6%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 1.9e-127;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 39 LILTRRSVMNQPFVIEEYAGPEPVLLIGKLSHSDVDRGEGRTKYLITGEGAGTVFIDEAT 98
DB 49 LNRKRGVMNQMFVLEFSGPEPILVGRHTDLDPSGSKIKYILSDGAGTIFQINDVT 108
QY 99 GNHVTSLDREKQAVVLLAQAVDRASNRPLEPPSEFIKQDINDNPIFPLGPHAT 158
DB 109 GDHAIKRLDREKAEVYLLTAQAVDMETSKPLPPSEFIKQDINDNAPFELNGPYHAT 168
QY 159 VPENSVGTSVIQTVAHDADDPSTYNSAKLVYTVLDGLPFSVDPQTVGVRTAIPMDRE 218
DB 169 VPENSIIGTSTVNTATADDDPYGNSAKLVYSLBGPYFSLPEPTAIKTLAPMDRE 228
QY 219 TQSEFLVVIQAKMGHNGVLSGSTVTVTLSDVNDNPPKPSLYQFSVETAGGTLV 278
DB 229 AKSEYLVVIOAKMGHSGSLSGTTLTVTLTVNDNPPKFAQSLYHFSVEDVVLGTAI 288
QY 279 GRLRAQPDLDGNALMAYSLIDGSGEAFSITDLOGRDLVLRPELDFESQRSFV 338
DB 289 GRVANDODIGENAKOSSYDILIDGDTALFEITSDAQODITILKRLPLDETSTYLLR 348
QY 339 EATNTLIDPAYLRGPKDYAVRVAVQDAPEPPAFTQAAYHLLVDEKRAFGTLVQOISA 398
DB 349 EAANVHIDPFRSGGPKDTATKIVIEDADEPPVSSPYLLLEVENAALNSIQVTA 408
QY 399 ADDSPASPIRYSITLPSDPERCESTOPEEGTIHTMAPIIDREARAHNTLVATLGMRW 458
DB 409 RDPDITSSPIRFSIDRTDLERQNTINADGKTLTLPDLRELSVHNHTITATEI--- 464
QY 459 GPERGWVLLVWMSAPAPORSVPGSAVGIPODSQAQSRVQVAIQTLIDENDAPQLA 518
DB 465 -----RHNSQISRPVAILKVLVDNANPBA 490
QY 519 EPYDTFVCSAARQGLIQTVAIRALDRDEVGNSHVSQGPGLPD---ANFTQDNDR--- 571

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DB 491 SEYAFLENGKPGVITQTVASMDKDPKNGHY--FLYSLLEPMVNNPFIKKNEDSL 548
QY 572 -----LPAWHPPLMASASSMLWHPAERGNOQASQKSSSL-PCG-RLPGA 616
DB 549 SIILAKNGFNROKQEVYLLPITII-----SDSGNPPLSSTSTLIRVCCGSDNGV 597
QY 617 LPSCQ-----LPFGI---PALGIYLC 634
DB 598 VQSCNVEAVLPIGLSMGALLITAILAC 623

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RESULT 12
US-08-332-643-48
/ Sequence 48, Application US/08332643
/ Patent No. 5639634
/ GENERAL INFORMATION:
/ APPLICANT: Suzuki, Shintaro
/ TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
/ NUMBER OF SEQUENCES: 56
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
/ STREET: Two First National Plaza, 20 South Clark
/ STREET: Street
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/332,643
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/872,643
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5639634and, Greta E.
/ REFERENCE/DOCKET NUMBER: 27866/30795
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 793 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-332-643-48

```

```

Query Match 45.6%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 1.9e-127;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 39 LILTRRSVMNQPFVIEEYAGPEPVLLIGKLSHSDVDRGEGRTKYLITGEGAGTVFIDEAT 98
DB 49 LNRKRGVMNQMFVLEFSGPEPILVGRHTDLDPSGSKIKYILSDGAGTIFQINDVT 108
QY 99 GNHVTSLDREKQAVVLLAQAVDRASNRPLEPPSEFIKQDINDNPIFPLGPHAT 158
DB 109 GDHAIKRLDREKAEVYLLTAQAVDMETSKPLPPSEFIKQDINDNAPFELNGPYHAT 168
QY 159 VPENSVGTSVIQTVAHDADDPSTYNSAKLVYTVLDGLPFSVDPQTVGVRTAIPMDRE 218
DB 169 VPENSIIGTSTVNTATADDDPYGNSAKLVYSLBGPYFSLPEPTAIKTLAPMDRE 228

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QY 21 TOEEFLVIAKMGHMGMSLGSSTVTVTLSDVNNDNPKPQOSLYQPSVETLPGTLV 278
Db 229 AKSEYLVVIAKMGHSGSLGSLTTLTVTLTDVNDNPKPQOSLYHVSVEDEVLTGTAI 268
QY 279 GRLEADPDLGDNALMAYSILDGESEAFSISTDLQGRDGLTVRKPLDFESQRSYFRV 338
Db 289 GRVYANDQDQIGENAOQSYYDIDGDDGTALFEITSDAQODGIIIRLKKPLDFETKKSYYTLKD 348
QY 339 EANTTLIDPVLARSGEKVAVSRVAVODAPPEPAFTQAAVHLTVENKAGTLVGOISA 398
Db 349 EAAVHIDDFESGRGPKDTATKIVEDADBPVFSSTYLLVEHENAALNSVIGQVTA 408
QY 399 ADLDPSPAPRYSILPHSDPERCFCSIQPEEGTHTAPLDRPARAMHVLVATELGMSW 458
Db 409 RDPDITSSPIRFSIDHTDLERQFNINADQKITLATPLDRLSVMHNITITATEI---- 464
QY 459 GPERGWVPLVAEMASAPAPRQKSPVGSAGVIGPOSSAQASVQVATIGTLDENNAQOLA 518
Db 465 -----RHSQISISVPALIKVLVDNNAPEFA 490
QY 519 EPYDTVCDSAPAGOLIQVIALDRDEVGNSSHSVFOGPIGPD-----ANFTVQDNRD-- 578
Db 491 SEYBAFCEHKGKQGVQIVYASADKDDPKNGHY--FLYSLDPEMNNNNFIIKXNEDNSL 548
QY 572 -----LPWFHPLMASASMLWHPPARERGNQPASQKSSSL-PCG-RUPGA 618
Db 549 SIILAKNGFNRKQOEVLPLFIIL-----SPSGNPPILSSTLTIIRVCGCSNDGV 597
QY 617 LPSCQ-----LPLGI---PALGI-VLC 634
Db 598 VQSCNVEAVVPLTGLSKGALIALIILAC 623

RESULT 13
US-08-332-638--54
; Sequence 54, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:

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:      LENGTH: 793 amino acids
:      TYPE: amino acid
:      TOPOLOGY: 1linear
:      MOLECULE TYPE: protein
US-08-332-638-54

Query Match          45.6%; Score 1529.5; DB 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 1.9e-127;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9

QY      39  L L R T R S W M N P F I E E X A G P E P V L L G K L H S D V D E E G T K Y L L L G E G A G T F V I D E A T
      49  L N R S K G W M N M F L E E S G P E P L V G R L H T D L D P E S K K I K I L S G D G G I T F Q I N D V T
QY      99  G N I H W T S L D R E E K A Q Y V L L A Q A V D R A S N P L E P E S F I I K G D I N D N P I P L G E Y A T
      109  G D I H A I K L R D R E K A E Y L T L T A Q A D W E I S K R L E P S E F I I K V G D I N D N A P E F L N G Y A T
QY      159  V P E M S V G T S V I Q V T A H A D D P S I G N S A K L Y T V L D L P F F S V D P Q T G V R T A I P M D E
      169  V P M S I T G T S V N V A T D A D P V Y G N S A K L Y S I L E Q P F S L E P F A I I K T A L P M D E
QY      219  T O E F I V I V I Q A D M G A H G G L S G S T T V V T L S V N D N P P K F P Q S I Y O F S V E T A G P T I V
      229  A K E Y I V I V I Q A D M G H G S G L S G T L T L V I L T D V N D N P P K F A S I V H F S V P E V I V G T A I
QY      279  G R L R A D P L G N A L M A Y S I I D G E S E A F S I S T D L G R D G L L V R K P L D E S O R S I S F R V
      289  G R Y K A D O D I G E N A O S S Y D I I D G T A L F E I T S D A Q A D G I I R K R P L D F E T K S Y T L D
QY      339  E A N T L I D A Y L I R G P E F D V A S V R A V G D A P E P A F Q A A Y H L T P E N K A P G T L V Q I S A
      349  E A A N V H I D R F S G R G P F O D T A T V K I V A E D A E P F E S S P T Y L L E V H E N A L N S I V Q V T A
QY      399  A D D S P A S E I R S I L P H S D P E R C F S I O P E B G T I H T A P L D R E A R W N L T V L A T E L G S W N
      409  R D P D I T S P I R S I D R H T D L E R Q F I N A D D K I T L A P L P R E L S W M I N I I T A E I
QY      459  G P E R G W P L L V A E K S A P A P P O R S V G S A V G I P O D S S A Q S R V A I Q T L D E D N A P O L A
      465  -----
QY      519  E P Y D T F V C S A A P G O L I C V I R A L D E D E V G N S H V S F G G L P D ----- A N F V O D N D -----
      491  S E Y E A L C E N G R P G V I T Q V S A M D D P K N G H Y - F L Y S L L P E M V N N P N T I I K N E N S L
QY      572  ----- L P A W F H P L I M A S A S S W L H M P P A E R G N O P A S G K S S L P G C - R L F G A
      549  S I L A K N G F R K O K E V Y L L P I I I ----- S D S G N P L S T S T L T I R V C G S C S N D V
QY      617  L P S C Q ----- L P L G I ----- P A L G I V A C 634
      598  V O S C N V E A Y V L I G L S M G A L I A I L A C 623
      597

RESULT 14
US-08-738-349-12
; Sequence 12; Application US/08738349
; Patent No. 5863638
; GENERAL INFORMATION:
; APPLICANT: Takeshita, Sunao
; APPLICANT: Okazaki, Makoto
; APPLICANT: Kawai, Shinji
; APPLICANT: Tsujimura, Atsushi
; APPLICANT: Amano, Egon
; TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
; TITLE OF INVENTION: Process for Its Production
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington

```

```

/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/738,349
/ FILING DATE: 25-OCT-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/364,439
/ FILING DATE:
/ APPLICATION NUMBER: US 08/112,061
/ FILING DATE: 26-AUG-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Barker, M. P.
/ REGISTRATION NUMBER: 32,013
/ REFERENCE/DOCKET NUMBER: 02481.1323-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 615 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-738-349-12

Query Match          44.5%; Score 1493; DB 2; Length 615;
Best Local Similarity 50.9%; Pred. No. 2,3e-124;
Matches 308; Conservative 92; Mismatches 123; Indels 82; Gaps 15;

Cy 36 GALLRRSRVWVNOQFVIEBYAGPEPVLLGKLSHDVDRGEGRTKYLITGEGAGTVFVID 95
Db 39 GQVLRSGRGVWVNOQFVIEBYETTPDPVLRGLHSDIDSGDNKITLSEGGGTVFVID 98
Cy 96 EATGNIHVTKSLDEEKAQVYLLAQAVRASNRPLEPSPFFIIKGGDINDNPIPLGPY 155
Db 99 DKSNGIHATKTLDEEKAQVYLLAQAVRDTNRPLEPSPFFIYKVDINDNPIPLGPY 157
Cy 156 HATVPKSNVGTSTVQYTAHDADDPSSYNSAKLVYTVLDLPFSVDPOGVVRAIPLMK 215
Db 158 HANVPKSNVGTSTVQYTAHDADDPYTGNSAKLVYSLBQPFYSVAQGIIRLALPNM 217
Cy 216 DRETQSEFLVVIQAKMGHNGLSGSTVTVTLSDVNDNPKPFPOSLYQFSVETAGCG 275
Db 218 DRAKEEYHVYIQAQKMGHNGLSGSTTVTLTLTDVNDNPKPFPOSVQ-SVSEAIVG 276
Cy 276 TLVGRLAQDPDLGDMALMAVSLIDGSEAFSTLDLQGRDLIVRKPLDRESQRTS 335
Db 277 BEVGRVAKDPDIDENGLVTYINIVDGDG--FEITTDYETQG--VKLKKPVDDETRAYS 332
Cy 336 FRVEATNTLLDPATLRGPFKDVAVAVQADAPPAFTQAAVHLTVENKAPGTLVGO 395
Db 333 LK-EAANVHIDPKRISNGPFKDTVTYKL-VEDADEPMTFLAPYIHEVQENAAAGTVGR 390
Cy 396 ISAADLDSAPSPRIYSLPHSDPERGCSIQPEEGTHTTAAPLDREAPAMNLTVALTEIG 455
Db 391 VHAQDPDPAANSPIRYSIDRHTDLDRFETINPDEGFIKTKPLDREETAMINI-VFAAEI- 448
Cy 456 MSWGPBGMVPLVAEWSADPAAPQSPVSAVGIPQDSSAQASRQVAVIQLTDEMDNP 515
Db 449 -----HNRQEKVPAIRIVLDVNDNP 470
Cy 516 QLAEPYDTVCDSAPGQLIQVIRALDRDEVGNSSHVSPQGIPLPD---ANFTVQDNRL 572
Db 471 KFAAPYEGFICSDKLSNQ-PIVTSADDDDDTANGPFIISLP--PEIHNPNFTVRNDRN 527
Cy 573 PA-----WFHPLMASASSWLHWPAERNGQPAQSQKSSLP-CG-RLPG 615

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Db 528 TAGVYARRGFSRQKQDYLLPVI-----SDGIRPMSTNTLITKVGCGDVNG 576
Cy 616 ALPSC 620
Db 577 ALLSC 581

RESULT 15
US-08-188-228-44
/ Sequence 44, Application US/08188228
/ Patent No. 5597725
/ GENERAL INFORMATION:
/ APPLICANT: Suzuki, Shintaro
/ TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
/ NUMBER OF SEQUENCES: 62
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/188,228
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/049,460
/ FILING DATE: 19 APR 1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/872,643
/ FILING DATE: 17 APR 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5597725and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31340
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELER: 25-3856
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 532 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-188-228-44

Query Match          43.8%; Score 1468; DB 1; Length 532;
Best Local Similarity 54.6%; Pred. No. 3,1e-122;
Matches 271; Conservative 89; Mismatches 98; Indels 38; Gaps 1;

Cy 39 LLRTSRVWVNOQFVIEBYAGPEPVLLGKLSHDVDRGEGRTKYLITGEGAGTVFVID 98
Db 56 LNRSGRGVWVNOQFVIEBFSGPPIILVGRHTDLPSSKIKITLSDGAGTIFQINDIT 115
Cy 99 GNHVTKSLDEEKAQVYLLAQAVRASNRPLEPSPFFIIKGGDINDNPIPLGPYHAT 156
Db 116 GDHAIKRLDEEKAETLLNQAQVDMETNRPLEPSPFFIIKVDINDNAPFLNGPYHAT 175
Cy 159 VPKSNVGTSTVQYTAHDADDPSSYNSAKLVYTVLDLPFSVDPOGVVRAIPLMK 218
Db 176 VPKSNVGTSTVQYTAHDADDPYTGNSAKLVYSLBQPFYSVAQGIIRLALPNM 235
Cy 219 TQSEFLVVIQAKMGHNGLSGSTVTVTLSDVNDNPKPFPOSLYQFSVETAGCGTV 278

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Db 236 AKEEYLVIQAVDMGSHSGLSGTTTLTVTLTDVNDNPPKFAQSLYHFSVPEDEVLTGTAI 295
Qy 279 GRLAODPPLGDNALMAYSIIDEGSEAFSISTDLOGRDGLTVKRPIDPFESORSYSPRV 338
Db 296 GRVXANDODIGENAOSSYDIIDGGTALFEITSDAOQDGYIRLKPIDFETKSYTLKV 355
Qy 339 EATNTLIDPAYLRGPFKDVASVRVAVODAPPEPAFTAAYHLTVPENKAPGTLVGQISA 398
Db 356 EANATHIDPRFSGRGPFDATATVKIIVEDADEPPVFSSPTYLLEVENAALNSVIGQVTA 415
Qy 399 ADLDSAPSPIRYSILPHSDPERCFISIOPEEGTHTAAPLDREARAHNLTVLATELGSMW 458
Db 416 RDPDITSSPIRFSIDRHIDLERQFNINADGKITLATPDLRELSVWHNISITATEI---- 471
Qy 459 GPERGMVPLLVAMWSAPAPQORSFVGSVAGIPQDSAOASRVQYAIOTLDENDNAPOLA 518
Db 472 -----RNHSQISRVPAIKVLVDNDNAPPEFA 497
Qy 519 EPYDTFVCDASAPQOL 534
Db 498 SEYEAFLENGKPGQV 513
```

Search completed: December 8, 2004, 10:01:08
Job time : 78.8394 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.29398 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-6

Perfect score: 95

Sequence: 1 MGVRLILAMLGWG 16

Scoring table: BIOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	56.8	408	2 B83333	probable MFS trans
2	53	55.8	172	1 DMECHD	3-hydroxydecanoyl-
3	53	55.8	172	2 AF0626	D-3-hydroxydecanoyl-
4	53	55.8	172	3 F90758	3-hydroxydecanoyl-
5	53	55.8	172	4 D85622	3-hydroxydecanoyl-
6	53	55.8	172	5 AH0174	3-hydroxydecanoyl-
7	52.5	55.3	222	6 C75250	hypothetical prote
8	51	53.7	172	7 D82194	3-hydroxydecanoyl-
9	51	53.7	177	8 G64116	3-hydroxydecanoyl-
10	50	52.6	490	9 D86879	arginine/ornithine
11	49	51.6	621	2 T46851	conserved hypotet
12	48	50.5	303	3 B83470	hypothetical prote
13	47.5	50.0	383	2 AD0183	probable exported
14	47	49.5	170	2 F87710	hypothetical prote
15	46	48.4	126	2 C97946	conserved hypotet
16	46	48.4	126	2 F95078	conserved hypotet
17	46	48.4	344	2 T12378	NADH dehydrogenas
18	46	48.4	554	2 T13585	probable spermidin
19	46	48.4	927	2 A48085	transcription fact
20	45	47.4	55	2 T10356	hypothetical prote
21	45	47.4	212	2 S53229	e antigen precursor
22	45	47.4	305	2 B65048	hypothetical prote
23	45	47.4	394	2 B85916	probable transport
24	45	47.4	394	2 AD0842	probable transport
25	45	47.4	394	2 G81071	probable transport
26	45	47.4	445	2 D82184	quinol oxidase, ch
27	45	47.4	786	2 F83292	probable sensor/re
28	45	47.4	1133	2 A54164	steroid regulatory
29	44.5	46.8	347	2 A46567	tetracycline resis

30	44	46.3	255	2 A60515	Deda family integr
31	44	46.3	307	2 F95949	probable oligopept
32	44	46.3	322	2 AE2160	glycosyltransferas
33	44	46.3	323	2 F95398	probable ABC trans
34	44	46.3	431	1 SAVLC2	large surface anti
35	44	46.3	472	2 AC3534	glu/aspartic acid
36	43.5	45.8	270	2 F70878	hypothetical prote
37	43.5	45.8	415	2 AG2044	hypothetical prote
38	43	45.3	124	2 AB2178	hypothetical prote
39	43	45.3	211	1 A53532	metalloprotease
40	43	45.3	211	2 JC4630	metalloprotease
41	43	45.3	216	2 B75469	hypothetical prote
42	43	45.3	263	2 T09841	hypothetical prote
43	43	45.3	281	2 XMECCF	glycerol facilitat
44	43	45.3	281	2 D91235	glycerol facilitat
45	43	45.3	281	2 D86082	facilitated diffus

ALIGNMENTS

RESULT 1
B83333
Probable MFS transporter PA2500 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83333
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:1094043
A:Accession: B83333
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-408 <STO>
A:Cross-references: UNIPROT:Q910Y2; GB:AE004677; GB:AE004091; NID:99348548; PIDN:AA0581
A:Experimental source: strain PA01
C:Genetics:
A:gene: PA2500
C:Superfamily: cynx protein

Query Match 56.8%; Score 54; DB 2; Length 408;
Best Local Similarity 76.9%; Pred. No. 3;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GVVRLILAMLGW 15
DB 72 GLVALLPLWGRW 84

RESULT 2
DMECHD
3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) - Escherichia coli (s
W:Alternate names: beta-hydroxydecanoyl thioester dehydratase
C:Species: Escherichia coli
C:Date: 30-Jun-1990 #sequence_revision 21-Nov-1997 #text_change 09-Jul-2004
C:Accession: A64836; A28140
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-172 <BIAT>
A:Cross-references: UNIPROT:P18391; GB:AE000197; GB:U00096; NID:q1787180; PIDN:AACT4040
A:Experimental source: strain K-12, substrain MG1655
R:Cronan Jr., U.E.; Li, W.B.; Coleman, R.; Narasimhan, M.; de Mendoza, D.; Schwab, J.M.
J. Biol. Chem. 263, 4641-4646, 1988
A:Title: Derived amino acid sequence and identification of active site residues of Esch

A:Reference number: A28140; MUID:88169574; PMID:2832401
 A:Accession: A28140
 A:Molecule type: DNA
 A:Residues: 1-169, 'LF' <CRO>
 C:Genetics:
 A:Gene: fabA
 A:Map position: 22 min
 C:Function:
 A:Description: catalyzes two reversible reactions, the dehydration of (R)-3-hydroxydecan
 C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
 C:Keywords: carbon-oxygen lyase; fatty acid biosynthesis; homodimer; hydro-lyase
 F:70/Active site: Cys #status predicted
 F:71/Active site: His #status experimental

Query Match 55.8%; Score 53; DB 1; Length 172;
 Best Local Similarity 62.5%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
 DB 87 MMQLVGFYLGWLGGEG 102

RESULT 3
 AF0626
 D-3-hydroxydecanoyl-[acyl-carrier-protein] [imported] - Salmonella enterica subsp. enter
 C:Species: Salmonella enterica subsp. enterica serovar Typh
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AF0626
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
 th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moul, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF0626
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD08193.1; PID:gl502242; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1088
 C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase

Query Match 55.8%; Score 53; DB 2; Length 172;
 Best Local Similarity 62.5%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
 DB 87 MMQLVGFYLGWLGGEG 102

RESULT 4
 F90758
 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) [similarity] - Escher
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: F90758
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
 A:Reference number: A9629; MUID:21156231; PMID:11258796
 A:Accession: F90758
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 <HAV>
 A:Cross-references: UNIPROT:P18391; GB:BA000007; PIDN:BA034461.1; PID:gl3360498; GSPDB:G
 A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:
 A:Gene: ECE1038
 C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.8%; Score 53; DB 2; Length 172;
 Best Local Similarity 62.5%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
 DB 87 MMQLVGFYLGWLGGEG 102

RESULT 5
 D85622
 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) [similarity] - Escher
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: D85622
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: D85622
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 <STO>
 A:Cross-references: UNIPROT:P18391; GB:AE005174; NID:912514136; PIDN:AAG55440.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: fabA
 C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.8%; Score 53; DB 2; Length 172;
 Best Local Similarity 62.5%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
 DB 87 MMQLVGFYLGWLGGEG 102

RESULT 6
 AH0174
 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) [imported] - Yersinia
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AH0174
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AH0174
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 <KUR>
 A:Cross-references: UNIPROT:Q8ZG80; GB:AL590842; PIDN:CAC90259.1; PID:gl5979478; GSPDB:G
 C:Genetics:
 A:Gene: fabA
 C:Superfamily: 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 55.8%; Score 53; DB 2; Length 172;
 Best Local Similarity 62.5%; Pred. No. 1.9;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16

Db 87 MMQLVGFYLGWLGSG 102

RESULT 7

C75250 hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: C75250

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Ullrich, T.; Zaleski, C.; Ma

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: C75250

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <WHI>

A:Cross-references: UNIPROT:Q9RR69; GB:AE002092; GB:AE00513; NID:G6460455; PIDN:AAF1217

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2628

A:Map position: 1

C:Superfamily: Deinococcus radiodurans hypothetical protein DR2628

Query Match 55.3%; Score 52.5; DB 2; Length 222;
Best Local Similarity 66.7%; Pred. No. 2.8;

Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 3 GLVRLILAWLGWG 16

Db 154 GLARVLAWGLSGWG 168

RESULT 8

DB2194 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase VC1463 [imported] - Vibrio cholerae

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: DB2194

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.W.

Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: DB2194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <HEI>

A:Cross-references: UNIPROT:Q9RS00; GB:AE004226; GB:AE003852; NID:G9655979; PIDN:AAF9463

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1463

A:Map position: 1

C:Superfamily: 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase

Query Match 53.7%; Score 51; DB 2; Length 172;
Best Local Similarity 56.2%; Pred. No. 3.7;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGWG 16

Db 87 MMQLVGFYLGWLGSG 102

RESULT 9

G64116 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase (EC 4.2.1.60) - Haemophilus influenzae

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C:Accession: G64116

R:Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.

; Gockayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

, D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: G64116

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-177 <FIG>

A:Cross-references: UNIPROT:P45159; GB:U32812; GB:L42023; NID:G1574784; PIDN:AA022972.1

C:Genetics:

A:Gene: fabA

C:Function:

A:Description: catalyzes two reversible reactions, the dehydration of (R)-3-hydroxydecan

A:Pathway: unsaturated fatty acid biosynthesis

C:Superfamily: 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase

C:Keywords: carbon-oxygen lyase; fatty acid biosynthesis; hydro-lyase

F15/16/Active site: Cys, His #status predicted

Query Match 53.7%; Score 51; DB 2; Length 177;
Best Local Similarity 56.2%; Pred. No. 3.8;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGWG 16

Db 92 MMQLVGFYLGWLGSG 107

RESULT 10

C86879 arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL14

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: C86879

R:Polstein, A.; Wincker, P.; Manger, S.; Tallon, O.; Malarme, K.; Weissbach, J.; Ehrli

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: C86879

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-490 <STO>

A:Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:G12725084; PIDN:AA006133.1; GSPDB:

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: arcD1

C:Superfamily: L-lysine transport protein

Query Match 52.6%; Score 50; DB 2; Length 490;
Best Local Similarity 64.3%; Pred. No. 13;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GLVRLILAWLGWG 16

Db 288 GLVRLILAWLGWG 301

RESULT 11

T46851 conserved hypothetical protein yba [imported] - Rhodobacter sphaeroides

C:Species: Rhodobacter sphaeroides

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C:Accession: T46851

R:Mackenzie, C.; Simmons, A.E.; Kaplan, S.

Genetics 153, 525-538, 1999

A:Title: Multiple chromosomes in bacteria. The yin and yang of tnp gene localization in

A:Reference number: Z24108; MUID:99442363; PMID:10511537

A:Accession: T46851

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-621 <MAC>

A/Cross-references: UNIPROT:Q9ZFB1; EMBL:AF108766; NID:94185542; PIDN:AA09115.1; PID:G4
A/Experimental source: strain 2.4.1
C/Genetics:
A/Gene: ybat

Query Match 51.6%; Score 49; DB 2; Length 621;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 MGLVRLIAMLGNG 16
DB 22 MGLVGLMAVGLGSG 36

RESULT 12
B83470
hypothetical protein PA1411 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: B83470
R/Steve, C.K.; Pham, X.Q.; Ervin, A.L.; Micozucht, S.D.; Martener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.W.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lartig, K.; Lim,
; Lory, S.; Olson, M.V.
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83470
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-303 <STO>
A/Cross-references: UNIPROT:Q913T3; GB:AE004570; GB:AE004091; NID:99947350; PIDN:AA00480
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA1411
C/Superfamily: hypothetical protein yded

Query Match 50.5%; Score 48; DB 2; Length 303;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LVRLIAMLGNG 15
DB 50 LVGLMLCMGRGW 61

RESULT 13
AD0183
probable exported protein YP01504 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AD0183
R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586560
A/Accession: AD0183
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-383 <XLR>
A/Cross-references: UNIPROT:Q8ZG16; GB:AL590842; PIDN:CA09027.1; PID:G15979546; GSPDB:G
C/Genetics:
A/Gene: YP01504

Query Match 50.0%; Score 47.5; DB 2; Length 383;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 W-GVRLIAMLGNG 15
DB 93 WGLVRLPAIGWASGW 107

RESULT 14
F87710
hypothetical protein CC3720 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: F87710
R/Nietman, W.C.; Feldlym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.R.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: F87710
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-170 <STO>
A/Cross-references: UNIPROT:Q9A246; GB:AE005673; NID:913425488; PIDN:AAK25682.1; GSPDB:G
C/Genetics:
A/Gene: CC3720
C/Superfamily: 3-hydroxydecanoyl-(acyl-carrier-protein) dehydratase

Query Match 49.5%; Score 47; DB 2; Length 170;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MMGLVRLIAMLGNG 16
DB 85 MMGLVGLFLGWSGPG 100

RESULT 15
C97946
conserved hypothetical protein spr0595 [imported] - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: C97946
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.D.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zock, C.; Baltz, R.H.; Jaskunas, S.R.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: C97946
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-126 <XLR>
A/Cross-references: UNIPROT:Q97RV8; UNIPROT:Q8DGM7; GB:AE007317; PIDN:AAK9399.1; PID:G1
C/Genetics:
A/Gene: spr0595
C/Superfamily: glpB protein

Query Match 48.4%; Score 46; DB 2; Length 126;
Best Local Similarity 46.2%; Pred. No. 14;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MMGLVRLIAMLG 13
DB 6 LMALILMALMMG 18

Search completed: December 8, 2004, 10:27:03
Job time : 5.25398 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.41322 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-6
Perfect score: 95
Sequence: 1 MMGLVRLLLAWLGSGW 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	241	2 Q6ETS8	Q6ETS8 homo sapien
2	95	100.0	493	2 Q6ELQ7	Q6ELQ7 homo sapien
3	95	100.0	781	2 Q6EFX6	Q6EFX6 mus musculu
4	95	100.0	781	2 AAH57373	AAH57373 mus muscu
5	95	100.0	819	1 CADC_HUMAN	CADC_HUMAN
6	54	56.8	172	1 PABA_PHOLL	PABA_PHOLL
7	54	56.8	408	2 Q910Y2	Q910Y2 pseudomonas
8	53	55.8	171	1 PABA_ECOLI	PABA_ECOLI
9	53	55.8	171	1 PABA_ECOLI	PABA_ECOLI
10	53	55.8	171	1 PABA_SALTY	PABA_SALTY
11	53	55.8	172	1 PABA_YERPE	PABA_YERPE
12	53	55.8	172	2 Q6D6D7	Q6D6D7 erwinia car
13	53	55.8	177	1 PABA_WIGBR	PABA_WIGBR
14	52.5	55.3	222	2 Q9RFE9	Q9RFE9 delnoccoc
15	52	54.7	176	1 PABA_HAEDU	PABA_HAEDU
16	52	54.7	194	2 Q7NCAS	Q7NCAS glieobacter
17	52	54.7	328	2 Q6ZET7	Q6ZET7 synecocyst
18	52	54.7	328	2 BAD01813	BAD01813 synecoc
19	51	53.7	172	1 PABA_CANBF	PABA_CANBF
20	51	53.7	172	1 PABA_VIBCH	PABA_VIBCH
21	51	53.7	172	1 PABA_VIBPA	PABA_VIBPA
22	51	53.7	172	1 PABA_VIBTU	PABA_VIBTU
23	51	53.7	172	1 PABA_VIBTY	PABA_VIBTY
24	51	53.7	177	1 PABA_HAELN	PABA_HAELN
25	51	53.7	177	1 PABA_PASWU	PABA_PASWU
26	51	53.7	348	2 Q9TDS7	Q9TDS7 cynopocellu
27	51	53.7	361	2 Q21680	Q21680 alopias pel
28	51	53.7	542	2 Q7U446	Q7U446 synecococc
29	50	52.6	391	2 Q6KX24	Q6KX24 pseudomonas
30	50	52.6	391	2 Q6BD91	Q6BD91 pseudomonas
31	50	52.6	447	2 Q7NV89	Q7NV89 chromobacte

32	50	52.6	490	2 Q9CE15	Q9CE15 lactococcus
33	50	52.6	526	2 Q9K574	Q9K574 lactococcus
34	49	51.6	170	2 Q6EFS1	Q6EFS1 uncultured
35	49	51.6	170	2 AAR38141	AAR38141 unculture
36	49	51.6	175	1 PABA_RHOPA	PABA_RHOPA
37	49	51.6	621	2 Q9ZFB1	Q9ZFB1 rhodospseudo
38	49	51.6	2042	2 Q8TZ07	Q8TZ07 methanopyru
39	48.5	51.1	253	2 Q7YHW4	Q7YHW4 glieobacter
40	48	50.5	171	2 Q6TR96	Q6TR96 photobacter
41	48	50.5	171	2 CAG20180	CAG20180 photobact
42	48	50.5	292	2 Q7VX52	Q7VX52 chromobacte
43	48	50.5	292	2 Q7ZHX9	Q7ZHX9 thermus the
44	48	50.5	296	2 AAS81695	AAS81695 thermus t
45	48	50.5	303	2 Q913T3	Q913T3 pseudomonas

ALIGNMENTS

RESULT 1					
ID	Q6ETS8	PRELIMINARY;	PRT;	241 AA.	
AC	Q6ETS8;				
DT	01-JUN-2003 (TREMBLrel. 24, Created)				
DT	01-OCT-2003 (TREMBLrel. 24, Last sequence update)				
DE	Full-length cDNA 5-PRIME end of clone CS0DE010YPI9 of Placenta of Homo sapiens (human) (Fragment).				
DE	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCB1_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RA	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.				
CC	-1- SIMILARITY: Contains 2 cadherin domains.				
DR	EMBL; BX248750; CAD6557.1; -.				
DR	HSSP; F12830; 1065.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0005509; F:calcium ion binding; IEA.				
DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.				
DR	InterPro; IPR002126; Cadherin.				
DR	Pfam; PF00028; Cadherin_2.				
DR	PRINTS; PR00205; CADHERIN.				
DR	SMART; SM00112; CA; 2.				
DR	PROSITE; PS00232; CADHERIN_1; 1.				
DR	PROSITE; PS00268; CADHERIN_2; 2.				
KW	Calcium; Calcium-binding.				
FT	NON TER 241				
SQ	SEQUENCE 241 AA; 26348 MW; 4649831B5424604 CRC64;				
Query Match					
Best Local Similarity 100.0%; Score 95; DB 2; Length 241;					
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 MMGLVRLLLAWLGSGW 16				
DB	1 MMGLVRLLLAWLGSGW 16				
RESULT 2					
ID	Q96LQ7	PRELIMINARY;	PRT;	493 AA.	
AC	Q96LQ7;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ25193.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Nimomiyu K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kanahara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
 RA Nakagawa K., Munro S., Morikawa M., Kawamura M., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isega T., Sugano S.,
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; AK057922; BAB1613.1; -
 DR HSSP; P12830; 106S.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 4.
 KM Calcium; Calcium-binding; CADHERIN_2; 4.
 SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;
 Query Match 100.0%; Score 95; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGGVRLLLAWLGWG 16
 DB 1 MGGVRLLLAWLGWG 16
 ID QEPFX6 PRELIMINARY; PRT; 781 AA.
 AC QEPFX6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=cdh24;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kusterberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Rana S.S., Loughran N.A., Peters K.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pothey J., Helton E., Kettelman A., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzyszewski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.L.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC057373; AAH57373.1; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835A CRC64;
 Query Match 100.0%; Score 95; DB 2; Length 781;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGGVRLLLAWLGWG 16
 DB 1 MGGVRLLLAWLGWG 16
 ID AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kusterberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Rana S.S., Loughran N.A., Peters K.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pothey J., Helton E., Kettelman A., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

```

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC057373, AAH57373.1..
SQ SEQUENCE      781 AA;  84104 MW;  15996D6E6C9335A CRC64;.

Query Match          100.0%; Score 95; Db 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches    16; Conservative     0; Mismatches   0; Indels   0; Gaps   0

QY      1 MMGLVLLLAAGGWSG 16
Db       1 MMGLVLLLAAGGWSG 16

RESULT 5
CAO_HUMAN
ID ID CAD_O_HUMAN STANDARD; PRT; 819 AA.
AC Q86U90; Q86U91; Q9N184;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN RN
RP RP
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
CAENININS.
RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA Kattilaas B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
RL "Characterization of cadherin-24, a novel alternatively spliced type
II cadherin.";
RJ J Biol. Chem. 278:27513-27519(2003).
[2]
SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Marx W., Robble E., Sanchez C., Schenfeld J.,
RA Seeshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vargas A.,
RA Vanden R., Weanabe C., Wiand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Gowdski P., Gray A.;
RL "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RJ Genome Res. 13:2265-2270(2003).
[3]
SEQUENCE FROM N.A. (ISOFORM 3).
RX TISSE=Testis;
RA Blum H., Baerach S., Neues H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells; cadherins may thus contribute to the
sorting of heterogeneous cell types. Cadherin-24 mediate strong
cell-cell adhesion.
CC SUBUNIT: Associates with alpha-, beta- and delta-catennins.
-1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=long form;
Name=0=Q86UP0-1; Sequence=DIsplayed;
Name=2; Synonyms=short form;
Name=3;
Name=0=Q86UP0-2; Sequence=VSP_008717;
Name=3;
IsoId=Q86UP0-3. Sequence=VSP_008718 VSP_008719.

```

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CC      Note=No experimental confirmation available;
CC      -I- SIMILARITY: Contains 5 cadherin domains.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; AY260900; AAP20580.1; -
DR      EMBL; AY260901; AAP20581.1; -
DR      EMBL; AY358199; AAO8856.1; -
DR      PIR; T4617477; CABY0758.1; -
DR      PIR; T46418; T46418.
DR      HSSP; P09803; 117W.
DR      Genew; HGNC:14265; CDH24.
DR      InterPro; IPR002126; Cadherin.
DR      InterPro; IPR002033; Cadherin_C_term.
DR      Pfam; PF00028; Cadherin_5.
DR      Pfam; PF01049; Cadherin_C/1.
DR      PRINTS; PR00205; CADHERIN.
DR      PROSITE; PS00232; CADHERIN_1; 2.
DR      PROSITE; PS50268; CADHERIN_2; 5.
KW      Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW      Multigene family; Repeat; Signal; Transmembrane.
FT      SIGNAL          1
FT      PROSEP          19
FT      CHAIN           21
FT      DOMAIN          45
FT      TRANSMEM        45
FT      DOMAIN          642
FT      DOMAIN          663
FT      DOMAIN          819
FT      DOMAIN          819
FT      DOMAIN          819
FT      DOMAIN          819
FT      DOMAIN          819
FT      DOMAIN          819
FT      DOMAIN          819
FT      CARBOHYD         446
FT      CARBOHYD         548
FT      CARBOHYD         563
FT      VASPLIC          455
FT      FT              427
FT      VARSPPLIC        1
FT      FT              427
FT      VARSPPLIC        1
FT      FT              428
FT      FT              492
SQ      SEQUENCE       819 AA; 87751 MW; 90830304F18BA7E4A CEC64;
Query Match               100.0%; Score 95; DB 1; Length 819;
Best Local Similarity     100.0%; Pred. No. 3e-05;
Matches    16; Conservative   0; Mismatches      0; Indels    0; Gaps    0.
Cc      1 MMGLVRLLLAWLGNG 16
Cc      1 MMGLVRLLLAWLGNG 16
-----
RESULT 6
FABA_PROHL
AC      C7MB46;
ID      FABA_PROHL STANDARD; PRT; 172 AA.
DT      05-JUN-2004 (Rel. 44, Created)
DT      05-JUL-2004 (Rel. 44, Last sequence update)
DE      3-hydroxydecanoyl-lacyl-carrier-protein (update)
DE      3-hydroxydecanoyl-lacyl-carrier-protein dehydratase (EC 4.2.1.60)
GN      (Beta-hydroxydecanoil thioester dehydrase).
GN      Name=faba; OrderedLocuNames=plu1772;
GC      Photobacterium luminescens (Subsp. laumouillii).
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales.

```

CC Enterobacteriaceae; Photorhabdus.
 RX NCBI_TaxID=141679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
 RA Duchaud S., Kustnok C., Frangeul L., Buchrieser C., Giraudon A.,
 RA Taouit S., Bocs S., Boursaux-Ende C., Chandler M., Charles J.-F.,
 RA Dassa B., DeRose R., Derzelle S., Freysinet G., Gaudreau S.,
 RA Médigue C., Lancia A., Powell K., Sigulier P., Vincent R., Wingate V.,
 RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
 RT "The genome sequence of the entomopathogenic bacterium *Photorhabdus*
 RT *luminescens*.";
 RL Nat. Biotechnol. 21:1307-1313(2003).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 CC fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 CC ACP to E-(2)-decenoyl-ACP and then its isomerization to Z-(3)-
 CC decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 CC = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 CC carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 CC acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC
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 CC
 CC EMBL; EX571865; CAE14065.1; -
 CC PhotoList; pln1772; -
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; FabA.
 DR TIGRFAMs; TIGR01749; fabA; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 71 71 By similarity.
 SQ SEQUENCE 172 AA; 18999 MW; 72D63DF044DAE4E CRC64;
 Query Match 56.8%; Score 54; DB 1; Length 172;
 Best Local Similarity 62.5%; Pred. No. 6.1;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MGGLVRLLLAWLGSGW 16
 DB 87 MMQLVGFPLQWLGSG 102
 RESULT 7
 ID Q910Y2 PRELIMINARY; PRT; 408 AA.
 AC Q910Y2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Probable MFS transporter.
 GN OrderedLocuNames=PA2500;
 OS *Pseudomonas aeruginosa*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RX SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10964043;
 RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; AB004677; AAG05888.1; -
 DR PIR; B83333; B83333.
 KM Complete proteome.
 SQ SEQUENCE 408 AA; 43089 MW; A34FDB70FC656972 CRC64;
 Query Match 56.8%; Score 54; DB 2; Length 408;
 Best Local Similarity 76.9%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GLVRLLLAWLGW 15
 DB 72 GLVRLLLAWLGW 84
 RESULT 8
 ID FABA_ECOL6 STANDARD; PRT; 171 AA.
 AC Q8FJ83;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 3-Hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 DE (Beta-hydroxydecanoyl) thioester dehydratase.
 GN Name=faba; OrderedLocuNames=c1090;
 OS *Escherichia coli* O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Ison S.-R., Boutin A., Heckert J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 CC fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 CC ACP to E-(2)-decenoyl-ACP and then its isomerization to Z-(3)-
 CC decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 CC = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 CC carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 CC acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC
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 CC
 CC EMBL; AE016758; AAN79558.1; ALT_INIT.
 DR HSSP; P18931; IMKA.
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; FabA.
 DR TIGRFAMs; TIGR01749; fabA; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT INIT_MET 0 0 By similarity.

FT ACT SITE 70 70 By similarity.
SQ SEQUENCE 171 AA, 18665 MW, 3D8C55A01DD72220 CRC64;
Query Match 55.8%; Score 53; DB 1; Length 171;
Best local Similarity 62.5%; Pred. No. 8.5;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 MMGLVRLTLAWLGGWG 16
DB 86 MMGLVGYFLGMDGGEG 101

RESULT 9

FABA_ECOLI STANDARD; PRT: 171 AA.

AC P18351, O59383, 31-NOV-1980 (Rel. 16, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
OS Name=faba; OrderedLocustNames=b0954, z1304, ECol038, SF0354, S1020;
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562, 83334, 623;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=86169574; PubMed=2832401;
RA Cronan J.E., Jr., Li W.-B., Coleman R., Narasimhan M., de Mendoza D.,
RA Schwab J.M.,
RT "Derived amino acid sequence and identification of active site
RT residues of Escherichia coli beta-hydroxydecanoyl thioester
RL dehydratase";
RL J. Biol. Chem. 263:4641-4646(1988).

REVISION TO 169-171.

RC SPECIES=E.coli;
RX MEDLINE=92370687; PubMed=1505031;
RA Henry M.F., Cronan J.E., Jr.,

RT "A new mechanism of transcriptional regulation: release of an
RT activator triggered by small molecule binding.";
RL Cell 70:671-679(1992).

SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.T.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).

SEQUENCE FROM N.A.

RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905322;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Horio A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashiuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampedro G., Seki Y., Takami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano W., Horinouchi T.,
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).

SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobleck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatter F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).

SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shida T., Hattori M., Shinagawa H.,
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).

SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.,
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).

SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590224; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G., III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blatter F.R.,
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).

MUTANTS FABA6 AND FABA2.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=96404784; PubMed=8808925;
RA Rock C.O., Tsay J.-T., Heath R., Jackowski S.,
RT "Increased unsaturated fatty acid production associated with a
RT suppressor of the faba6(fbs) mutation in Escherichia coli.";
RL J. Bacteriol. 178:5382-5387(1996).

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC SPECIES=E.coli;
RX MEDLINE=96398612; PubMed=8805534;
RA Leesong M., Henderson B.S., Gillig J.R., Schwab J.M., Smith J.L.,
RT "Structure of a dehydratase-isomerase from the bacterial pathway for
RT biosynthesis of unsaturated fatty acids: two catalytic activities in
RT one active site.";
RL Structure 4:253-264(1996).

FUNCTION: Necessary for the introduction of cis unsaturation into
fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
decanoyl-ACP.

CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
= 2,3-decanoyl-[acyl-carrier protein] or 3,4-decanoyl-[acyl-
carrier protein] + H(2)O.

PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
acid synthesis in bacteria.

SUBUNIT: Homodimer.

SIMILARITY: Belongs to the thioester dehydratase family.

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CC EMBL; J01186; AA96496.1; ALT INT.
 CC EMBL; AE000197; AAC74040.1; -
 CC EMBL; D90733; BAA35712.1; -
 CC EMBL; AE005285; AAG55440.1; -
 CC EMBL; AP002554; BAB34461.1; -
 CC EMBL; U37057; AAC4389.1; -
 CC EMBL; U56977; AAC4399.1; -
 CC EMBL; AE015125; AAM42583.1; -
 CC EMBL; AE016981; AAP6468.1; -
 CC PIR; A64836; DMECHD.
 CC PIR; D85622; D85622.
 CC PIR; F90758; F90758.
 CC PDB; IMKA; X-ray; A/B=1-171.
 CC PDB; IMKB; X-ray; A/B=1-171.
 CC ECODBASE; H017.2; 6TH EDITION.
 CC ECHOBASE; EB0263; -
 CC EcGene; EG10273; faba.
 CC HAMAP; MF_00405; -; 1.
 CC InterPro; IPR010083; Faba.
 CC TIGRfams; TIGR01749; faba; 1.
 CC 3D-structure; Complete proteome; Direct protein sequencing;
 CC Fatty acid biosynthesis; Lyase.
 CC INT MET 0
 CC ACT SITE 70 70 P -> L (in allele FBA6; TS).
 CC VARIANT 75 75 G -> D (in allele FBA2; TS).
 CC VARIANT 101 101 R -> H (in Ref. 8).
 CC CONFLICT 17 17 M -> I (in Ref. 8).
 CC CONFLICT 36 36 M -> I (in Ref. 8).
 CC CONFLICT 151 151 G -> C (in Ref. 8).
 CC STRAND 7 7
 CC HELIX 9 16
 CC TURN 17 18
 CC TURN 31 33
 CC STRAND 38 43
 CC TURN 47 50
 CC STRAND 53 59
 CC TURN 62 63
 CC HELIX 65 68
 CC TURN 69 73
 CC HELIX 79 96
 CC TURN 97 98
 CC STRAND 102 108
 CC TURN 111 113
 CC STRAND 119 120
 CC TURN 123 135
 CC STRAND 139 149
 CC TURN 150 151
 CC STRAND 152 165
 CC TURN 169 171
 CC SEQUENCE 171 AA; 18838 MM; 3D8C55A01DCD0B20 CRC64;
 Query Match 55.8%; Score 53; DB 1; Length 171;
 Best Local Similarity 62.5%; Pred. No. 8.5;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 MMGLVRLIAMIIGMG 16
 |||||
 Db 86 MMGLVRYLGLGSGS 101

RESULT 10
 FABA_SALT
 ID FABA_SALT STANDARD; PRT; 171 AA.
 AC O8XEV3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

01-OCT-2004 (Rel. 45, Last annotation update)
 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 (Beta-hydroxydecanoyl thioester dehydratase)
 DE Name=faba; OrderedLocNames=TM1067, STY1068, t1853;
 GN Name=faba; OrderedLocNames=TM1067, STY1068, t1853;
 OS Salmonella typhimurium, and
 CC Salmonella typhi.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 CC NCBI_TaxID=602, 601;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S. typhi; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali U., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of salmonella enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parhill U., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Hague A., Hlen T.T., Holroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Goira P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S. typhi; STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
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CC EMBL; AE008746; AAL20000.1; -
 CC EMBL; AL627269; CAD08193.1; -
 CC EMBL; AE016840; AAO69471.1; -
 CC HSSP; P18391; IMKA.
 CC StyGene; SG27277; faba.
 CC HAMAP; MF_00405; -; 1.
 CC InterPro; IPR010083; Faba.

DR TIGR01749; fabA; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT INIT_MET 0 By similarity.
 ACT SITE 70 By similarity.
 SQ SEQUENCE 171 AA; 18916 MW; 3D9FC816D520B8C20 CRC64;

Query Match 55.8%; Score 53; DB 1; Length 171;
 Best Local Similarity 62.5%; Pred. No. 8.5;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLLLAMLGWG 16
 Db 86 MMGLVGFYLGWLGEG 101

RESULT 11

FABA_YERPE STANDARD; PRT; 172 AA.
 AC Q8ZG80;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 42, Last annotation update)
 DE 3-Hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 GN Name=faba; OrderedLocustNames=YF01430, Y2740, YP0875;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Yersinia.
 OX NCBI_taxid=632;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parthill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebailha M., James K.D., Chuchter C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarazaga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moulé S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.W., Watson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 RN (3)
 RP SEQUENCE FROM N.A.

RC STRAIN=91001 / Biovar Mediaevalis;
 RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
 RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
 RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
 RA Yang R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Necessary for the introduction of cis unsaturation into
 fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 decenoyl-ACP (By similarity).
 CC -!- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 carrier protein] + H(2)O.
 CC -!- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 acid synthesis in bacteria.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the thioester dehydratase family.

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 CC -----

DR EMBL; A014148; CAC90259.1; -
 DR EMBL; A013876; AAM86292.1; ALT_INIT.
 DR EMBL; A017130; AAS61132.1; ALT_INIT.
 DR PIR; A0174; A0174.
 DR HSSP; P18391; 1MKA.
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR01083; Faba.
 DR TIGR01749; fabA; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 71 By similarity.
 SQ SEQUENCE 172 AA; 18810 MW; 19037054D0A721EC CRC64;

Query Match 55.8%; Score 53; DB 1; Length 172;
 Best Local Similarity 62.5%; Pred. No. 8.6;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLLLAMLGWG 16
 Db 87 MMGLVGFYLGWLGEG 102

RESULT 12

Q6D6D7 PRELIMINARY; PRT; 172 AA.
 ID Q6D6D7;
 DT 01-OCT-2004 (TEMBLrel. 28, Created)
 DT 01-OCT-2004 (TEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
 DE 3-Hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC
 4.2.1.60).
 GN Name=faba; ORFNames=BCA1748;
 OS Yersinia carotovora subsp. atroseptica SCRI1043.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Pectobacterium.
 OX NCBI_taxid=218491;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCRI1043;
 RA Ball K.S., Sebailha M., Pritchard L., Holden M., Hyman L.J.,
 RA Holeva M.C., Thomson N.R., Bentley S.D., Chuchter C., Mungall K.,
 RA Aklin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moulé S., Nordertczak H.,
 RA Omond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Barrett B.G., Parthill J., Toth I.K.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX950851; CAG74653.1; -.

KM Lyase.
 SQ SEQUENCE 172 AA; 18963 MW; 6B4C06941629DA4 CRC64;

Query Match 55.8%; Score 53; DB 2; Length 172;
 Best Local Similarity 62.5%; Pred. No. 8.6;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MMGLVRLLLAMLGWG 16
 Db 87 MMGLVGFYLGWLGEG 102

RESULT 13
 FABA_WIGER STANDARD; PRT; 177 AA.
 ID Q8D204;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 GN Name=faba; OrderedLocNames=MIGR3000;
 OS Wigglesworthia glosindia brevipalpis.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Wigglesworthia.
 CX NCBI_TaxID=36870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2229718; PubMed=12219091; DOI=10.1038/ng986;
 RA Akman L., Yamashita A., Matanabe H., Oshima K., Shiba T., Hattori M.,
 RA Akeoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT files, Wigglesworthia glosindia."
 RL Nat. Genet. 32:402-407(2002)
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 CC fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 CC ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 CC decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 CC = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 CC carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 CC acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC -----
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 CC -----
 DR EMBL; AB063522; BAC24446.1; -
 DR HSSP; P18391; IMKA.
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; Faba.
 DR TIGRFAMs; TIGR01749; faba; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 71 71
 SQ SEQUENCE 177 AA; 20109 MW; 53237E5162914988 CRC64;
 QY Query Match 55.8%; Score 53; DB 1; Length 177;
 Best Local Similarity 62.5%; Pred. No. 8.8;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 MNGVRLLLAMGSG 16
 Db 87 MNGVRLLLAMGSG 102
 RESULT 14
 ID Q9RR69 PRELIMINARY; PRT; 222 AA.
 AC Q9RR69;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
 DE Hypothetical protein DR2628.
 GN OrderedLocNames=DR2628;
 OS Deinococcus radiodurans.
 CC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
 CC Deinococcaceae; Deinococcus.
 CX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L.A., Uitterlinden T.R., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002092; AAP12174.1; -
 DR TIGR; C75250; C75250.
 DR PIR; DR2628; -
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 222 AA; 24482 MW; A1B9F407DF89A9A CRC64;
 QY Query Match 55.3%; Score 52.5; DB 2; Length 222;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 3 GLAVLLIALLVGGWG 16
 Db 154 GLAVLLIALLVGGWG 168
 RESULT 15
 ID FABA_HAEU STANDARD; PRT; 176 AA.
 AC Q7U343;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60)
 DE (Beta-hydroxydecanoyl thioester dehydratase).
 GN Name=faba; OrderedLocNames=HD0181;
 OS Haemophilus ducreyi.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 CC Pasteurellaceae; Haemophilus.
 CX NCBI_TaxID=730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3500HP / ATCC 700724;
 RA Munson R.S. Jr., Ray W.C., Mahatras G., Sabo P., Mungur R.,
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
 RT "The complete genome sequence of Haemophilus ducreyi."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Necessary for the introduction of cis unsaturation into
 CC fatty acids. Catalyzed the dehydration of (3R)-3-hydroxydecanoyl-
 CC ACP to E-(2)-decanoyl-ACP and then its isomerization to Z-(3)-
 CC decenoyl-ACP (By similarity).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxydecanoyl-[acyl-carrier protein]
 CC = 2,3-decenoyl-[acyl-carrier protein] or 3,4-decenoyl-[acyl-
 CC carrier protein] + H(2)O.
 CC -1- PATHWAY: Key step in the anaerobic pathway of unsaturated fatty
 CC acid synthesis in bacteria.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioester dehydratase family.
 CC -----
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 CC -----
 DR EMBL; AE017151; AAP5174.1; -
 DR HAMAP; MF_00405; -; 1.
 DR InterPro; IPR010083; Faba.
 DR TIGRFAMs; TIGR01749; faba; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lyase.
 FT ACT_SITE 75 75
 SQ SEQUENCE 176 AA; 19280 MW; 21DE115843D568DC CRC64;

Wed Dec 8 11:46:32 2004

us-09-788-051-6.rup

Page 9

Query Match 54.7%; Score 52; DB 1; Length 176;
Best Local Similarity 56.2%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Oy 1 MMGLVRLILAWIGGKG 16
Db 91 MMGLVGFPLGWIGGKG 106

Search completed: December 8, 2004, 10:24:35
Job time : 8.41322 secs

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OK protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.62102 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-6

Sequence: 1 MWGLVRLILMLGSGWG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*\n2: Geneseqp1990s:*\n3: Geneseqp2000s:*\n4: Geneseqp2001s:*\n5: Geneseqp2002s:*\n6: Geneseqp2003as:*\n7: Geneseqp2003bs:*\n8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	16	7	ADD29447 Human cad
2	95	100.0	493	5	AD116946 Human NOV
3	95	100.0	607	5	AB553295 Human pol
4	95	100.0	636	7	ADD29445 Human pol
5	95	100.0	781	5	AB553296 Human pol
6	95	100.0	781	5	AAM48736 Human pad
7	95	100.0	781	5	ABG34078 Human PRO
8	95	100.0	781	5	AD116604 Human NOV
9	95	100.0	781	5	AD116606 Human NOV
10	95	100.0	781	6	ABR40114 Human cel
11	95	100.0	781	6	ADA01366 Human PRO
12	95	100.0	781	6	ADA43795 Human sec
13	95	100.0	781	6	ADA43563 Human sec
14	95	100.0	781	6	ADA01238 Human PRO
15	95	100.0	781	7	ADA01122 Human sec
16	95	100.0	781	7	ADA43679 Human sec
17	95	100.0	781	7	ADA06941 Human PRO
18	95	100.0	781	7	ADA08429 Human hum
19	95	100.0	781	7	ADB99722 Human PRO
20	95	100.0	781	7	ADB87005 Human PRO
21	95	100.0	781	7	ADB66160 Human sec
22	95	100.0	781	7	ADB99638 Human PRO
23	95	100.0	781	7	ADB99493 Human hum
24	95	100.0	781	7	ADB66044 Human sec
25	95	100.0	781	7	ADC23442 Human tra

26	95	100.0	781	7	ADC26135 Human PRO
27	95	100.0	781	7	ADB04962 Human PRO
28	95	100.0	781	7	ADE11268 Human PRO
29	95	100.0	781	7	ADB88199 Human PRO
30	95	100.0	781	7	ADD95494 Human sec
31	95	100.0	781	7	AD306424 Human PRO
32	95	100.0	781	7	AD358199 Human PRO
33	95	100.0	781	7	ADD88315 Human PRO
34	95	100.0	781	7	ADD90896 Human sec
35	95	100.0	781	7	ADP99451 Human sec
36	95	100.0	781	7	ADG06544 Human PRO
37	95	100.0	781	7	ADG05495 Human PRO
38	95	100.0	781	7	ADG82496 Human PRO
39	95	100.0	781	8	ADE51749 Human sec
40	95	100.0	781	8	ADE51865 Human sec
41	95	100.0	781	8	ADE37723 Human sec
42	95	100.0	781	8	ADE37607 Human sec
43	95	100.0	781	8	ADD95378 Human PRO
44	95	100.0	781	8	AD38078 Human PRO
45	95	100.0	781	8	ADE76167 Human PRO

ALIGNMENTS

RESULT 1
ID ADD29447 standard; protein, 16 AA.
AC ADD29447;
DT 15-JUN-2004 (first entry)
DE Human cadherin-like protein signal peptide.
XX cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytotactin; osteopetrotic; cancer;
KW osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumor; human.
XX Homo sapiens.
OS US200314491-A1.
PN 31-JUL-2003.
PD 16-FEB-2001; 2001US-00788051.
PF 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX (GDB/) GODBOLE S D.
PA (KLOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (DRMA/) DRMANAC R T.
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI Liu C, Drmanac RT;
XX WPI; 2003-829799/77.
XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteopetrosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX Claim 11; SEQ ID NO 6, 63pp; English.
XX This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutic useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the signal peptide of the human
CC secreted cadherin-like protein which was used during the exemplification
CC of the invention.

XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 95; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MGVLRLLAMLGWG 16
D6 1 MGVLRLLAMLGWG 16

RESULT 2
AD116946
ID AD116946 standard; protein: 493 AA.
AC AD116946;
XX
XX AD116946;
XX
XX 15-APR-2004 (first entry)
XX
XX Human NOVX protein homologue SeqID 482.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; str.
XX
XX Homo sapiens.
XX
XX WO200268649-A2.
XX
XX 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266757P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.

PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0280992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285139P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

XX (CURA-) CURAGEN CORP.
XX
XX Tchernov VT, Spytek KA, Zernusen BD, Patnrajan M, Shinkets RA;
PI Li L, Gangolli EA, Patisgaru M, Anderson DM, Rastell L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolanc AR, Pena CEA;
PI Furtak K, Grosse WM, Alsobrook JP, Iepley DM, Rieger DK, Burgess CE;
XX
XX WPI: 2002-706998/76.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 482; 1498pp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular atrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiautismic, nephroprotective, antiautistic, hepatoprotective,
CC neuroprotective, nootropic, antibacterial, vitacide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX Sequence 493 AA;
SQ

Query Match 100.0%; Score 95; DB 5; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMGLVRLILAWLGWG 16
 |||||
 DB 1 MMGLVRLILAWLGWG 16

RESULT 3
 ABB53295
 ID ABB53295 standard; protein; 607 AA.

XX ABB53295;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #35.

XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquilizer; antiarrhythmic; cardiact; antidiabetic;
 KW antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
 KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.

OS Homo sapiens.

FN WC200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

FR 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.
 (SMIK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdock FR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;
 PI Lai Y, Xie Q;

DR WPI: 2002-041392/05.

DR N-PSDB; ABA90360.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

XX Claim 1; Page 106-108; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneoplastic palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including

CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketocidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX Sequence 607 AA;

Query Match 100.0%; Score 95; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 5.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMGLVRLILAWLGWG 16
 |||||
 DB 1 MMGLVRLILAWLGWG 16

RESULT 4
 ADD29445
 ID ADD29445 standard; protein; 636 AA.

XX ADD29445;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein amino acid sequence.

XX cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytotstatic; osteopetrosis; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.

OS Homo sapiens.

FN Key Location/Qualifiers

FT Peptide 1..16

FT Protein /label=Signal_peptide

FT /label=636

XX US2003144491-A1.

PD 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

XX (GODE/) GODEBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LITC/) LIT C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
 PI Liu C, Drmanac RT;

DR WPI: 2003-829799/77.

DR N-PSDB; ADD29461, ADD29446.

XX Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteoporosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.

PS Claim 11; SEQ ID NO 4; 63pp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of

XX Claim 9; Page 105; 11pp; English.
PS
XX
CC The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
CC neuroprotective, antiarthritic, antirheumatic, dermatological,
CC immunosuppressive, antineoplastic, antipruritic, antiallergic,
CC antiallergic, antileptotic, haemostatic, antipruritic, antiallergic,
CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecules are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune disease including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy; cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MMGLVRLLLAWLGWG 16
Db 1 MMGLVRLLLAWLGWG 16
RESULT 7
ABG34078
ID ABG34078 standard; protein; 781 AA.
XX
AC ABG34078;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Pro peptide #49.
XX
KM Human, PRO; secreted protein; transmembrane protein; genetic disorder;
KM tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US027099.
XX
PR 01-SEP-2000; 2000US-0228986P.
PR 05-SEP-2000; 2000US-0230621P.
PR 22-SEP-2000; 2000US-0235147P.
PR 10-NOV-2000; 2000WO-US030873.
PR 12-JAN-2001; 2001US-0261878P.
PR 16-JAN-2001; 2001US-0261910P.
PR 16-JAN-2001; 2001US-0261939P.
PR 16-JAN-2001; 2001US-0262150P.
PR 25-JAN-2001; 2001US-0264385P.
PR 02-FEB-2001; 2001US-0266421P.
PR 09-FEB-2001; 2001US-0267623P.
PR 28-FEB-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-0274399P.
PR 03-APR-2001; 2001US-0280982P.

PR 04-APR-2001; 2001US-0282129P.
PR 04-APR-2001; 2001US-0282199P.
PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2002-362426/39.
DR N-PSDB; ABK70009.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
XX genetic analysis of individuals with genetic disorders.
XX
PS Claim 11; Fig 98; 21pp; English.
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. Polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding, reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a human PRO protein of the invention
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 MMGLVRLLLAWLGWG 16
Db 1 MMGLVRLLLAWLGWG 16
RESULT 8
AD116604
ID AD116604 standard; protein; 781 AA.
XX
AC AD116604;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein to treat human pathological conditions SeqID140.
XX
KM human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KM inflammation; autoimmune disorder; allergy; blood disorder;
KM acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KM immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KM Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KM cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
KM haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KM antisthmatic; nephrotropic; antiarthritic; hepatotropic;

XX	WC000268649-A2.
FN	
XX	
XX	
PD	06-SEP-2002.
PF	
31-JAN-2002;	2002WC-US002785.
XX	
31-JAN-2001;	2001US-0265395P.
PR	31-JAN-2001;
PR	2001US-0265412P.
PR	31-JAN-2001;
PR	2001US-0265517P.
PR	31-JAN-2001;
PR	2001US-0265514P.
PR	02-FEB-2001;
PR	2001US-0266406P.
PR	03-FEB-2001;
PR	2001US-0266767P.
PR	07-FEB-2001;
PR	2001US-0266755P.
PR	07-FEB-2001;
PR	2001US-0267057P.
PR	08-FEB-2001;
PR	2001US-0267459P.
PR	09-FEB-2001;
PR	2001US-0267823P.
PR	15-FEB-2001;
PR	2001US-0268974P.
PR	26-FEB-2001;
PR	2001US-0271664P.
PR	27-FEB-2001;
PR	2001US-0271839P.
PR	27-FEB-2001;
PR	2001US-0271855P.
PR	02-MAR-2001;
PR	2001US-0272788P.
PR	02-MAR-2001;
PR	2001US-0273046P.
PR	14-MAR-2001;
PR	2001US-0275925P.
PR	14-MAR-2001;
PR	2001US-0275947P.
PR	14-MAR-2001;
PR	2001US-0275950P.
PR	14-MAR-2001;
PR	2001US-0275989P.
PR	15-MAR-2001;
PR	2001US-0276448P.
PR	15-MAR-2001;
PR	2001US-0276450P.
PR	16-MAR-2001;
PR	2001US-0276397P.
PR	16-MAR-2001;
PR	2001US-0276765P.
PR	20-MAR-2001;
PR	2001US-0278652P.
PR	26-MAR-2001;
PR	2001US-0278775P.
PR	26-MAR-2001;
PR	2001US-0278778P.
PR	29-MAR-2001;
PR	2001US-0279682P.
PR	29-MAR-2001;
PR	2001US-0279684P.
PR	30-MAR-2001;
PR	2001US-0280147P.
PR	11-APR-2001;
PR	2001US-0282992P.
PR	11-APR-2001;
PR	2001US-0283083P.
PR	20-APR-2001;
PR	2001US-0285133P.
PR	23-APR-2001;
PR	2001US-0285749P.
PR	03-MAY-2001;
PR	2001US-0286327P.
PR	03-MAY-2001;
PR	2001US-0288504P.
PR	29-MAY-2001;
PR	2001US-0294074P.
PR	30-MAY-2001;
PR	2001US-0294473P.
PR	08-JUN-2001;
PR	2001US-0296964P.
PR	18-JUN-2001;
PR	2001US-0298959P.
PR	19-JUN-2001;
PR	2001US-0299324P.
PR	13-AUG-2001;
PR	2001US-0312020P.
PR	16-AUG-2001;
PR	2001US-0312889P.
PR	16-AUG-2001;
PR	2001US-0312908P.
PR	21-AUG-2001;
PR	2001US-0313390P.
PR	28-AUG-2001;
PR	2001US-0315470P.
PR	31-AUG-2001;
PR	2001US-0316447P.
PR	07-SEP-2001;
PR	2001US-0318115P.
PR	07-SEP-2001;
PR	2001US-0318118P.
PR	12-SEP-2001;
PR	2001US-0318740P.
PR	19-SEP-2001;
PR	2001US-0323379P.
PR	18-OCT-2001;
PR	2001US-0330245P.
PR	18-OCT-2001;
PR	2001US-0330308P.
PR	14-NOV-2001;
PR	2001US-0332701P.
XX	
PA	
XX	(CURA-) CURAGEN CORP.
XX	
PI	Tchernev VT, Spytek KA, Zethusen BD, Faturajan M, Shinkets RA;
PI	Li L, Gangolfi EA, Padgugan M, Anderson DW, Rattelli L, Miller CB;
PI	Gielach VL, Tappier RJ, Guev VY, Colman SD, Wolenc AR, Pena CEA;
PI	Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE
XX	WP1; 2002-706998/76.
XX	N-PSDB; AD11605.
XX	

Pt	treating NOXV-associated disorders", e.g. cancer, cardiomyopathy,
Pt	atherosclerosis, or diabetes), and in chromosome mapping, tissue typing or
Pt	pharmacogenomics.
Xx	
PS	Claim 1; SEQ ID NO 142; 1498pp; English.
Cc	This invention relates to a novel nucleic acids, and encoded polypeptides
Cc	thereof, which have properties related to the stimulation of biochemical
Cc	or physiological responses in a cell, tissue, organ or organism.
Cc	Specifically, it refers to the use of biologically active fragments for
Cc	diagnostic and prognostic assays and furthermore in the treatment of
Cc	diverse pathological conditions. The present invention describes novel
Cc	human and murine NOXV proteins, as well as methods to modulate their
Cc	expression using antisense oligos, ribozymes and peptide nucleic acids.
Cc	The NOXV polypeptides, polymucleotides and antibodies are useful in
Cc	treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
Cc	atherosclerosis, cancer and diabetes. Furthermore, they may be used in
Cc	treating or preventing diseases such as inflammation, autoimmune
Cc	disorders, allergies, blood disorders, acquired immunodeficiency syndrome
Cc	(AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
Cc	arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
Cc	and epilepsy. Accordingly, these molecules have many activities including
Cc	cycostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
Cc	haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anoecttic,
Cc	antianasthetic, nephrotropic, antiarthritic, hepatotropic,
Cc	neuroprotective, nootropic, antibacterial, vitucide, antiparasitic,
Cc	relaxant and anticovulsant. In addition, they are useful in screening
Cc	assays to identify small molecules that modulate or inhibit, for example,
Cc	neurogenesis, wound healing and angiogenesis. The nucleic acids are also
Cc	used as in chromosome mapping, tissue typing, preventive medicine and
Cc	pharmacogenomics. This polypeptide is a human NOXV protein of the
Cc	invention.
Sq	
SQ	Sequence 781 AA;
Yy	
Query Match	100.0%; Score 95; DB 5; Length 781;
Best local similarity	100.0%; Pred. No. 6,9e-05;
Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Dd	
1 MMGVRLLMLMGSGWG 16	
1 MMGVRLMLLMGSGWG 16	
RESULT 10	
ID	ABR40114 standard; protein; 781 AA.
AC	XX ABR40114;
DT	XX 04-JUL-2003 (first entry)
DE	Human cell adhesion and extracellular matrix protein, CADECW-11.
KM	Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
KM	anticovulsant; nootropic; neuroprotective; immunosuppressive;
KM	dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KM	gene therapy; cell adhesion; extracellular matrix; CADECW;
KM	immune system disorder; AIDS; allergy; neurological disorder; stroke;
KM	Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KM	cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
KM	genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
OS	Homo sapiens.
XX	WO2003027230-A2.
PN	03-APR-2003.
PD	02-AUG-2002; 2002WO-USO24649.
PF	
XX	

PR 03-AUG-2001; 2001US-0310119P.
PR 17-AUG-2001; 2001US-0313051P.
PR 31-AUG-2001; 2001US-0316771P.
PR 07-SEP-2001; 2001US-0317896P.
PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
XX (INCYTE GENOMICS INC.)
XX
XX Burford N, Warren BA, Duggan BW, Mason PM, Richardson TW, Yue H;
PI Forsythe JF, Elliott VS, Griffith JA, Gorvad AE, Azimzai Y;
PI Kallik DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
PI Waila NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
DR WPI; 2003-354645/33.
DR N-PSDB; ACC00402.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
XX Claim 1; Page 192-194; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACC00392-ACC00413, and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX CC lusus erythematous), genetic disorders (e.g. Alport's syndrome) or cell
XX CC proliferative disorders (e.g. cancer or atherosclerosis)
XX
XX Sequence 781 AA;
SQ
XX
XX Query Match 100.0%; Score 95; DB 6; Length 781;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMGLVRLILAWLGWG 16
Db 1 MMGLVRLILAWLGWG 16

RESULT 11
ADA01366
ID ADA01366 standard; protein: 781 AA.
XX
XX ADA01366;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human PRO polypeptide #49.
DE
XX
XX Human, PRO; secreted polypeptide; transmembrane polypeptide;
KM tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KM adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KM microvascular endothelial cell; endothelial cell tube formation;
KM sports-related joint problem; articular cartilage defect; osteoarthritis;
KM rheumatoid arthritis; osteoporosis; antirheumatic; antirheumatic;
XX
XX Homo sapiens.
OS
XX US2003068779-A1.
FN
XX 10-APR-2003.
PD
XX 16-SEP-2002; 2002US-00245107.
PF

XX 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001US-0290709P.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENT) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Rivaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WT, Zhang Z;
PI Fong S;
DR WPI; 2003-625484/59.
DR N-PSDB; ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for inducing endothelial cell
XX tube formation and for treating sports-related joint problems, articular
XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
XX represents a human PRO polypeptide of the invention.
XX
XX Sequence 781 AA;
SQ
XX
XX Query Match 100.0%; Score 95; DB 6; Length 781;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-05;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMGLVRLILAWLGWG 16
Db 1 MMGLVRLILAWLGWG 16

RESULT 12
ADA43795
ID ADA43795 standard; protein: 781 AA.
XX
XX ADA43795;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human secreted/transmembrane polypeptide PRO34009.
DE
XX
XX Human, PRO; secreted protein; transmembrane protein;
KM endothelial cell tube formation; chondrocyte cell differentiation;
KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
KM liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX US2003064474-A1.
FN

XX 03-APR-2003.
PD 16-SEP-2002; 2002US-00245859.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX (GENTH) GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI: 2003-605867/57.
DR N-PSDB; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO2183, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 11; Fig 98; 308pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acid encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6000, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO133, PRO20080
CC and PRO2183 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. NO. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 20-NOV-2003 (first entry)
XX Human secreted/transmembrane polypeptide PRO34009.
DE
XX Human; PRO: secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour, lung tumour, colon tumour;
XX breast tumour, prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
XX US2003073196-A1.
XX
XX 17-APR-2003.
XX
XX 18-SEP-2002; 2002US-00246210.
XX
XX 04-APR-2001; 2001US-0282199P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI: 2003-743814/70.
XX N-PSDB; ADA43562.
XX
XX
XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
XX PRO2183 useful for stimulating the proliferation or differentiation of
XX chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
XX polypeptide, having at least 80% sequence identity to a sequence selected
XX from any one of the 57 amino acid sequences given in specification, or to
XX a sequence encoded by a nucleic acid molecule selected from any one of
XX the nucleic acids deposited under any of the ATCC accession numbers given
XX in specification, or a sequence having at least 80% identity to PRO
XX lacking its associated signal peptide, an extracellular domain of PRO
XX with or without its associated signal peptide. Also included are vectors,
XX transformed host cells, anti-PRO antibodies, the nucleic acid encoding
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6000, PRO6000,
XX PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX an oligonucleotide probe derived from any one of the above nucleotide
XX sequences. PRO6018 polypeptide is useful for stimulating the
XX proliferation or differentiation of chondrocyte cells. PRO133, PRO20080
XX and PRO2183 polypeptides are useful for stimulating the proliferation of
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX polypeptides are useful for inhibiting the proliferation of human
XX microvascular endothelial cells. PRO polypeptides are useful for
XX detecting the presence of tumour in a mammal, including tumours of lung,
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX PRO189, PRO4499, PRO6000, PRO10275, PRO21207, PRO20933 and
XX PRO34274 polypeptides are useful for inducing endothelial cell tube
XX formation. PRO or the antibody are useful in the preparation of a
XX medicament for treating a condition responsive to PRO polypeptide. The
XX oligonucleotide probes are useful for isolating genomic and cDNA
XX nucleotide sequences, for measuring or detecting the expression of an
XX associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX hybridisation probe, in chromosome and gene mapping, in the generation of
XX antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 95; DB 6; Length 781;

CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;

Query Match 100.0%; Score 95; DB 7; Length 781;
Best Local Similarity 100.0%; Pred. NO. 6.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGWG 16
|||
1 MMGLVRLLLAWLGWG 16

Search completed: December 8, 2004, 10:13:03
Job time : 7.62102 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 16.3495 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-6

Perfect score: 95

Sequence: 1 MWGLVRLJLMLGSGWG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 segs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	95	100.0	16	10	US-09-788-051-6
2	95	100.0	493	15	US-10-072-012-482
3	95	100.0	607	15	US-10-258-851-74
4	95	100.0	636	10	US-09-788-051-4
5	95	100.0	781	9	US-09-860-868-2
6	95	100.0	781	14	US-10-245-752-98
7	95	100.0	781	14	US-10-245-859-98
8	95	100.0	781	14	US-10-245-103-98
9	95	100.0	781	14	US-10-245-107-98
10	95	100.0	781	14	US-10-245-143-98
11	95	100.0	781	14	US-10-245-771-98
12	95	100.0	781	14	US-10-245-851-98
13	95	100.0	781	14	US-10-245-883-98

14	95	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
15	95	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
16	95	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
17	95	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
18	95	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
19	95	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
20	95	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
21	95	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
22	95	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
23	95	100.0	781	14	US-10-239-136-98	Sequence 98, Appl
24	95	100.0	781	14	US-10-243-024-98	Sequence 98, Appl
25	95	100.0	781	14	US-10-243-409-98	Sequence 98, Appl
26	95	100.0	781	14	US-10-245-621-98	Sequence 98, Appl
27	95	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
28	95	100.0	781	14	US-10-245-023-98	Sequence 98, Appl
29	95	100.0	781	14	US-10-243-035-98	Sequence 98, Appl
30	95	100.0	781	14	US-10-243-185-98	Sequence 98, Appl
31	95	100.0	781	14	US-10-245-427-98	Sequence 98, Appl
32	95	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
33	95	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
34	95	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
35	95	100.0	781	14	US-10-243-370-98	Sequence 98, Appl
36	95	100.0	781	14	US-10-162-435-13	Sequence 98, Appl
37	95	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
38	95	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
39	95	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
40	95	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
41	95	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
42	95	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
43	95	100.0	781	14	US-10-238-411-98	Sequence 98, Appl
44	95	100.0	781	14	US-10-243-124-98	Sequence 98, Appl
45	95	100.0	781	14	US-10-243-425-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-6
Sequence 6, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-6

Query Match 100.0% ; Score 95; DB 10; Length 16;
Best Local Similarity 100.0% ; Pred. No. 1.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLVRLJLMLGSGWG 16

Db 1 MMGLVRLLLAWLGGWG 16

RESULT 2

US-10-072-012-482
; Sequence 482, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchermey, Velizar
; APPLICANT: Szytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esna
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 482
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-482

Query Match 100.0%; Score 95; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGGWG 16
DB 1 MMGLVRLLLAWLGGWG 16

RESULT 3

US-10-258-951-74
; Sequence 74, Application US/10258951
; Publication No. US20040033504A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnick, Karen
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 95; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLLLAWLGGWG 16
DB 1 MMGLVRLLLAWLGGWG 16

RESULT 4

US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radjoe T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 95; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MMGLVRLILAWLGWG 16
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DB 1 MMGLVRLILAWLGWG 16

RESULT 5
US-09-860-868-2

Sequence 2, Application US/09860868
Patent No. US20020076757A1
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J.
TITLE OF INVENTION: 57805, A NOVEL HUMAN CACHERIN FAMILY
FILE REFERENCE: 1048-050001
CURRENT APPLICATION NUMBER: US/09/860,868
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 60/205,674
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 95; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.0002; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MMGLVRLILAWLGWG 16
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DB 1 MMGLVRLILAWLGWG 16

RESULT 6
US-10-245-752-98

Sequence 98, Application US/10245752
Publication No. US20030064473A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watcane, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C66
CURRENT APPLICATION NUMBER: US/10/245,752
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-752-98

CY 1 MMGLVRLILAWLGWG 16
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DB 1 MMGLVRLILAWLGWG 16

RESULT 7
US-10-245-859-98

Sequence 98, Application US/10245859
Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watcane, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C78
CURRENT APPLICATION NUMBER: US/10/245,859
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT

ORGANISM: Homo Sapien
US-10-245-859-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGSGW 16
DB 1 MMGLVRLILAWLGSGW 16

RESULT 8
US-10-245-103-98

Sequence 98, Application US/10245103
Publication No. US2003006878A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C12
CURRENT APPLICATION NUMBER: US/10/245,103
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-103-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGSGW 16
DB 1 MMGLVRLILAWLGSGW 16

RESULT 9
US-10-245-107-98

Sequence 98, Application US/10245107
Publication No. US2003006879A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C17
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGSGW 16
DB 1 MMGLVRLILAWLGSGW 16

RESULT 10
US-10-245-143-98

Sequence 98, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

```
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C90
CURRENT APPLICATION NUMBER: US/10/245,143
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match      100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMGLVRLILANLWGSG 16
DB      1 MMGLVRLILANLWGSG 16

RESULT 11
US-10-245-771-98
Sequence 98, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
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PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-771-98

Query Match      100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMGLVRLILANLWGSG 16
DB      1 MMGLVRLILANLWGSG 16

RESULT 12
US-10-245-851-98
Sequence 98, Application US/10245851
Publication No. US20030068782A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C93
CURRENT APPLICATION NUMBER: US/10/245,851
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
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SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-851-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGWG 16
DB 1 MMGLVRLILAWLGWG 16

RESULT 13
US-10-245-883-98
Sequence 98, Application US/10245883
Publication No. US20030068783A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C70
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-883-98

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMGLVRLILAWLGWG 16
DB 1 MMGLVRLILAWLGWG 16

RESULT 14
US-10-237-535-98
Sequence 98, Application US/10237535
Publication No. US20030073188A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C3
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/134459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09

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PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
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PRIOR FILING DATE: 1999-07-20
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PRIOR FILING DATE: 1999-08-31
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PRIOR FILING DATE: 1999-10-29
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PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/186921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
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PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150

PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
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PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
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PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MMGLVRLILAVTGGWG 16
DB 1 MMGLVRLILAVTGGWG 16
RESULT 15
US-10-238-183-98
Sequence 98, Application US/10238183
Publication No. US20030073189A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C11
CURRENT APPLICATION NUMBER: US/10/238,183
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09

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PRIOR APPLICATION NUMBER: 60/274399
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PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match: 100.0%; Score 95; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MMGLVRLLLAWLGGWG 16
1 MMGLVRLLLAWLGGWG 16

Search completed: December 8, 2004, 11:34:26
Job time: 16.3495 secs

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OM protein - protein search, using sw model
Run on: December 8, 2004, 09:16:13 ; Search time 1.90791 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-6
Perfect score: 95
Sequence: 1 MWGLVLLMLLWLGWG 16

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 478139 segs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	54	56.8	555	4	US-09-252-991A-31521
2	53	55.8	173	4	US-09-543-681A-7869
3	53	55.8	195	4	US-09-489-039A-12028
4	48	50.5	86	4	US-09-513-999C-4272
5	48	50.5	373	4	US-09-252-991A-24381
6	47	49.5	500	4	US-09-540-236-3439
7	46	48.4	126	4	US-09-583-110-2867
8	45	47.4	860	4	US-09-252-991A-26112
9	45	47.4	1147	2	US-08-131-365B-38
10	45	47.4	1147	2	US-08-668-123-38
11	44	46.3	169	4	US-09-328-352-6931
12	44	46.3	273	4	US-09-489-039A-12374
13	44	46.3	346	5	PCR-US96-10602-2
14	44	46.3	582	4	US-09-488-1039A-10786
15	43.5	45.8	361	4	US-09-328-352-7040
16	43	45.3	12	2	US-08-764-640-136
17	43	45.3	12	2	US-08-973-225-136
18	43	45.3	12	3	US-09-244-238A-136
19	43	45.3	12	3	US-09-516-704-136
20	43	45.3	12	4	US-09-540-090-136
21	43	45.3	12	4	US-09-832-233A-136
22	43	45.3	439	4	US-09-583-110-3057
23	42.5	44.7	112	4	US-09-205-258-1097
24	42	44.2	157	4	US-09-270-767-32124
25	42	44.2	157	4	US-09-270-767-47341
26	42	44.2	210	3	US-08-849-764C-4
27	42	44.2	210	3	US-09-262-087-4

28	42	44.2	210	4	US-08-463-261B-10	Sequence 10, Appl
29	42	44.2	211	1	US-08-588-163-4	Sequence 4, Appl
30	42	44.2	211	2	US-09-111-070-4	Sequence 4, Appl
31	42	44.2	211	4	US-09-540-530-3	Sequence 3, Appl
32	42	44.2	211	4	US-08-134-231C-13	Sequence 13, Appl
33	42	44.2	211	4	US-08-728-160-13	Sequence 13, Appl
34	42	44.2	309	4	US-09-489-039A-10582	Sequence 10582, A
35	42	44.2	317	2	US-08-864-799-4	Sequence 4, Appl
36	42	44.2	317	2	US-08-864-799-5	Sequence 5, Appl
37	42	44.2	348	4	US-09-489-039A-8632	Sequence 8632, Ap
38	42	44.2	538	3	US-09-040-005-2	Sequence 2, Appl
39	42	44.2	538	3	US-09-522-217-115	Sequence 115, App
40	42	44.2	538	4	US-09-404-641-2	Sequence 2, Appl
41	42	44.2	538	4	US-09-923-246-115	Sequence 115, App
42	42	44.2	538	4	US-10-295-723-115	Sequence 115, App
43	42	44.2	538	4	US-10-414-186-2	Sequence 2, Appl
44	42	44.2	538	4	US-09-825-561A-2	Sequence 2, Appl
45	42	44.2	539	4	US-09-248-796A-16542	Sequence 16542, A

ALIGNMENTS

```
RESULT 1
US-09-252-991A-31521
; Sequence 31521, Application US/09252991A
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31521
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31521

Query Match      56.8%; Score 54; DB 4; Length 555;
Best Local Similarity 76.9%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3  GLVRLMLLWLGW 15
Db      219  GLVRLMLLWLGW 231

RESULT 2
US-09-543-681A-7869
; Sequence 7869, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRENNON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7869
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7869
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Query Match 55.8%; Score 53; DB 4; Length 173;
Best Local Similarity 62.5%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1 MGVLRLLIWLWGNG 16
Db 88 MMQLVGFYLGWLGSEG 103

RESULT 3

US-09-489-039A-12028
; Sequence 12028, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12028
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12028

Query Match 55.8%; Score 53; DB 4; Length 195;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 1 MGVLRLLIWLWGNG 16
Db 110 MMQLVGFYLGWLGSEG 125

RESULT 4

US-09-513-999C-4272
; Sequence 4272, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59,US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4272
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -22..-1
; OTHER INFORMATION: score 10
; OTHER INFORMATION: seq FILATLTIASTWA/LT
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 13
; OTHER INFORMATION: Xaa=Glu or Gly
US-09-513-999C-4272

Query Match 50.5%; Score 48; DB 4; Length 86;
Best Local Similarity 72.7%; Pred. No. 6.9;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Cy 5 VRLILWLWGNG 15
Db 70 VRLILSWWSGW 80

RESULT 5

US-09-252-991A-24381
; Sequence 24381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24381
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24381

Query Match 50.5%; Score 48; DB 4; Length 373;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 4 LVRLILWLWGNG 15
Db 120 LVGLIMCWRCGW 131

RESULT 6

US-09-540-236-3439
; Sequence 3439, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709,2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3439
; LENGTH: 500
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3439

Query Match 49.5%; Score 47; DB 4; Length 500;
Best Local Similarity 87.5%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 8 LLAWLWGW 15
Db 164 LVAWLWGW 171

RESULT 7

US-09-583-110-2867
; Sequence 2867, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2867
LENGTH: 126
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-2867

Query Match 48.4%; Score 46; DB 4; Length 126;
Best Local Similarity 46.2%; Pred. No. 19;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 MMGLVRLIAMLG 13
DB 6 LMALILAMLMWG 18

RESULT 8
US-09-252-991A-26112
Sequence 26112, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26112
LENGTH: 860
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26112

Query Match 47.4%; Score 45; DB 4; Length 860;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 GLVRLIAMLG 16
DB 624 GLAQLQTLPRWG 637

RESULT 9
US-08-131-365B-38
Sequence 38, Application US/08131365B
Patent No. 5527690
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston

STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/131,365B
FILING DATE: 01-OCT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-131-365B-38

Query Match 47.4%; Score 45; DB 1; Length 1147;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

OY 1 MMGLVRLI-AMLG 15
DB 628 LMLIRHLGLRLVGRW 644

RESULT 10
US-08-668-123-38
Sequence 38, Application US/08668123
Patent No. 5891631
GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
APPLICANT: Goldstein, Joseph L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-123-38

Query Match 47.4%; Score 45; DB 2; Length 1147;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 1 MGGLVRL--AVLGM 15
DB 628 LMLIRHLQRLWYGRM 644
RESULT 11
US-09-328-352-6931
Sequence 6931, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-035A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6931
LENGTH: 169
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-6931

Query Match 46.3%; Score 44; DB 4; Length 169;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 VRLILAVLWLGWG 16
DB 113 IGLIVAVLWLGWG 124
RESULT 12
US-09-489-039A-12374
Sequence 12374, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12374
LENGTH: 273
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12374

Query Match 46.3%; Score 44; DB 4; Length 273;
Best Local Similarity 87.5%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
PCT-US96-10602-2
Sequence 2, Application PC/TUS9610602
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10602
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,814
FILING DATE: 20-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/282001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10602-2

Query Match 46.3%; Score 44; DB 5; Length 346;
Best Local Similarity 47.6%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 8; Gaps 1;

QY 2 MGVLRL-----LAVLGG 14
DB 285 WALARLSWNLVPLWLG 305
RESULT 14
US-09-489-039A-10786
Sequence 10786, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10786
LENGTH: 582
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10786

Wed Dec 8 11:46:31 2004

us-09-788-051-6.rat

Page 5

Query Match 46.3%; Score 44; DB 4; Length 582;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 MMGLVRL--LWLVGGWG 15
: ||| ||| : |||
Db 20 LMLVALLVITIGAM 34

RESULT 15
US-09-328-352-7040
; Sequence 7040, Application US/09328352
; Patent No. 6562358
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7040
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7040

Query Match 45.8%; Score 43.5; DB 4; Length 361;
Best Local Similarity 42.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

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: ||| ||| : |||
Db 101 VMGIPVILIGLWLVWVG 119

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Job time: 2.90791 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 50.1417 Seconds

(without alignments)
1189.717 Million cell updates/sec

Title: us-09-788-051-7

Perfect score: 3259

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Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: PIR2:*
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4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	49.2	796	2	A38992
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3	1593	48.9	796	2	148277
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5	1529.5	46.9	793	2	D38992
6	1441	44.2	789	2	152701
7	1440	44.2	790	2	137016
8	1431.5	43.9	785	2	150180
9	1412.5	43.3	790	2	G02678
10	1400	43.0	790	2	150178
11	1389.5	42.6	790	2	151638
12	1368.5	42.0	794	2	159372
13	935.5	28.7	784	1	10HUC5
14	601	18.4	906	1	10HUCN
15	596	18.3	913	1	10HUCR
16	594.5	18.2	906	1	10HUC2
17	594	18.2	906	1	10HUCN
18	592	18.2	877	1	10HUCN
19	591	18.1	912	1	10HUCN
20	586	18.0	887	1	10HUCN
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22	581	17.8	882	1	10HUC5
23	581	17.8	905	1	10HUC2
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25	574.5	17.6	717	2	151206
26	567	17.4	916	2	C38992
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44					G-cadherin-15 precu
45					G-cadherin-15 precu

30	531	16.3	732	1	10HUCB
31	531	16.3	783	2	150116
32	524	16.1	884	2	10HUC5
33	523.5	16.1	896	2	145858
34	521	16.0	884	2	S34438
35	519	15.9	871	2	S47518
36	512	15.7	3034	2	T14119
37	510.5	15.7	826	2	B53363
38	510.5	15.7	896	2	A55363
39	507	15.6	730	1	10HUCN
40	502.5	15.4	822	1	10HUCP
41	502.5	15.4	829	1	10HUCP
42	486	15.2	3097	2	T00021
43	481	15.1	840	2	137281
44	481	15.1	894	2	137281
45	487	14.9	770	2	B48910

ALIGNMENTS

RESULT 1

A38992

cadherin 11 precursor - human

N/Alternate names: OB-cadherin, osteoblast

C/Species: Homo sapiens (man)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: A38992

R/Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: A38992

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-796 <SUZ>

A/Cross-references: UNIPROT:P55287; GB:U34056; MUID:9506403; PIDN:AAA5622.1; PID:950640

C/Genetics:

A/Gene: GDB:CDH11; OB

A/Cross-references: GDB:512891; OMIM:600023

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication

F/56-159/Domain: cadherin repeat homology <CR1>

F/162-268/Domain: cadherin repeat homology <CR2>

F/211-383/Domain: cadherin repeat homology <CR3>

F/386-488/Domain: cadherin repeat homology <CR4>

Query Match

Best Local Similarity 50.4%; Score 1602; DB 2; Length 796;

Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

QY	1	CMGRLLA-----APAR-----AMAGSR--HGQPALLRFRSGWVNNQFVIEEYAGPEPV	47
DB	13	CLQMLCHSAFAPBERGHLPSPFHGHEKKGQVQIRKRGWVNNQFVIEEYTPDDV	72
QY	48	LICKLMSVDYRGGRKTYLLTGEAGTVFVIDEATGNHVTSLDREERQAQVLLAQAVD	107
DB	73	LVGRLLMSDSDGDNIKYILSGGAGTIVIDDKSGNIAHTKLDREERQAQVLLAQAVD	132
QY	108	RASNRLPEPSEFIIIGQDINNPFIPLGPHATPEMSNGTSVIOYADADDPSTG	167
DB	133	RDNRPLPEPSEFIVQDINDNPEFLHETTHANVPESNGTSVIOYADADDPSTG	192
QY	168	NSAKLVYVLDGLPFESVDPQGTGVVTAIPNDRETQEEFLVVIQAKDGMGNGGLSGST	227
DB	193	NSAKLVYSILDEQPYFSVEAQGTGIRTPALPNDRKEEYHVVIQAKDGMGNGGLSGST	252
QY	228	TIVTITSDVVDNPPKPPQSIYQFSVETAGPGLVGRRLAQPDDGLNMLMYSLIDGGG	287
DB	253	KVITITLVDVNDPPKPPQRIYQMSVSEAAVGGSEVERVAKPPDGENGLVTYNIVDGGG	312
QY	288	SEAFSISTDQGDGLITVRKPLDFESQSRYSFRVETATLLIDPAYLRGPFEDVASVAV	347

Db 313 MESEFITDYEFGVILKKKPVDFETERAVSLKVEANVHIDPKFISNGPFDOTVTKI 372
Qy 348 AVQAPREPAFTQAAHNLTVPENKAPGLVQGISAADLSPASIRSYILPHSDPERCSF 407
Db 373 SVEDDEPMPFLASVYHEVQENAAAGVGRVAKAPDPAANSPIRISIDRHLDLDFFT 432
Qy 408 IQPEEGTHTAAPLDREARAHNLTVLATELGMSWGPGRGVPLLVAMSAAPAPQSRP 467
Db 433 INPEDGFIKTKTLPDLREBTALNITVPAELI-----463
Qy 468 VGSAGVIGPQSSAQAQVAVIQTLDENDNAPOLAEYDIFVCDSDS---AAPQGLQVIR 523
Db 464 -----NHRHQEAQVPAIRVLVDNDNAPKFAAYEGFICESDQTKPLSNQPIVTS 514
Qy 524 ALDRDEVNSSHVSFFQGP--LGPDPANFTVQDNRLDPA-----WPHPLM 565
Db 515 ADDXDDPDANGBRFLFSLPPEIHNPNFTVQDNNTAGVYARRGGRKQKODLYLPIVI 574
Qy 566 ASASSWLHWPFAERGNQAPASOGKSSLP-CG-RIPGALPSC 604
Db 575 -----SDGIIPPMSTNTLTIKVGCGDVNGALJSC 604

RESULT 2

OB-cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kido, A.; Mann, E. J. Biol. Chem. 269, 12092-12098, 1994
A:Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin A; Reference number: A53584; MUID:94216322; PMID:8163513
A:Accession: A53584
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:g994774; PIDN:BA04797.1; PID:g994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
C:Keywords: transmembrane protein
F:156-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:386-488/Domain: cadherin repeat homology <CR4>

Query Match 49.0%; Score 1596; DB 2; Length 796;
Best Local Similarity 50.7%; Pred. No. 2.8e-98;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;
Qy 15 SREHP-----GPAIIKTRRSVWVNOFFVIEEYAGPEPVLIGKLSHDVDRGERT 63
Db 29 SHLHPSFHGHKEKKEQVLRKSKGWVWNOFFVIEEYAGPEPVLIGKLSHDVDRGERT 88
Qy 64 KYLLTGAGAGTVFVIDATGNIHVTKSLDREKQAVYLLAQAVIDRASNPRLPEPSEFIK 123
Db 89 KYLLSGGAGTIFVIDKSGNIHATKTLDBEERAOYTLMAQAVIDRDTNRPLEPSEFIK 148
Qy 124 GODINDNPPFLPGPYHATVPENSNVGTSVIQTADHADDPSYGNSAKLYTVLDDLPF 183
Db 149 VQDINDNPPFLHETIYHANVPERSNVGTSVIQTADHADDPSYGNSAKLYTVLDDLPF 208
Qy 184 SVDPOGTVARAIINMRETOEFLVYIOAKDGMGNGISGTTVTLVTLSDVNDNPPK 243
Db 209 SVZAQGTGIRTAIPNDREAKEHETVYIOAKDGMGNGISGTTVTLVTLSDVNDNPPK 268
Qy 244 POSLYQSVYETAGPGLVGRLAODPDLDGNALMAYSILDEGSEAFSISTDLQGRDL 303
Db 269 POSYQMSVEEAAPGEEVGRVAKAPDIDGENGLVTYNIYDGGIELFETITDYETQDV 328
Qy 304 LTVAKPLDEPSSQSYSRVATNTLIDPALREGPKDVAAYVAVQDAPEPAFTQAA 363
Db 329 VKLKKPVDFETKAYSLKIEANVHIDPKFISNGPFDOTVTKISVEDADEPMPFLASV 388

Qy 364 HLTVPENKAPGLVQGISAADLSPASIRSYILPHSDPERCSFIOPEEGTHTAAPLDR 423
Db 389 IHEVQENAAAGTVGRVAKAPDPAANSPIRISIDRHLDLDFFTINPEDGFIKTKPLDR 448
Qy 424 EARAHNLTVLATELGMSWGPGRGVPLLVAMSAAPAPQSRVGSAGVIGPQSSAQAQ 483
Db 449 EETAMNLSVPAELI-----HNRHQET 470
Qy 464 RYQVAVIQTLDENDNAPOLAEYDIFVCDSDSAP-----GGLQVIRALDRDEVNSSHVSFQ 539
Db 471 KYPVALIRVLVDNDNAPKFAAYEGFICESDHPKLSNQPIVTVASDADDODDPAANPRIF 530
Qy 540 GP--LGPDPANFTVQDNRLDPA-----WPHPLMASASSWLHWPFAERGN 581
Db 531 LPPEIHNPNFTVQDNNTAGVYARRGGRKQKODLYLPIVI-----SDGII 579
Qy 582 QPASGKSSLP-CG-RIPGALPSC 604
Db 580 PMSSTNTLTIKVGCGDVNGALJSC 604

RESULT 3

cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48277
R:Hoffmann, I.; Balling, R. Dev. Biol. 169, 337-346, 1995
A:Title: Cloning and expression analysis of a novel mesodermally expressed cadherin. A:Reference number: I48277; MUID:95262886; PMID:7750649
A:Accession: I48277
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <RES>
A:Cross-references: UNIPROT:P55288; EMBL:X77557; NID:g642796; PIDN:CA054674.1; PID:g666606
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4.4e-98;
Matches 316; Conservative 96; Mismatches 127; Indels 84; Gaps 8;
Qy 15 SREHP-----GPAIIKTRRSVWVNOFFVIEEYAGPEPVLIGKLSHDVDRGERT 63
Db 29 SHLHPSFHGHKEKKEQVLRKSKGWVWNOFFVIEEYAGPEPVLIGKLSHDVDRGERT 88
Qy 64 KYLLTGAGAGTVFVIDATGNIHVTKSLDREKQAVYLLAQAVIDRASNPRLPEPSEFIK 123
Db 89 KYLLSGGAGTIFVIDKSGNIHATKTLDBEERAOYTLMAQAVIDRDTNRPLEPSEFIK 148
Qy 124 GODINDNPPFLPGPYHATVPENSNVGTSVIQTADHADDPSYGNSAKLYTVLDDLPF 183
Db 149 VQDINDNPPFLHETIYHANVPERSNVGTSVIQTADHADDPSYGNSAKLYTVLDDLPF 208
Qy 184 SVDPOGTVARAIINMRETOEFLVYIOAKDGMGNGISGTTVTLVTLSDVNDNPPK 243
Db 209 SVZAQGTGIRTAIPNDREAKEHETVYIOAKDGMGNGISGTTVTLVTLSDVNDNPPK 268
Qy 244 POSLYQSVYETAGPGLVGRLAODPDLDGNALMAYSILDEGSEAFSISTDLQGRDL 303
Db 269 POSYQMSVEEAAPGEEVGRVAKAPDIDGENGLVTYNIYDGGIELFETITDYETQDV 328
Qy 304 LTVAKPLDEPSSQSYSRVATNTLIDPALREGPKDVAAYVAVQDAPEPAFTQAA 363
Db 329 VKLKKPVDFETKAYSLKIEANVHIDPKFISNGPFDOTVTKISVEDADEPMPFLASV 388
Qy 364 HLTVPENKAPGLVQGISAADLSPASIRSYILPHSDPERCSFIOPEEGTHTAAPLDR 423
Db 389 IHEVQENAAAGTVGRVAKAPDPAANSPIRISIDRHLDLDFFTINPEDGFIKTKPLDR 448

QY 424 EAAAHNLTATLTELGLWGWPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQAS 483
| : : : : :
DB 449 EETAMNLSVPAADI-----HNNHQT 470
QY 484 RVQVAITQTLDBNDNAPOLAEPTFTVCDSPAAP-----GQLIQVIRALDRDEVGSSHVSPQ 539
| : : : : :
DB 471 KVPVAIRVLVDNDAPKFAAPYEGFICSDHPKALSNQPIVTSADQDDTANGPRTFS 530
QY 540 GP--LGPDAFTVQDNRLDPA-----WFHPLMASASWMLWPPAERGN 581
| : : : : :
DB 531 LPPEIMNPNFTVRNDNDNTAGVYARRGFSROKQDPYLLPIV-----SDGGI 579
QY 582 QPASQKSSSLP-CG-RLPGALPSC 604
| : : : : :
DB 580 PPMSTNTLTITKVCQDVNGALLSC 604

RESULT 4

149556
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R:Kimura, Y.; Matsumi, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169,347-358, 1995
A/Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A/Reference number: 149556; MUID:95269887; PMID:7750650
A/Accession: 149556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; GB:D11963; NID:g974190; PIDN:BA06730.1; PID:g974191
C/Superfamily: cadherin; cadherin repeat homology
F:56-159/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 1593; DB 2; Length 796;
Best Local Similarity 50.6%; Pred. No. 4,4e-98;
Matches 317; Conservative 95; Mismatches 128; Indels 86; Gaps 8;

QY 15 GREHP-----GPA.LRTRSWVWNOFVIEEYAGPEPVLIGKLSDVDRGEGRT 63
| : : : : :
DB 29 SHLPSPFGHHEKGEQVLQSRKRWVWNOFVIEETGDPVLVGRHLSDIDSGDGN 88
QY 64 KYLLTGBGAGTVFVDEATGNVHTKS.LDREKAQVYLLAQAVRASNPPEPSEPIIK 123
| : : : : :
DB 89 KYLLSGGAGTIFVYIDKSGNTHAKTIDREERAOYLLMAQAVRDNRPLEPSEPIIVK 148
QY 124 QODINDNPFILPGLPYAHATVPEKSNVGTSVIQVTAHADADPSYNSAKLYVTYVLDGLPFF 183
| : : : : :
DB 149 VQDINDNPEFLHEIYHANVPEKSNVGTSVIQVTAHADADPSYNSAKLYVSIIEGQPYF 208
QY 184 GVDQGTGVVRAIPMDRETOEFLVYVQAQDMGSHGSGSTTVYVTLSDVNDNPKF 243
| : : : : :
DB 209 SVEAQGTIRTAIPMDREAEYHVYVQAQDMGSHGSGSTTVYVTLSDVNDNPKF 268
QY 244 POSLYQFSVETAGFGLVGRLLRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRGL 303
| : : : : :
DB 269 POSYQMSVSAAVGEVGRVAKADPDIGENGLVTVNIVDGDGELFEITDDETQGV 328
QY 304 LTVKPELDFESQKSFVENVNTLIDPAYLRGPFQDVASVRAVQDAPPPAFQAY 363
| : : : : :
DB 329 VKLKRPVDFETKRAVSLKIEANVHIDKFTISNGFKDTVTKLSVEDADPPVFLAPSY 388
QY 364 HLTVENAPGTLVQGISAADSPASIRYSILPHSDPERCFSIQPEEGTITHAALDR 423
| : : : : :
DB 389 IHEQENAAAGTVVGRVAKDPDANSIRYSIDHDTLDRFNTINPDGFIKTKPLDR 448
QY 424 EAAAHNLTATLTELGLWGWPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQAS 483
| : : : : :
DB 449 EETAMNLSVPAADI-----HNNHQT 470
QY 484 RVQVAITQTLDBNDNAPOLAEPTFTVCDSPAAP-----GQLIQVIRALDRDEVGSSHVSPQ 539

DB 471 KVPVAIRVLVDNDAPKFAAPYEGFICSDHPKALSNQPIVTSADQDDTANGPRTFS 530
QY 540 GP--LGPDAFTVQDNRLDPA-----WFHPLMASASWMLWPPAERGN 581
| : : : : :
DB 531 LPPEIMNPNFTVRNDNDNTAGVYARRGFSROKQDPYLLPIVSD-----GG 578
QY 582 QPASQKSSSLP-CG-RLPGALPSC 604
| : : : : :
DB 579 IPPMSTNTLTITKVCQDVNGALLSC 604

RESULT 5

D38992
cadherin 8 - human
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: D38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-793 <SUZ>
A/Cross-references: GB:L34060; NID:g506411; PIDN:AAA35628.1; PID:g506412
C/Genetic: GDB:CDH8
A/Accession: GDB:CDH8
A/Cross-references: GDB:5822911
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 46.9%; Score 1529.5; DB 2; Length 793;
Best Local Similarity 47.8%; Pred. No. 7,4e-94;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

QY 23 L.LRTRSWVWNOFVIEEYAGPEPVLIGKLSDVDRGEGRTKYLLTGBGAGTVFVDEAT 82
| : : : : :
DB 49 LNRKRGWVWNOFVIEEESGPEPLVGRHLTDLPGRSKIKYLLSGDAGTIFQINDVT 108
QY 83 GNIVHTKSLDREKAQVYLLAQAVRASNPPEPSEPIIKQODINDNPFILPGLPYAT 142
| : : : : :
DB 109 GDHAIKRLDREKAEVYTLTAQAVDMETSKPEPSEPIIKQODINDNAPPELNGPYAT 168
QY 143 VPEMSVGTGSVYQVTAHADADPSYNSAKLYVTYVLDGLPFFSVDQGTGVVRAIPMDRE 202
| : : : : :
DB 169 VPEMSVGTGSVYQVTAHADADPSYNSAKLYVSIIEGQPYFIEETALIKRLPMDE 228
QY 203 TOEFLVYVQAQDMGSHGSGSTTVYVTLSDVNDNPKFPOSLYQFSVETAGFGLV 262
| : : : : :
DB 229 AKEEVLYVYVQAQDMGSHGSGSTTVYVTLSDVNDNPKFQOSLYHFSVPDVLVGTAI 288
QY 263 GRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGRGLTVKRLDFESQKSFV 322
| : : : : :
DB 289 GRKANDQDIGNAQSSYDIDGDTALPETISDQAQDGTIRLRKPLDFETKSYTLKD 348
QY 323 EATNTLIDPAYLRGPFQDVASVRAVQDAPPPAFQAYHILTVENAPGTLVQGIS 382
| : : : : :
DB 349 EAAAHNIDRFSGRGPFQDTATVYKIVEDADPPVSSPTYLLEVHENAALNSVIGQVTA 408
QY 383 ADIDSPASIRYSILPHSDPERCFSIQPEEGTITHAALDR EAAAHNLTATLTELGLW 442
| : : : : :
DB 409 RDEDITSSPIRSIDHDTLDRQFNINADGKITLATPDRHSVHNITITATET----- 464
QY 443 GPERGWVPLVAEWSAPAPQSPVGSANGIPQDSSAQASRVQVAITQTLDBNDNAPOLA 502
| : : : : :
DB 465 -----RNHSQISVPAIKVLDVNDAPAPA 490
QY 503 ERYDTVCSAAPGQLIQVIRALDRDEVGSSHVSPQGLPD-----ANFTVQDNRD 555
| : : : : :
DB 491 SEYEAFICENKRGQVYQVTSAMDKDPKNGHY--FLYSLLEPMVNNPFTIKQEDNSL 548

QY 556 -----LPAMFPLMLASASWLMWPPAEKGNQPAQSGKSSSL-PCG-RLPGA 600
DB 549 SLAKHNGFNKQKEVILPIL-----SDSGNPLPSTLTITRVCGCSNDGV 557
QY 601 LPSCQ-----LPLGI---PALGIYLC 618
DB 598 VQSCNVAEYVPLIGLSMGALITALLAC 623

RESULT 6

152701
K-cadherin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 152701
R/Xiang, Y. Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, Cancer Res. 54, 3034-3041, 1994
A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer A/Reference number: 152701; MUID:94243827; PMID:8187093
A/Accession: 152701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-789 <RES>
A/Cross-references: UNIPROT:P55280; GB:D25290; NID:g435460; PIDN:BAA04975.1; PID:g435461
C/Genetics:
A/Gene: KCAD
C/Superfamily: cadherin, cadherin repeat homology
F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 44.2%; Score 1441; DB 2; Length 789;
Best Local Similarity 45.0%; Pred. No. 5,7e-88;
Matches 289; Conservative 116; Mismatches 155; Indels 82; Gaps 7;

QY 13 AGSEHPGALLRRRWVWVNOFVIEYAGPEPVILGKLSVDVSGEGTKYLLTGEA 72
DB 42 ANSHNE-----LSRSKRSMWVNOFVIEYAGPEPVILGKLSVDVSGEGTKYLLTGEA 97
QY 73 GTFVVIDEATGNITHTKSLDREKQAYVLLAQAVDRASNPLEPSEFIIKQDINDNP 132
DB 98 GDLITINENGDILATRLDREKQAYVLLAQAVDRASNPLEPSEFIIKQDINDNP 157
QY 133 IFFLPYHATVPENSNVSVIQTATADADPSYNSAKLYTVTLDELPEFSYDPOGVV 192
DB 158 IFTKDVYATVPEMAADVGTFTVQYATADADPTYSNKAQVYISLQGPYFVSSTGII 217
QY 193 RTAENMDRETOEERFLVIAQXMGHMGSLGSTVTVTLSDVNNPKFPQSLYQESV 252
DB 218 KTAALNMDRENREBOYQVIAQXMGHMGSLGSTVTVTLSDVNNPKFPQSLYQESV 277
QY 253 VETAGPGLVGRLAQDPDLGDNALMAVSIIDEGSEAFSISTDLQGRDGLTVRKPLDF 312
DB 278 PESPPGTPGRKASADADVGENAEIEYSITDEGHMDPVIDQETGGIITVKLLDF 337
QY 313 ESQSYGFRVETATITLDPAVLRGPKVAVSVAVQDAPEPAFTQAAYHUTPENKA 372
DB 338 EKKRVYTLKVEASNPILBPRFLVIGPKSATVRIVDDVDEPVSKEAYILQIREDAQ 397
QY 373 PGLVQISADLDSPASFRYSILPHSDPERCFSTIOPEGITHTAAPLDREARAWNLT 432
DB 398 INTTIGVAADDPAAANPVKYSVDRTDMRIFNIDSGSIFTSKLLDRETLMNHT 457
QY 433 VLATELGMSWGPGRGWPLLVASMSAPAPQSPVGSAGVIGIPQSSAQSRYOVAIQT 492
DB 458 VITETI-----NNPKQSSRVPLIYIKVL 479
QY 493 DEQDNAPQALPEPYDTFVCDASAPQOLIQTALDRDEVGNSSHVSGPLGDA-----NF 548
DB 480 DVNDNAPFAEFYETFTVCEKAKADQLITLHAYDKDPPYSGHOFSS--LAPDAASGSNF 537
QY 549 TVQDNDR-----LPAMFPLMLASASWLMWPPA-----E 578
DB 538 TIDDKONTAGITRKXGYNRHEMSTYLLFVVISDND-----YVQSGSTGTVTVRVACDH 593

QY 579 RGNQPAQSGKSSSLPCGRLPGAALPSCQPLGIPLGIYLCAS 620
DB 594 HGNMQSCHAELIHPTGLSTGALVAILCTIYLLVTVLFLFA 635

RESULT 7

137016
cadherin-6 - human
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: 137016
R/Shimoyama, Y.; Gotob, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S. Cancer Res. 55, 2206-2211, 1995
A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the A/Reference number: 137016; MUID:95262134; PMID:7743525
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:g974184; PIDN:BAA06562.1; PID:g974185
C/Genetics:
A/Gene: GDB:CDH6
A/Cross-references: GDB:5822908
C/Superfamily: cadherin, cadherin repeat homology
F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 44.2%; Score 1440; DB 2; Length 790;
Best Local Similarity 45.1%; Pred. No. 6.6e-88;
Matches 285; Conservative 118; Mismatches 151; Indels 78; Gaps 6;

QY 23 LLRRRWVWVNOFVIEYAGPEPVILGKLSVDVSGEGTKYLLTGEAGTVVIDEAT 82
DB 48 LNRSKRSMWVNOFVIEYAGPEPVILGKLSVDVSGEGTKYLLTGEAGTVVIDEAT 107
QY 83 GNHHTKSLDREKQAYVLLAQAVDRASNPLEPSEFIIKQDINDNPPIPLGPHAT 142
DB 108 GDIQATKLDREKQAYVLLAQAVDRASNPLEPSEFIIKQDINDNPPIPLGPHAT 167
QY 143 VPENSNVSVIQTATADADPSYNSAKLYTVTLDELPEFSYDPOGVVRLAIPMDRE 202
DB 168 VPENSDVGTFTVQYATADADPTYSNKAQVYISLQGPYFVSSTGIIKTAALNMDRE 227
QY 203 TOSEFLVIAQXMGHMGSLGSTVTVTLSDVNNPKFPQSLYQESVETAGPGLV 262
DB 228 NREQYVIAQXMGHMGSLGSTVTVTLSDVNNPKFPQSLYQESVETAGPGLV 287
QY 263 GLRPAQDPDLGDNALMAVSIIDEGSEAFSISTDLQGRDGLTVRKPLDFESQSYGFRV 322
DB 288 GRKASADADVGENAEIEYSITDEGHMDPVIDQETGGIITVKLLDFEKKVYTLKY 347
QY 323 EATYTLDPATLRGPKVAVSVAVQDAPEPAFTQAAYHUTPENKAAGTLVQISA 382
DB 348 EASNPYHEPRFLVIGPKSATVRIVDDVDEPVSKEAYILQIREDAQINTTIGSVTA 407
QY 383 ADLDSPASPIRYSILPHSDPERCFSTIOPEGITHTAAPLDREARAWNLTVLATLGMSW 442
DB 408 QDPDAANPVKYSVDRTDMRIFNIDSGSIFTSKLLDRETLMNHTIATEI----- 463
QY 443 GPRGWPPLVAVMSAPAPQSPVGSAGVIGIPQSSAQSRYOVAIQTLDENNAQOLA 502
DB 464 -----NNPKQSSRVPLIYIKVLVDVNDNAPFA 489
QY 503 EPYDTFVCDASAPQOLIQTALDRDEVGNSSHVSGPLGDA-----NFTVQDNDR 555
DB 490 EFTFTVCEKAKADQLITLHAYDKDPPYSGHOFSS--LAPDAASGSNTTIDDKONTA 547
QY 556 -----LPAMFPLMLASASWLMWPPA-----ERGNQPAQSGK 588
DB 548 GILTRKXGYNRHEMSTYLLFVVISDND-----YVQSGSTGTVTVRVACDHGNNQSCHE 603
QY 589 SSSLPCGRLPGAALPSCQPLGIPLGIYLCAS 620
DB 604 ALIHPTGLSTGALVAILCTIYLLVTVLFLFA 635

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RESULT 8
150180
caderherin-7 - chicken
CISpecies: Gallus gallus (chicken)
CDate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
CAccession: I50180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-specific
A.Reference number: I50178; MUID:95309115; PMID:1540531
A.Accession: I50180
A>Status: preliminary; translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A.Residues: 1-785 <NAK>
A.Cross-references: UNIPROT:Q90763; GB:ID42150; NID:gs668000; PIDN:BA07721.1; PID:gs668000
C:Superfamily: caderherin; caderherin repeat homology <CDH>
F156-266/Domain: caderherin repeat homology <CDH>

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Query Match Similarity 43.9%; Score 1431.5; DB 2; Length 785;
Best Local Similarity 45.7%; Pred. No. 24e-87;
Matches 296; Conservative 103; Mismatches 166; Indels 83; Gaps 8;

QY 6 AARAPAMAGSRHP--GPALLPTRSRVMWNPQVIEEYAGPEPVILGHLSDVDREGERT 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 27 AEPSP-----SSKPEFGQGRTRTKRSWVMNPFVLEEYMGSDPLVYGGLHSDVVKGGSI 82
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 64 KYLLGEGAGYGVFVDEATGNTHVTKSLDREKQYVLAAVDNRASRNPPEPSEFIK 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 83 KYILSGEAGSSFTIIDENTGDIHATKRLDREQAYITLRAQHDLTNKPEPSEFYIK 142
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 124 GQDINDNPPIPLGPHATVPEMSVNGTSVIQVTAHADADDSYGNSAKLVTYVLIDGPEFF 183
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 143 IQDINDNPEPKFDGTYTAVGPEMSPVGTSTVQVATATDADDPYGNASARVYSILQGYXF 202
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 184 SVDPEQTVVRAIPMMDRETOEEFLVTOADMGMHMGISGSTVYVTLSDVNDNPEPKF 243
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 203 SVEPTGTGIKRALPMMDREAKDQYLLVTOADMGMQNGSLGTSVTVTLTDVNDNPEPF 262
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 244 POSTQSFVETVETAGTGTLVGRLRADDPDLDGNALMAYSILDGESEAFSISTDIQGRDL 303
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 263 PRSRQVNVPSLPLASVVARIKAADADVGRPAEHEYNIIVGDGLGVFKISVDDQTOEGI 322
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 304 LTVRKPLDPESORCSIFRVEATNTLIDPAYLRGCFKQVAVRAVQDAPPPAFTOAY 363
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 323 ITIQELDPEKATSYTLRIEAMNMAVDPRFSLGFSMTVTVKIIVEVDDEPPVFTSLY 382
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 364 HLTVPENKAPGLVQOISAADLDPASPIRYSILSPDPERCFSIQPEEGTIIHAAPLDR 423
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 383 SMVSEAKVGITIGTVAHADPDASNPVRSIDNTLEKRYFNIDANSGYITRAKSLDR 442
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 424 EAPAMHNTLVATELGMSWGPERGVPVLLVAEWSAPAAPQPSPVGSAVGIQDSSAQAS 483
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 443 ETNAVHNTITVLAME-----SQNPQIG 464
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 484 RVQVAVIQTLDEENDNAQLAAEPYDTFVCSAAPGQIIOYIRALDPREV--GNSSVHSPG 541
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 465 KQYVAVITLLIDINDNPEFRAMEYETTVCEADPGQIITQKISADKDDPPNGQPFSLTAE 524
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 542 LGPDANFTVQDNRDPA-----WEHPLIMASASSWLHPAERGN--- 581
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 525 AANNHNFLLQDKDKNTATVLTFRBNGFRROEGSVFLPFIYDSCS---PALSNTTLTI 580
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 582 -----QPASQKSSSLPCGRLPAL--PSCQPLGIPALGIY 616
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 561 RVCDCDADGIAQTCNAEATILPAGSLGTGLATIAACVTLVLVLLIV 628
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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C|Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C|Accession: G02678
R|Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A|Reference number: H01584
A|Accession: G02678
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-790 <SH>
A|Cross-references: UNIPROT:Q1634; EMBL:U59325; NID:g1389852; PIDN:AA802933.1; PID:g133
C|Superfamily: cadherin; cadherin repeat homology
F162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.3%; Score 1412.5; DB 2; Length 790;
Best Local Similarity 45.9%; Pred. No. 4.56-86;
Matches 288; Conservative 100; Mismatches 152; Indels 87; Gaps 9;

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QY 25 RTRSRWVNOQFVLEEYABEPPLVIGKLHSDVNGEERTKXLLGEGAGVFIWIDEATGN 84
Db 50 RPKGWVWNOQFVLEEHHGPDQYVYKGLHSDSDGDSGVKXILGEGAGTFFIIDDPTGD 109
QY 85 IHVWKSJLDREKQAVYLLAQVADBSNRPLEPPEEFLIIKQODINDNPPIPLGFIYHATVP 144
Db 110 IHSKSLDREKQTHYVLAQALDRINKPLEPEESEFLIIKQODINDNAPKFDGSIYATVP 169
QY 145 EMSNVGTSVILQVTAHADDDPSYGSANKLYVTVLDDGLPFSVDPQTGVVRIAPMMDRQTQ 204
Db 170 EMSMDGTSVILQVITATDADDPYGSNSARVWYSILGQFPFSVDPQTGVVRIALHMMDRAR 229
QY 205 EEPFLVIOAKMGHMGGLSGSTTVYVTLSPVNNPNPKFPQSLYQFSYVERPAGPTLYGR 264
Db 230 EHYEVLIOAKMQAGVGLSGSTTVNTITLVNDNPPRFQKHQLYVPESAQYGSANGK 289
QY 265 LRAODPDIGDNLMAVSIIDGEGSEAPFSISTDLOQRDGLTVRKPLDRESORSTFRVEA 324
Db 290 IKANDADGSNADMTYSIINGDGMGISISTDKETREGLISLKKPLNKKKSXYLNEBG 349
QY 325 TNLTIIDPAYLRGPFKCVASVVAOVADPEPPATQAAHYHLYVENKPAKGLVQGISAD 384
Db 350 ANTHLDPRFSHLGPFKQATMKIIVGDVDEPPLSMSEYMEYENAKIGIVGVYLAOD 409
QY 385 LDSPASPIRYSILPHSDPERCFSTQPEEGTITHAAPLDREARAMHNTLVLTALGWSWGP 444
Db 410 PDSSTLSLRYEINNVEDDFENIDANTGTRTKVLDREBTPYWNITVTASEI----- 463
QY 445 ERGWVPLLVAEWSAPAAPQKSPVGSANGVIPQSSAQSARQVVAIQOTLEDNDNAPQLAEP 504
Db 464 -----DNPDLISHVTGVRVLVDVANDNPPELLARE 491
QY 505 YDTFVCDGAAPGQLIQVIRALDREVGNSHVSF-----QGPGPDANFTVQDNRLPA-- 558
Db 492 YDIIVCENSKGQVITHISATDKDDFANGPRFNFELDERLTVNP--NTLLKDNBENTIASI 549
QY 559 -----WFHPLMASASWLMHWPARERGNOPASQKSSSL-----PCGRPLG 599
Db 550 LTRRRRFRRTYQDYYVLPIMISD-----GGTFF-SLSSSSTITIRVACACER-DG 595
QY 600 ALPGCQPLGIPALG-----IVLC 618
Db 596 RVRTCHAEAFLLSAGLSTGALITAILLC 622

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RESULT 9	Development 121, 132-133, 195
G02678	A>Title: Neural crest cell-adhesion controlled by sequential and subpopulation-spe
cadherin-14 - human	A,Reference number: I50178; PMID:95309115; PMID:7540331
C:Species: Homo sapiens (man)	A,Accession: I50178

A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: mRNA
A:Residues: 1-790 <NKA>
A:Cross-references: UNIPROT:Q09762; GB:D42149; NID:g867998; PIDN:BA07720.1; PID:g867999
C:Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 43.0%; Score 1400; DB 2; Length 790;
Best Local Similarity 49.0%; Pred. No. 3e-85;
Matches 263; Conservative 109; Mismatches 121; Indels 44; Gaps 3;

23 L L R F R S W M N Q F V I E E Y A G P E V L I G K L H S D V D R G E G T K L L T G E G A T V F I D E A T 82
D B L S R S K R S W M N Q F L I E E Y T G T D Y Q V G K L H S D Q D K D G S L K Y I L S G D G A G D L F I I N E A T 107
Q Y G N I V T S I D R E E A Q V L L A Q A V D R A S N R P L R P S P F I I K G O D I N D N P I F P L G P H A T 142
D B 108 G D I A T R L D E E P V I L R A Q A I N R T G R P E P S E F I I K I H D I N D N E P F K D Y N A S 167
Q Y 143 V P E M S N G T S V I Q T A D A D D P S Y G S A K L V Y T V D L G L P P S V D P O T G V R T A I P M M D E 202
D B 168 I P E M S D V G T F V Y Q T A D D P T G N S A K Y V S I L Q G P Y S E S E T G I I K I A L M D R E 227
Q Y 203 T Q E F L V I Q A K M G M G L S G T T V T V L S P V N N P R F P Q S I Q F S V E T A G C T L V 262
D B 228 N R E Q V V I Q A K M G G M G L S G T T V N I T L T V N D N P R F P Q S T Q F R A P E S T P D S P I 287
Q Y 263 G R L A Q D P D L G D N A L M A Y S I L D E G S E A F S I S T D L G R D G L L T V R K P L D F E S Q R S Y F R V 322
D B 268 G R I A N A D A D E N A E I Y S I T E G G Y D M F G I T D K O T Q E G I I V K K A L D P E N K N L V I K V 347
Q Y 323 E A T T L D P A Y L R G R P K V A S R V A V O D A P E P P A T Q A Y H L T P E N K A P G T L V Q I S A 382
D B 348 E A T T H A D P F L Y L G P K D S A T I R I Q E V D E P P V S R P A Y I I E V E D E P I N S I G T V A 407
Q Y 383 A D D S P A P I R Y S I L P H S D P E R C F S I O P E E G T I H T A P L D R E A R A M H N L T V L A T E L G W S M 442
D B 408 Q D P R A A C P Y K Y S I D R I T D M D R V F N I N S G S I F T K T I D R E L L M H N I T V I A E L - - - - 463
Q Y 443 G P E R G W P L L V A E W S A P A P P Q R S P V G S A V G I P D O S S A Q A S R V O A I Q T L D E N D N A P O L A E P 502
D B 464 - - - - - N N P K O S S R V P F I K V L D V N D N A P E R A 489
Q Y 503 E P Y D T F Y C S A A P G O L I Q V I R A L D R D E V G N S H V S F Q G P L G P D A - - - - - N F T V Q D N R D 555
D B 490 M F Y T F V C E N A K A E Q L I Q T L S A V D K D S Y S G H Q F S F S - I A P A S S N F T L Q D N R D 544

RESULT 11
151638
F:cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F51638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A:Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A:Reference number: F51638; MUID:96039533; PMID:7496667
A:Accession: F51638
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: mRNA
A:Residues: 1-790 <EBP>
A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:g85463; PIDN:CAAS9679.1; PID:g8546
C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 42.6%; Score 1389.5; DB 2; Length 790;
Best Local Similarity 45.9%; Pred. No. 1.5e-84;
Matches 282; Conservative 107; Mismatches 164; Indels 61; Gaps 9;

25 R T R S W M N Q F V I E E Y A G P E V L I G K L H S D V D R G E G T K L L T G E G A T V F I D E A T N 84
D B 49 R L R S W M N Q F V I E E Y T G T D Y Q V G K L H S D Q D K D G S L K Y I L S G D A G T M F I D E T D 108

Q Y 85 I H V T K S I D R E E A Q V L L A Q A V D R A S N R P L R P S P F I I K G O D I N D N P I F P L G P H A T V P 144
D B 109 I H A I O R L E R E S S Q T L K A Q L D R I T R P E P S E F I V K I Q D I N D N P K L D G P T Y T A S V P 168
Q Y 145 E M S N G T S V I Q T A D A D D P S Y G S A K L V Y T V D L G L P P S V D P O T G V R T A I P M M D E T Q 204
D B 169 E M S P V G T S I I Q V A T A D D P T G S A R V A V S I L Q G P Y S E S E T G I I R A L T M D R E S R 228
Q Y 205 E E P L V I Q A K M G M G L S G T T V T V L S P V N N P R F P Q S I Q F S V E T A G C T L Y G R 264
D B 229 D Y E V I I Q A K M G Q L G A G T T V N V T L S D V N N P R F P Q K H Q M S V L S L I N S T V G R 288
Q Y 265 L R A Q D P D L G D N A L M A Y S I L D E G S E A F S I S T D L G R D G L L T V R K P L D F E S Q R S Y F R V E A 324
D B 269 V L A M D L D E G V A E A K K Y N I I D D E F E F D I V T D P E N Q G V I T V K K P L D F E T R K S Y T L K I E G 348
Q Y 325 T N T L D P A Y L R G R P K V A S R V A V O D A P E P P A T Q A Y H L T P E N K A P G T L V Q I S A A D 384
D B 349 S N A H L E R F L M G P R D T S V H I V E V D E P P V G S S F Y E V E S E N D I Q T T Q I V S A K D 408
Q Y 385 L D S P A P I R Y S I L P H S D P E R C F S I O P E E G T I H T A P L D R E A R A M H N L T V L A T E L G W S G P 444
D B 409 P D A T N S V R Y S I D S S D P G R F Y D V T T G A L M T R P L D R E V S M H N I T I L A M E N - - - - 462
Q Y 445 E R G W P L L V A E W S A P A P P Q R S P V G S A V G I P D O S S A Q A S R V O A I Q T L D E N D N A P O L A E P 504
D B 463 - - - - - N N P A O I G V P V T I K V L D V N D N A P P P T K F 490
Q Y 505 Y D T F Y C S A A P G O L I Q V I R A L D R D E V G N S H V S F Q G P L G P D A - - - - - N F T V Q D N R D L P A W F 560
D B 491 S E T L M C E N A K A Q L I Q V S A V D Q D P O E G C H I S T S - L A P D A N N P F T L R D Q D N T A M I 548
Q Y 561 - - - H P L M A S A S W L M P - P A E R G N P A S Q G S S S L - - - P C G R L P G A L P S C Q - - - - - L P 607
D B 549 L T R R P G F Q S Q S F Y F L L I S D N G N P R L S T G L T I Q V C S D K - D G D I M S C N A E P Y T L P 607
Q Y 608 L G I - - - P A L G I V L C 618
D B 608 I S L S R G A L I A L T L T C 621

RESULT 12
159372
cadherin 12 - human
N:Alternate names: Br-cadherin
C:Species: Homo sapiens (man)
C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: F59372
R:Seilig, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.M.
Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
A:Title: Expressed cadherin pseudogenes are localized to the critical region of the spin
A:Reference number: F59372; MUID:95249541; PMID:7731968
A:Accession: F59372
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMB
A:Molecule type: mRNA
A:Residues: 1-794 <RES>
A:Cross-references: UNIPROT:F55289; GB:L33477; NID:g793942; PIDN:AB48539.1; PID:g793943
C:Genetics: GDB:CDH12
A:Gene: GDB:CDH12
A:Cross-references: GDB:596324
A:Map position: 5p13-5p14
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:57-160/Domain: cadherin repeat homology <CR1>
F:163-269/Domain: cadherin repeat homology <CR2>
F:272-384/Domain: cadherin repeat homology <CR3>
F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <INT>

Query Match 42.0%; Score 1368.5; DB 2; Length 794;

Best Local Similarity 44.4%; Pred. No. 3.6e-83;
Matches 282; Conservative 114; Mismatches 154; Indels 85; Gaps 11;

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QY 14 GSREHPGALLTRRSWVWNOFVIEEYAGEPVLLICKLHSDVDVRSGETKYLITGEGAG 73
Db 44 GQRSH---FQVRKRGWVWNOFVLEEMGESEPGYVSKLHSDLDKGEGLVYTLSDGAG 99
QY 74 TVFVIDATGNHITKSLDREKQAVYLLAQAIVRAANRPLREPESEFIIIGODINDNPI 133
Db 100 TVFVIDETGDIHAIKSLDREKQAVYLLAQAIVRAANRPLREPESEFIIIGODINDNPI 139
QY 134 FPLGPHATVEMSNVGTSVIQTVAHDADDPVSQSAKLYTVVLDGLPFPSVDPQTVVR 193
Db 160 FLDPGYATVEMSPVGAIVYLQVAKATDADDPYNSARVYSLIQGQPYSIDPKTGIVR 219
QY 194 TAIEMRETOEEELVYIQAQDMGNGHGLSGSTTVYTLSDVNDNPKPKPQSIYOSVY 253
Db 220 TALPMREVEKEQVQLIQAQDMGNGHGLSGSTTVYTLSDVNDNPKPKPQSIYOSVY 279
QY 254 ETAPRGTLVGRADPDLDGNALMAYSIIDEGSEAFSISTDQGRDGLTVAKPLDPE 313
Db 280 ESSPGISAKIRAVDPFGONAEIENVIVPGDGNLFDIVTDDEDTQEGVILKKEPDEF 339
QY 314 SQRSYSPVEAVNTLIDPAVIRGPFKDVASVAVADAPPPAFTQAAYHLTVPENKAP 373
Db 340 TKKAVTFKVDASNLHLDRFHSAGPFKDTATVKISLVDVDEPPVFSKPLTYMEVEDTPV 399
QY 374 GTIVGQISAALDPSASPIRYSILPHSDPERCFISIOPEEGTITHAALDSEARAHNTLV 433
Db 400 GTIIGAVIAQDLDDGSSAVRFTIDKSDGDSYFTIDNGEITANLDELDSRTHQVFSI 459
QY 434 LATELGMSWGPGRGVPLLVAEWMSAPAPQPSRPSVSAVGIPODSSAQASRVYAIOTLD 493
Db 460 IASKYS-----NFL-----TSKVNILINVL 481
QY 494 ENDNAPOLABPYDTFVCDASAPRGQLIQTALDRDEVNSHVSFOGRLGDA---NFT 549
Db 482 VNEPPEISVPEYETAVCNAPRGQIQLVSAADBDLSPAGQFSFR--LSEPAIKENFT 539
QY 550 VQDRNDLPA-----WEPHILMASAGSLWHPAERGNQPSAQCKSSSLP 593
Db 540 VRDRNNATAGIETRRNGSRROQELHFLPVVIEDSSV-----PQ-----SSTNMTIR 588
QY 594 CGRL--PGALPSCQ----LPLGIPA--LGIYIC 618
Db 589 VCRCDSDGTILSCNVEAIFLFPVGLSTGALIAILLC 623
```

RESULT 13

10HUC5
Cadenherin 5 precursor - human
N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
R/Accession: S49893; S24305; A43418
R/Breviario: F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Goley, D.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A/Description: Molecular and functional properties of VE-cadherin (784/cadherin-5) a nov
A/Reference number: S49893
A/Accession: S49893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-784

A/Cross-references: UNIPROT:P33151; EMBL:X79981; NID:9559833; P1DN:CAA56306.1; P1D:95998
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: S24305
A/Molecule type: mRNA
A/Residues: 5-516, 'I', 518-784 <SUZ>
A/Cross-references: EMBL:X59796; NID:9639976; P1DN:CAA42468.1; P1D:929593
R/Lampugnani, M.G.; Ratsel, M.; Pigott, R.; Pliascane, A.; Houen, G.; Rucco,

J. Cell Biol. 118, 1511-1522, 1992
A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contact
A/Reference number: A43418; MUID:92394977; PMID:1522121

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QY 14 GSREHPGALLTRRSWVWNOFVIEEYAGEPVLLICKLHSDVDVRSGETKYLITGEGAG 73
Db 44 GQRSH---FQVRKRGWVWNOFVLEEMGESEPGYVSKLHSDLDKGEGLVYTLSDGAG 99
QY 74 TVFVIDATGNHITKSLDREKQAVYLLAQAIVRAANRPLREPESEFIIIGODINDNPI 133
Db 100 TVFVIDETGDIHAIKSLDREKQAVYLLAQAIVRAANRPLREPESEFIIIGODINDNPI 139
QY 134 FPLGPHATVEMSNVGTSVIQTVAHDADDPVSQSAKLYTVVLDGLPFPSVDPQTVVR 193
Db 160 FLDPGYATVEMSPVGAIVYLQVAKATDADDPYNSARVYSLIQGQPYSIDPKTGIVR 219
QY 194 TAIEMRETOEEELVYIQAQDMGNGHGLSGSTTVYTLSDVNDNPKPKPQSIYOSVY 253
Db 220 TALPMREVEKEQVQLIQAQDMGNGHGLSGSTTVYTLSDVNDNPKPKPQSIYOSVY 279
QY 254 ETAPRGTLVGRADPDLDGNALMAYSIIDEGSEAFSISTDQGRDGLTVAKPLDPE 313
Db 280 ESSPGISAKIRAVDPFGONAEIENVIVPGDGNLFDIVTDDEDTQEGVILKKEPDEF 339
QY 314 SQRSYSPVEAVNTLIDPAVIRGPFKDVASVAVADAPPPAFTQAAYHLTVPENKAP 373
Db 340 TKKAVTFKVDASNLHLDRFHSAGPFKDTATVKISLVDVDEPPVFSKPLTYMEVEDTPV 399
QY 374 GTIVGQISAALDPSASPIRYSILPHSDPERCFISIOPEEGTITHAALDSEARAHNTLV 433
Db 400 GTIIGAVIAQDLDDGSSAVRFTIDKSDGDSYFTIDNGEITANLDELDSRTHQVFSI 459
QY 434 LATELGMSWGPGRGVPLLVAEWMSAPAPQPSRPSVSAVGIPODSSAQASRVYAIOTLD 493
Db 460 IASKYS-----NFL-----TSKVNILINVL 481
QY 494 ENDNAPOLABPYDTFVCDASAPRGQLIQTALDRDEVNSHVSFOGRLGDA---NFT 549
Db 482 VNEPPEISVPEYETAVCNAPRGQIQLVSAADBDLSPAGQFSFR--LSEPAIKENFT 539
QY 550 VQDRNDLPA-----WEPHILMASAGSLWHPAERGNQPSAQCKSSSLP 593
Db 540 VRDRNNATAGIETRRNGSRROQELHFLPVVIEDSSV-----PQ-----SSTNMTIR 588
QY 594 CGRL--PGALPSCQ----LPLGIPA--LGIYIC 618
Db 589 VCRCDSDGTILSCNVEAIFLFPVGLSTGALIAILLC 623
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Query Match 28.7%; Score 935.5; DB 1; Length 784;
Best Local Similarity 39.9%; Pred. No. 2.4e-54;
Matches 225; Conservative 83; Mismatches 201; Indels 55; Gaps 12;

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QY 1 CMGRLAAPARAWAGSREHPG-----PALTRRSWVWNOFVIEEYAGEPVLLICKL 52
Db 14 CIGLAIAVAANAAGA--NAQRDTHSLPETHRQRDMWNOHMLDEKNTSLPHNVGKI 71
QY 53 HSDVDRGEGRTYLLTGBCAGTVFVYIDEATGNHITKSLDREKQAVYLLAQAIVRAANR 112
Db 72 KSVSR--KNAAYLLKGEVGVGVFVDAETGVAFIERDRNISEYHLTAIVYKDTSE 129
QY 113 PLREPESEFIIIGODINDNPIPLPGPHATVEMSNVGTSVIQTVAHDADDPVSQSAK 172
Db 130 NLETPSSFTIKVDNDMFPVTHRLFNASVSSAGVSVISVAVADADDPVGDHNAV 189
QY 173 VYTVLDGLPFSVDPQTVVRTAIPMDRETOEEELVYIQAQDMGNGHGLSGSTTVYT 232
Db 190 WQILKGEVFAID-NSGRIITIKSLDREKQAVYLLAQAIVRAANR--LRGDSGATVLT 247
QY 233 LSDVNDNPKPKPQSIYOSVETAGGTLVGRADPDLDGNALMAYSIIDEGSEAFS 292
Db 248 LQDINDNPFPIQTATFVPEDTRVGSVGLFVDEDPQNRKMTKISILSGDYODAT 307
QY 293 ISTDLQGRDGLTVRKLDFESQRSYSPVEAVNTLIDPAVIRGPFKDVASVAVAD 352
Db 308 IENPNAHNGIILKPKMFLDYKIQGSFIVEATDPTIDRYN--SPAGRAQVINITDV 366
QY 353 PEPPATQAAYHLTVPEN-KAGTLYVQGISAADLDSAPSIYSLPHSDPERCSIQDE 411
Db 367 DEPPITQGFYHOLENKKP--LIGVLAADPPAARHSISYSLRPSDKQPFVY-CK 423
QY 412 EGTHTAALDREARAHNTLVATELGMSWGPGRGVPLLVAEWMSAPAPQPSVGS 471
Db 424 KGIIVNKKLDEHYVWYLVYAKEL-----DS 452
QY 472 VGIPDSSAQASRVYVYIQTLDENDNAPOLABPYDTFVCDASAPRGQLIQTALDR 531
Db 453 TGRP--TKGESIVQVHLEVDENNAPARFAPQKVCENAHQQLVQISAIKDI-- 507
QY 532 NSGHVAFQGLPDPAFTVQDNRD 555
Db 508 TPNAVFKETLTNTENNFTITDND 531
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RESULT 14

JMBCN
N-cadherin precursor, neuronal - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A/Accession: A46163
R/Miyatani, S.; Shimamura, K.; Hatta, M.; Nagafuchi, A.; Nose, A.; Matsunaga, M.; Hatta, Science 245, 631-635, 1999
A/Title: Neutral cadherin: role in selective cell-cell adhesion.
A/Reference number: A32759; MUID:9346748; PMID:2762814
A/Accession: A32759
A/Molecule type: mRNA
A/Residues: 1-906 <MTY>
A/Cross-references: UNIPROT:P15116; GB:M1131; NID:g192327; PIDN:AAA37353.1; PID:g309125
R/Miyatani, S.; Copeland, N.G.; Gilbert, D.D.; Jenkins, N.A.; Takeichi, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 8443-8447, 1992
A/Title: Genomic structure and chromosomal mapping of the mouse N-cadherin gene.
A/Reference number: A46163; MUID:92409532; PMID:11528849
A/Accession: A46163
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 835-906 <MT2>
A/Cross-references: GB:S45011; NID:g256010; PIDN:AA23356.1; PID:g256011
A/Note: sequence extracted from NCBI backbone (NCBIN:113759, NCBI:P.113760)
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C/Suprafamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F/1-27/Domain: signal sequence #status predicted <SIG>
F/128-153/Domain: propeptide #status predicted <PRO>
F/160-906/Product: N-cadherin #status predicted <EXT>
F/160-906/Product: extracellular #status predicted <EXT>
F/162-267/Domain: cadherin repeat homology <CR1>
F/232-242/Region: cadherin binding #status predicted
F/237-382/Domain: cadherin repeat homology <CR2>
F/385-487/Domain: cadherin repeat homology <CR3>
F/500-605/Domain: cadherin repeat homology <CR4>
F/606-714/Domain: cadherin repeat homology <CR5>
F/715-766/Domain: transmembrane #status predicted <TM>
F/747-906/Domain: intracellular #status predicted <INT>
F/865-878/Region: serine-rich
F/190,273,325,402,572,651,692/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match

Best Local Similarity 18.4%; Score 601; DB 1; Length 906;
Best Local Similarity 33.9%; Pred. No. 5,4e-32;
Matches 190; Conservative 76; Mismatches 214; Indels 80; Gaps 21;

17 EHPGALLRTRRSWVWVQFVIEYAGPEPVILGKLSHSDVDRGGRKTYLTGEGAGT-- 74
149 KHSG-ALQKQKRDVIRPILNPKSRGPFQBLVIRSDKXLS-LRISVIGSGADQPP 206
75 --VFVIDEATGNIHTVKSIDREKAQVYLLAQAVDRASNPFLPSEFIIKGGDINDNP 132
207 TGIPIINPISGQSVTKPLDRELARFHLRAHVDINGNQ-VENPIDIVINVIDMNDNP 265
133 IEPGPHATPEMSNVGTSVIQVTAHDADDPYGNASAKLYTVVLGDLP-----PFSVD 186
266 EFLHGVNKGVSPESSKGGTYVMTVTAIDADDPNALN-GMLRYILSCAPSTPEPMFTTN 324
187 PQTVGVTATAPNMDRETOEELVVIQAKDMGSH-MGSLSGSTVTVTLSDVNDNPKPFQ 245
325 NETSDITVAAGDREKQVYLLIQATDEGNPTGLSNTATAVATVTDVNDNPEPFA 384
246 SLVPSVETVETAGPTLVGLRAQDPDLG-----NALMAYSLIDGEGEASISITDLQGD 301
385 MTFPGVPEVNR-VDVITANLTVTDKQPHTPANNA-AVRISSGDEPTGRFALITDPSND 441
302 GLTLVRKPLDFESQSSVFEVATNTLIDPAYLRG---PFKDVASVRAVQDAPPEPPAF 358
442 GLVTVVAFIDFETRMVLTVAENQY----PLAKGIQHPQSTATVSVTVIVDNNPFF 497
359 TQAAHILTVBENKAGTLVGQISADLDS-PASPIRYSILPHSDPERCSIOPEBGTHT 417

DB

498 APNPKIIQEGELHAGTMTLTITADDPRIYQNIIRYTKL--SDPAMWIKIDPVNGQIT 555
418 AAPLDREA-----RAMNLTVLATELGWSWGERGVPLVAEWGAPAPQPSFVGA 473
556 IAVLDRESPYQNNIYNATFLASDNG-----IPPV-----SGTG 589
474 IPOSSAASAVQVAICITLDENDNAPOLASPYDFVDSAPGQIQLVIRALDESDGNS 533
590 TLQ-----IYLLDINDNAPVL-POEATCETPEPNSI--NIALDITDIPNA 634
534 SHVSQGLPG---DANFTV 550
635 GPFAFDLPLSPVTKRMNTI 654

RESULT 15

ICHCN
N-cadherin precursor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
A/Accession: JH0424
R/Inuzuka, H.; Miyatani, S.; Takeichi, M.
Neuron 7, 69-79, 1991
A/Title: R-cadherin: a novel Ca2+-dependent cell-cell adhesion molecule expressed in the
A/Reference number: JH0424; MUID:91299343; PMID:1712604
A/Accession: JH0424
A/Molecule type: mRNA
A/Residues: 1-913 <INT>
A/Cross-references: UNIPROT:P24503; GB:D14459; GB:D00849; NID:g222854; PIDN:BA03356.1;
A/Experimental source: retina
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought to
C/Suprafamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; retina; transmembr
F/1-26/Domain: signal sequence #status predicted <SIG>
F/127-166/Domain: propeptide #status predicted <PRO>
F/167-913/Product: R-cadherin #status predicted <EXT>
F/167-721/Domain: extracellular #status predicted <EXT>
F/169-721/Domain: cadherin repeat homology <CR1>
F/244-249/Region: cadherin binding #status predicted
F/273-389/Domain: cadherin repeat homology <CR2>
F/392-504/Domain: cadherin repeat homology <CR3>
F/507-612/Domain: cadherin repeat homology <CR4>
F/613-721/Domain: cadherin repeat homology <CR5>
F/722-753/Domain: transmembrane #status predicted <TM>
F/754-913/Domain: intracellular #status predicted <INT>
F/870-885/Region: serine-rich
F/180,409,554,629,658,699/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 18.3%; Score 596; DB 1; Length 913;
Best Local Similarity 33.3%; Pred. No. 1.2e-31;
Matches 185; Conservative 77; Mismatches 226; Indels 68; Gaps 19;

16 REH-FGPAALLRTRRSWVWVQFVIEYAGPEPVILGKLSHSDVDRGGRKTYLTGEGAG- 73
153 ROHOSAKGLRQKEDWVIRPINVPENSRGPPQQLVIRSDKX-ELHIRYSITGVADQ 211
74 ---TVFVIDEATGNIHTVKSIDREKAQVYLLAQAVDRASNPFLPSEFIIKGGDINDN 150
212 PMEVEFSDIPVSGMYVTRPDRERASVYHLRAVAVMNGK-VENPIDIYIVIDMNDN 270
131 PPIPLGPHATPEMSNVGTSVIQVTAHDADDPYGNASAKLYTVVLGDLP-----PFS 184
271 RPEFINGVYNSVDEGKPGTYVMTVTAIDADDPSTAN-GMVRRIYVTPQPSQNMFT 329
185 VDPQTVGVTATAPNMDRETOEELVVIQAKDMGSHG-GLSGSTVTVTLSDVNDNPKF 243
330 INSEGTDLVVAAGDREKQVYVIVQATDMENLVYGSNTATAITVTDVNDNPEP 389
244 POSLYQSVETVETAGPTLVGLRAQDPDL--GDVAMAYSLIDGEGEASISITDLQGD 301
390 TTSYSGVPEVNR-VVVVAVNLTMDQPHSRPMNAIYILISGDPBGHTIRIDPYTNE 448
302 GLTLVRKPLDFESQSSVFEVATNTLIDPAYLRG---PFKDVASVRAVQDAPPEPPAF 358

Db 449 GNVTVKAVDYEMNRAFMLTVMVSN---QAPLASGIQMSFQSTAGVTISVTDVNEAPYF 504
QY 359 TQAAVH/LTPENKAPGTLVGQISADLDS-PASPIRYSILPHSDPERCFSIQPEEGTIHT 417
Db 505 PTNHKLIRLEGVPTGTVLTFPSAVDPDRFMQAVRSKL--SDPANWLNINATNGQIT 562
QY 418 AAPIDREARAWHNLTVLATELGMSWGPGRGWPVLVAEMSAAPAPORSPVGSAGIPOD 477
Db 563 AAVLDRESPTYIKNNVYEAT-----FLADNGIIPA-----SGTGTLO- 599
QY 478 SSAQASRVQVAICTLDENDNAPOLAEPTYDFVCDSAPGQLIQVIRALDRDEVGNSSHS 537
Db 600 -----IYIDINDNAPELL-FKXAQICEK--PNLNVINITTAADIDPNVGPV 645
QY 538 FQGPLGPPDA---NETV 550
Db 646 FELPSVPSAVKKNWTI 661

Search completed: December 8, 2004, 10:27:05
Job time : 52.1417 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 248.512 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-7

Perfect score: 3259

Sequence: 1 CMGRLAAPARAMAGSRHPC.....LPSCQLPLGIPALGIYVCAS 620

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %

Maximum Match 100 %

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2897.5	88.9	819	1 CAD0_HUMAN	Q86UP0 Homo sapien
2	2511	77.0	781	2 Q6PFK6	Q6PFK6 mus musculu
3	2511	77.0	781	2 AAH57373	AAH57373 mus muscu
4	2291	70.3	493	2 Q96LQ7	Q96LQ7 homo sapien
5	1602	49.2	796	1 CAD8_HUMAN	P55287 homo sapien
6	1601	49.1	796	2 Q96CZ8	Q96CZ8 homo sapien
7	1596	49.0	796	1 CAD8_MOUSE	P55288 mus musculu
8	1595.5	48.6	796	2 Q8C7Q6	Q8C7Q6 mus musculu
9	1582.5	48.6	794	2 Q93264	Q93264 xenopus lae
10	1558	47.8	792	1 CAD8_CHICK	O93319 gallus gall
11	1536.5	47.1	716	2 AAH57581	AAH57581 mus muscu
12	1536.5	47.1	716	2 AAH57581	AAH57581 mus muscu
13	1536.5	47.1	799	1 CAD8_HUMAN	P55286 homo sapien
14	1536.5	47.0	794	2 Q8BRK4	Q8BRK4 mus musculu
15	1530.5	47.0	799	1 CAD8_RAT	O54800 ratu
16	1528.5	46.9	799	1 CAD8_MOUSE	P97291 mus musculu
17	1528.5	46.8	716	2 Q8C375	Q8C375 mus musculu
18	1486.5	45.6	370	2 Q86T00	Q86T00 homo sapien
19	1446.5	44.4	788	1 CAD8_HUMAN	O96768 mus musculu
20	1441.5	44.2	801	1 CAD8_HUMAN	P55285 homo sapien
21	1441	44.2	789	1 CAD6_RAT	P55280 ratu
22	1440	44.2	790	1 CAD6_HUMAN	P55285 mus musculu
23	1435.5	44.0	789	1 CAD8_CHICK	O90763 gallus gall
24	1431.5	43.9	785	1 CAD7_CHICK	O90763 gallus gall
25	1430.5	43.9	788	2 Q8V168	Q8V168 mus musculu
26	1429.5	43.9	788	2 Q8W0S7	Q8W0S7 mus musculu
27	1429.5	43.9	788	2 AAH62962	AAH62962 mus muscu
28	1425	43.7	801	2 Q9Z0M3	Q9Z0M3 mus musculu
29	1423	43.7	551	2 Q8AMW2	Q8AMW2 gallus gall
30	1422	43.6	798	2 Q7ZYV7	Q7ZYV7 gallus gall
31	1422	43.6	798	2 Q8GCH3	Q8GCH3 gallus gall

32	1420	43.6	789	1 CAD9_HUMAN	Q9ULB4 homo sapien
33	1415.5	43.4	785	1 CAD7_HUMAN	Q9ULB5 homo sapien
34	1413	43.4	790	1 CAD6_MOUSE	P97326 mus musculu
35	1412.5	43.3	790	1 CAD1_HUMAN	Q13634 homo sapien
36	1412	43.3	630	2 Q81Y78	Q81Y78 homo sapien
37	1407.5	43.2	785	2 Q8BM92	Q8BM92 mus musculu
38	1400	43.0	790	1 CAD6_CHICK	Q90762 gallus gall
39	1395.5	42.8	790	2 Q8W5Z2	Q8W5Z2 homo sapien
40	1389.5	42.6	790	2 Q91838	Q91838 xenopus lae
41	1372.5	42.1	508	2 Q6PANA	Q6PANA mus musculu
42	1372.5	42.1	508	2 AAH60200	AAH60200 mus muscu
43	1372.5	42.1	794	2 Q86UD2	Q86UD2 homo sapien
44	1368.5	42.0	794	1 CAD6_HUMAN	P55289 homo sapien
45	1344	41.2	792	2 Q9DF50	Q9DF50 xenopus lae

ALIGNMENTS

RESULT 1	ID	CAD0_HUMAN	STANDARD	PRT	819 AA.
AC	Q86UF0	Q86UF0	Q86UF0		
DT	25-MAR-2004	(Rel. 43, Created)			
DT	25-MAR-2004	(Rel. 43, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Cadherin-24 precursor (UNQ2834/PRO34009).				
GN	Name=CDH24; Synonyms=CDH11L;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH				
RP	SCENTININS				
RX	MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;				
RA	Katagiri B.J., Nieman M.T., Wheelock M.D., Johnson K.R.;				
RT	"Characterization of cadherin-24, a novel alternatively spliced type				
RT	II cadherin.";				
RL	J. Biol. Chem. 278:27513-27519(2003).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RX	MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gr.1293003;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,				
RA	Eaton D., Fester J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Seshagiri S., Simons L., Singh J., Smith V., Srinon J., Vagstad A.,				
RA	Vandlen R., Watanabe C., Wileand D., Woods K., Xie M.-H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang X., Zhang Z., Goddard A., Wood W.L.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment.";				
RL	Genome Res. 13:2265-2270(2003).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 3).				
RP	TISSUE=Testis;				
RA	Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;				
RA	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.				
CC	- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.				
CC	- They preferentially interact with themselves in a homophilic				
CC	manner in connecting cells; cadherins may thus contribute to the				
CC	sorting of heterogeneous cell types. Cadherin-24 mediate strong				
CC	cell-cell adhesion.				
CC	- SUBUNIT: Associates with alpha-, beta- and delta-catenins.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein (potential).				
CC	- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=;				
CC	Name=1; Synonyms=long form;				
CC	Isoid=Q86UF0-1; Sequence=displayed;				
CC	Name=2; Synonyms=short form;				

Db	19	PFPSVDPQGVKVRTALPNMDEFTQEEFLVVIQAKMGGMGLSGSTTVVITLSDVNDP	256
QY	241	KRPKPSLIQPSVETVETGPGTIVGRIRAADPDLGNALMAYSILIDGESSPAFISTDLQGR	3000
Db	257	KRPKPSLIQPSVETVETGPGTIVGRIRAADPDLGNALMAYSILIDGESSPAFISTDLQGR	316
QY	301	DGLITVRKPELDFESQSFVFRVEANTLIDEPAYLRGCFPKVASVRAVADAPPAFTQ	360
Db	317	DGLITVRKPELDFESQSFVFRVEANTLIDEPAYLRGCFPKVASVRAVADAPPAFTQ	376
QY	361	AAVHLTVPENKAPGTLVGOISAAADLSPASPIRISILPHSPPECFSIOPEEGITHAP	420
Db	377	AAVHLTVPENKAPGTLVGOISAAADLSPASPIRISILPHSPPECFSIOPEEGITHAP	436
QY	421	LDEEAPAMNLVTLATELCMXSGPERGVPLLVEMWSPAAPPPORSVYSGAVGIPDSSA	480
Db	437	LDEEAPAMNLVTLATELCMXSGPERGVPLLVEMWSPAAPPPORSVYSGAVGIPDSSA	496
QY	481	QASRVQVAIQTLDENDNAPQLAEPYDTVCDSAAFGQLIQVIRALDRDEVGNSSHSFQG	540
Db	497	QASRVQVAIQTLDENDNAPQLAEPYDTVCDSAAFGQLIQVIRALDRDEVGNSSHSFQG	556
QY	541	PLGPDANFTVQGNRD-----LPA-----WPHILMASASWHL---573	
Db	557	PLGPDANFTVQGNRDQASALLPSRPPAPPRHAPVPIELMDWQPLASTATVTVSVCR	616
QY	574	-----WPPAERGNQPSAQG 587	
Db	617	CQPDGVSASQWPEAHLSAAGLSTG 640	
RESULT 2			
Q6PFY6	ID	PRELIMINARY; PRT; 781 AA.	
Q6PFY6	Q6PFY6		
DT	05-JUL-2004 (TEMBLrel. 27, Created)		
DT	05-JUL-2004 (TEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TEMBLrel. 27, Last annotation update)		
DE	Cadherin-like 24.		
GN	Name=Cdh24;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins P.S., Wagner L., Sheman C.M., Schuler G.D.,		
RA	Altschul S.F., Zedberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Mex S.I., Wang J., Hien P.,		
RA	Diatchenko L., Marcuana K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Sapichenko M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinini P., Prange C.,		
RA	Raba S.S., Locantello N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McEwan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Rodriguez S., Prange C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywnicki M.I., Skatska U., Smalusz D.E., Scherch A., Schein J.E.,		
RA	Jones S.J., Maier M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Brain;		
RA	Strausberg R.,		
RA	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: BC057373; AAH57373.1; -
 DR InterPro: IPR002126; Cadherin_C.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR02005; CADHERIN.
 DR SMART: SM00112; CAI_4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS50268; CADHERIN_2; 5.
 DR KEGG: Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;

Query Match 77.0%; Score 2511; DB 2; Length 781;
 Best Local Similarity 78.6%; Pred. No. 76-148;
 Matches 502; Conservative 24; Mismatches 47; Indels 66; Gaps 7;

QY 1 CMGRILAPARAMAGSREHPGALLRTRRSWMNQPFVIEEYAGEPVLIGKLSHDVDRGE 60
 DB 17 CMGRILAPARAMAGSREHPGALLRTRRSWMNQPFVIEEYAGEPVLIGKLSHDVDRGE 76
 QY 61 GRTKYLLTGBAGTGVFIDEATGNHVTKSLDREKQCYLLAQAVDRASNPLEPPSEF 120
 DB 77 GRTKYLLTGBAGTGVFIDEATGNHVTKSLDREKQCYLLAQAVDRASNPLEPPSEF 136
 QY 121 IIKGQDINDNPPFLPGPYHATVPEMSNVGTSVIQVTAHADDPSTGNSAKLVYTVLDGL 180
 DB 137 IIKQDINDNPPFLPGPYHATVPEMSNVGTSVIQVTAHADDPSTGNSAKLVYTVLDGL 196
 QY 181 PFFSVDPQTGVVTRTALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYTVLSDVNDP 240
 DB 197 PFFSVDPQTGVVTRTALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYTVLSDVNDP 256
 QY 241 PKFPQSLYQSFVETAGTGLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 300
 DB 257 PKFPQSLYQSFVETAGTGLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 316
 QY 301 DGLLTVRKPLDPESQSSYFVEATNTLIDPAYLRGPFKVAVSVYVQAPEPPAFQ 360
 DB 317 DGLLTVRKPLDPESQSSYFVEATNTLIDPAYLRGPFKVAVSVYVQAPEPPAFQ 376
 QY 361 AAYHLTVPENKAPGTLVGOISADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 420
 DB 377 AAYHLTVPENKAPGTLVGOISADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 436
 QY 421 LDREARAHNTLVATLGLGMSWGPGRGWPLLVAEWSAPAAPQSPVGSANGIPQDSSA 480
 DB 437 LDREARAHNTLVATLGLGMSWGPGRGWPLLVAEWSAPAAPQSPVGSANGIPQDSSA 496
 QY 481 QASRQOVAIOTLDEDNAPQLAEPYDTVCDSAAFGOLIOVTRALDDEVGNSSHYVFG 540
 DB 499 QASRQOVAIOTLDEDNAPQLAEPYDTVCDSAAFGOLIOVTRALDDEVGNSSHYVFG 518
 QY 541 PLGPANFTVQDNRLPAMFPLMASASWLMHPAER-----GNQPSQCKSS 590
 DB 519 PLGPANFTVQDNRLPAMFPLMASASWLMHPAER-----GNQPSQCKSS 571
 QY 581 -----SLPGRLFGALPSCQL-PLGTPA---LGIYVC 618
 DB 572 VTVSVCRCRPGDSVASCWPEAQLSPTGLSTGALLATVTC 610

RESULT 3
 AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373;
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.

GN CDH24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywicki M.J., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC057373; AAH57373.1; -
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;

Query Match 77.0%; Score 2511; DB 2; Length 781;
 Best Local Similarity 78.6%; Pred. No. 76-148;
 Matches 502; Conservative 24; Mismatches 47; Indels 66; Gaps 7;

QY 1 CMGRILAPARAMAGSREHPGALLRTRRSWMNQPFVIEEYAGEPVLIGKLSHDVDRGE 60
 DB 17 CMGRILAPARAMAGSREHPGALLRTRRSWMNQPFVIEEYAGEPVLIGKLSHDVDRGE 76
 QY 61 GRTKYLLTGBAGTGVFIDEATGNHVTKSLDREKQCYLLAQAVDRASNPLEPPSEF 120
 DB 77 GRTKYLLTGBAGTGVFIDEATGNHVTKSLDREKQCYLLAQAVDRASNPLEPPSEF 136
 QY 121 IIKGQDINDNPPFLPGPYHATVPEMSNVGTSVIQVTAHADDPSTGNSAKLVYTVLDGL 180
 DB 137 IIKQDINDNPPFLPGPYHATVPEMSNVGTSVIQVTAHADDPSTGNSAKLVYTVLDGL 196
 QY 181 PFFSVDPQTGVVTRTALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYTVLSDVNDP 240
 DB 197 PFFSVDPQTGVVTRTALPNMDRETOEELVYVIAQDMGGMGSLGSTTVYTVLSDVNDP 256
 QY 241 PKFPQSLYQSFVETAGTGLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 300
 DB 257 PKFPQSLYQSFVETAGTGLVGRRAQDPDLGNALMAYSILDEGSEAFSISTDLQGR 316
 QY 301 DGLLTVRKPLDPESQSSYFVEATNTLIDPAYLRGPFKVAVSVYVQAPEPPAFQ 360
 DB 317 DGLLTVRKPLDPESQSSYFVEATNTLIDPAYLRGPFKVAVSVYVQAPEPPAFQ 376
 QY 361 AAYHLTVPENKAPGTLVGOISADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 420
 DB 377 AAYHLTVPENKAPGTLVGOISADLSPASPIRYSILPHSDPERCFSIQPEEGTHTAAP 436
 QY 421 LDREARAHNTLVATLGLGMSWGPGRGWPLLVAEWSAPAAPQSPVGSANGIPQDSSA 480
 DB 437 LDREARAHNTLVATLGLGMSWGPGRGWPLLVAEWSAPAAPQSPVGSANGIPQDSSA 496

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QY 481 QASRQVAIQTLDENDNAPOLAEFPYFVCDASAPGQLIQTALDRDEVGNSSHVSG 540
DB 459 QSSRQVAIQTLDENDNAPOLAEFPYFVCDASAPGQLIQTALDRDEVGNSSHVSG 518
QY 541 PLGDPANFTVDNFDLPWFHPLIMASASSWLMHPAER-----GNQPSQKSS 550
DB 519 FVGDPANFTVDNFDNDSGA---SLILPSRPA---PPRCAPYLPIELMDWGCPALSTAT 571
QY 591 -----SLPCGRPLGALPSCQL-PLGIPA---LGIYLC 618
DB 572 VTVSVCRCPDGSYSASCWPEAQSLPTGLSTGALLAIVTC 610

RESULT 4
Q96LQ7 PRELIMINARY; PRT; 493 AA.
ID 096LQ7
AC 096LQ7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Nimmiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL -1 SIMILARITY: Contains 4 cadherin domains.
CC EMBL: AK057922; BAB71613.1; -.
DR HSSP; p12830; 106S.
DR Genew; HGNC:14265; CDR24.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; Cadherin; 4.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SMO0112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS02068; CADHERIN_2; 4.
DR Calcium; Calcium-binding.
SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;

Query Match 70.3%; Score 2291; DB 2; Length 493;
Best Local Similarity 93.3%; Pred. No. 1.9e-134;
Matches 446; Conservative 2; Mismatches 8; Indels 22; Gaps 2;

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DB 257 PKFQSLQFVSFVETAGTGLVGRRAQDPDLGNALMAYSILDGESEAFSISTDLQGR 316
QY 301 DGLLIVRPKLPDPSRSRSFVEATNTLIDPAYLRGCFKVASVAVQDAPPPPAFTQ 360
DB 317 DGLLIVRPKLPDPSRSRSFVEATNTLIDPAYLRGCFKVASVAVQDAPPPPAFTQ 376
QY 361 AAYHLLTVENKAPGTLVQGISAADLSPASIRYSILPHSDPERCFISIQPEEGTHTAAP 420
DB 377 AAYHLLTVENKAPGTLVQGISAADLSPASIRYSILPHSDPERCFISIQPEEGTHTAAP 436
QY 421 LDREKARAHNLTVALTEIG-----WSKQPEGWPLVVAEMSAAR 460
DB 437 LDREKARAHNLTVALTEIGEDSRAHKAAMASWPSRCPWV---GMRRLVTAIPSPA 490

RESULT 5
CADB_HUMAN STANDARD; PRT; 796 AA.
ID CADB_HUMAN
AC P55287; Q15065; Q15066; Q9UQ93; Q9UQ94;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN Name=CDH11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95073006; PubMed=7882033;
RA Tanhara H., Sano K., Helmark R.L., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin.";
RL Cell Adhes. Commun. 2:15-26 (1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Osteosarcoma;
RX MEDLINE=94216322; PubMed=8163513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
RA Amano E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts.";
RL J. Biol. Chem. 269:12092-12098 (1994).
RN [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanhara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RT nervous tissue.";
RL Cell Regul. 2:261-270 (1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Kools P.F.J., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
RT molecules are detectable in both human cancer and normal cells.";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=displayed;
CC Name=2;
CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC other tissues. Expressed in neuroblasts.

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Query Match	Best Local Similarity	Score 1602:	DB 1:	Length 796:
Matches 323;	Conservative 98;	Mismatches 134;	Indels 86;	Gaps 10
1	CMGRLA-----APAR-----	AMASRR--HPGPALLTRRSWVWQFVIEEYAGPEV	47	
13	CLGLCLGSHNAFAERERGHLPBFGHHEKKEGGVLQSGSKGVMWQFVIEEYTPDPV		72	
48	LIGLTHSDVDVRGGRKRYLLTGEGAGYVVIDEAGNTHYKSLDREPKQVYLLAAQVD		107	
73	LVGLGHSDDSGGNTKYLISGGAGTFLVIDDSGNHAKYLLDREKRAQVYLLMAQVD		132	

QY		106	RASNRPLEPSEFIIKGGDINDNPEIFLPGVHATVEMSVGVSIVQTAAHADDPISYG	166
D92		133	RLTNRPLEPSPFIKYKODINDNPFEIHEHYTHANVPERSVGTSVIQVTAAADDPITYG	192
QY		168	NSAKLYTVTLVDGLPFPSVDPOTGVVRITAIENMDRETOEEFLVITIQAOMGGNGGSLGST	227
D92		193	NSAKLYVSIILEEQPFPSVEAQGTIGTIRLTALPNMDEAKEEYHVIVIAQDMGGHGSLGTT	252
QY		228	TVALTVLSDVNDRPKFPPOSLYGFSTVERTAGPOTLVGRJADDPPLDGNAAMAYSILDGEQ	287
D92		253	KTIITLLIDNDNPFRFPQOLIYMSSEANAAGEEVGRKAKDPPIGENGLVITVAIVDGDG	312
QY		288	SEAFTSISTDLQGRDGLTLVRKPLDFESORSYSFRVEATNTLIDPAYLRGCPFKDVASRV	347
D92		313	MESFFETITTYEQEGVIKLKKEPVDETERAVSLKYEANAHIDKFLINSNGFFXTQIVKI	372
QY		348	AVODAEPAEPFOQAAYHLTPENKAPGTLVGOISAADLDSPAFIRISLIHPSPERCFS	407
D92		373	SVEDAEPMPFLAPSTIEHVEGNAAAGVGVAKPDPAANSIRISIDRHDLDFEFT	432
QY		408	IQEEECTGHTAAPLPDREARAMNLTVLATELGWSGPERGWPLLVAEWSAPAAPPORSP	467
D92		433	INPEDGFIKTTRPLDREETAAMINTVFPAEI-----	463
QY		468	VGSAAVGIPODSGAQSRVOVALQTLDENDNM.POLAEPYDTFCDS----AAPGLIQIR	523
D92		464	-----HNHQEQVFAIRKVLVDVNDNPKFAAPFEGFICSDQTKPLSNOPYTIS	514
QY		524	ALDRDEVGNSSHVSPFGGP--LGPDANFTVODNRDLPA-----WFHBLM	555
D92		515	ADDKDXTANGPRFITFELPEIITHNFNFTVRNDRDTAGVARAGSGFEROKODYLTPLIVI	574
QY		566	ASASSWLHWPPAERGNQPAPSQCKSSLP-CG-RLPGAIPSC	604
D92		575	-----SDGGIPPMSTNTLTLTKVCGCDVNGALLSC	604

RESULT 6
 Q96CZ9 PRELIMINARY; PRT: 796 AA.
 ID Q96CZ9 Q96CZ9;
 AC Q96CZ9; 01-DEC-2001 (TEMBIREl. 19, Created)
 DT 01-DEC-2001 (TEMBIREl. 19, Last sequence update)
 DT 01-MAR-2004 (TEMBIREl. 26, Last annotation update)
 DN Caderhin 11, type 2, isoform 1 preproprotein.
 GE Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI TaxID=9606;
 EN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Peltingold E.A., Gronow L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buettow K.H., Scheifter C.F., Bat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hestek F.,
 Diatchenko L., Marushina K., Farmer A.X., Rubin G.T., Hong L.,
 Stadelman M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udell T.B., Rothkyuk J.S., Carinini P., Prange C.,
 Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Huliy S.W.,
 Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Ketterman W., Madan A.C., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Schechenko Y., Bouffard G.-G.,
 Blakeley R.A., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Kravitski M.I., Skalka U., Smalls D.E., Scherch A., Schein J.E.,
 Jones S.U., Matra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human

RT "Generation and initial analysis of more than 15,000 full-length human

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE FROM N.A.

Strasbourg R.;

Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

FUNCTION: Cadherins are calcium dependent cell adhesion proteins (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

EMBL: BC013609; AAH13609.1; .

GO: GO:0016020; C:membrane; IEA.

GO: GO:0005509; F:calcium ion binding; IEA.

GO: GO:0007156; P:homophilic cell adhesion; IEA.

InterPro: IPR000233; Cadherin_C-term.

InterPro: IPR001901; SECD.

Pfam: PF00028; Cadherin_5.

PRINTS: PRO0205; CADHERIN.

SMART: SM00112; CA; 5.

PROSITE: PS00232; CADHERIN_1; 3.

PROSITE: PS02668; CADHERIN_2; 5.

PROSITE: PS01067; SECD; SEC61G; UNKNOWN_1.

Calcium-binding; Cell adhesion; Transmembrane.

SEQUENCE 796 AA; 87979 MW; 84979B834F7547C CRC64;

Query Match 49.1%; Score 1601; DB 2; Length 796;

Best Local Similarity 50.4%; Pred. NO. 3.5e-91;

Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

1 CMGRLA-----APAR-----AMAGSRE--HPGALARTRRSWMVNFVIEBAGPEPV 47

13 CLGMLCHSAAPAFRRGHLPSPFGHHEKGEQGLRSRGWVMVNFVIEBTPDDV 72

48 LIGLHSDVDGREGRTYTLTGEGAGTVFIDATGNTGHTKSLDSEKQVYLAQAVD 107

73 LVGLHSDVDGREGRTYTLTGEGAGTVFIDATGNTGHTKSLDSEKQVYLAQAVD 132

108 RASRPLEPPEPSEFFIKQDINDNPPLPLGPHATVEKMSNVGTSVYQVTAHDADPSYG 167

133 RDTNRPLEPPEPSEFFIKQDINDNPPLPLGPHATVEKMSNVGTSVYQVTAHDADPSYG 192

168 NSACLVYTVLDGLPFESVDPTQGVVTRATNMDFEETOEELVYIOAKMGHNGISGST 227

193 NSACLVYTVLDGLPFESVDPTQGVVTRATNMDFEETOEELVYIOAKMGHNGISGST 252

228 TVYTVLSDVNDNPKPFQSLYQFSVETAGPTLVGLRAQDDPLDGNALMAYSLDGG 287

253 KWTTLVDVNDNPKPFQSLYQFSVETAGPTLVGLRAQDDPLDGNALMAYSLDGG 312

288 SEAFSISTDIOGRDGLTVKPLDFESQSYFRVATNTLIDPAYLRGPFQDVASVY 347

313 MESEFITTDTYETQGVKTKKPPVDFETKRAVSLKVAANVHIDPKFISNGPFDVTVKI 372

348 AVODAPPPAFPTQAAVHLTVENKAPGTLVGOISADLDSPASPIYSLPSDPRCS 407

373 AVEADAPPPAFPTQAAVHLTVENKAPGTLVGOISADLDSPASPIYSLPSDPRCS 432

408 IQPEEGITHTAAPLDREARAHNLTVLATELGWSGWERGWVPLVAEMSAAPQSP 467

433 INPDGKITTKPLDRETAHNLTVFAAI----- 463

468 VGSANGVTPQSSAQAASVQVATQTLDENDNAPQALAPYDTFVDS-----AARGQLQVIR 523

464 -----HNRQEAQVPAIRVLDVNDAPKFAAPYEGFICSDQTKPLSNQPIVTS 514

524 ALPDREYGNSSHVSFOGP--LGPDAFTVQDNNDLPA-----WFHPLLM 565

515 ADDKDPANGPRIFFSLPEIINHPFTVRNDNDNAGVYARAGGFSRQKQDLYLLPIYI 574

566 ASASSMLHWPAPERGNQAPASQGSSSLP--CG-RLPALPSC 604

DB 575 -----SDGIPMSSSTNTLTIKVCQDVNGALISC 604

RESULT 7

CADB MOUSE

ID CADB MOUSE STANDARD; PRT: 796 AA.

AC P55288;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).

GN Name=Cdh11; Synonyms=Cad-11;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=95269886; PubMed=7750649;

RA Hoffmann I.H.; Balling R.;

RT "Cloning and expression analysis of a novel mesodermally expressed cadherin."

RL Dev. Biol. 169:337-346(1995).

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=95269887; PubMed=7750650;

RA Kimura Y.; Matsunami H.; Inoue T.; Shimamura K.; Uchida N.; Ueno T.; Miyazaki T.; Takeichi M.;

RT "Cadherin-11 expressed in association with mesenchymal morphogenesis in the head, somite, and limb bud of early mouse embryos."

RL Dev. Biol. 169:347-358(1995).

RN (3)

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6; TISSUE=Calvaria;

RA MEDLINE=94216322; PubMed=8163513;

RA Okazaki M.; Takeshita S.; Kawai S.; Kikuno R.; Tsujimura A.; Kudo A.; Aman E.;

RT "Molecular cloning and characterization of OB-cadherin, a new member of cadherin family expressed in osteoblasts."

RL J. Biol. Chem. 269:12092-12098(1994).

RN (4)

RP SEQUENCE FROM N.A.

RC TISSUE=Olfactory epithelium;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strassberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RA Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.; Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Heile F.; Diachenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.; Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schaefer T.E.; Brownstein M.J.; Ueda N.A.; Toshiyuki S.; Carninci P.; Prange C.;

RA Rana S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.; Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.; Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Faley J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.; Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

RA Butterfield Y.S.N.; Krzyzinski M.I.; Skalek U.; Skallus D.E.;

RA Scherch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN (5)

RP DEVELOPMENTAL STAGE.

RC STRAIN=C57BL/6; TISSUE=Testis;

RX MEDLINE=9703837; PubMed=8879495;

RA Munro S.B.; Blaschuk O.W.;

RT "A comprehensive survey of the cadherins expressed in the testes of fetal, immature, and adult mice utilizing the polymerase chain reaction."

RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL databank.
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X77557; CAA54674.1; -;
 DR EMBL; D31963; BAA06730.1; -;
 DR EMBL; D21253; BAA04797.1; -;
 DR EMBL; BC046314; AAA46314.1; -;
 DR PIR; A53584; A53584.
 DR PIR; I48277; I48277.
 DR PIR; I49556; I49556.
 DR HSSP; P09803; 117W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005866; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C term.
 DR Pfam; PF00028; Cadherin_1.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KEGG; K04468; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> M (in Ref. 1).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641D5529 CRC64;

Query Match 49.0%; Score 1596; DB 1; Length 796;
 Best Local Similarity 50.7%; Pred. No. 7, 1e-91;
 Matches 317; Mismatches 97; Mismatches 127; Indels 84; Gaps 8;

QY 15 SREHP-----GRLALTRRSWTWNOFVIEEYVAGPEPVILIGLHSDVDRGEGRT 63
 DB 29 SLHLSFPGHHEKKEGQVLYQSKRGWVNWQFVIEEYTGDPVLYGRLHSDIDSGDNT 88
 QY 64 KYLLTGEAGATVFVIDEATGNHVTKSLDREKAQYVLLAQAVDFASNRPEPSEFIK 123

DB 89 KYLLTGEAGATVFVIDEATGNHVTKSLDREKAQYVLLAQAVDRDTRPEPSEFIK 148
 QY 124 GODINDNPEIPFELGAYATVPEMSNVGTSVIQTVAHADDPSYGNAXLYVTVDGPEF 183
 DB 149 VQDINDNPEIPFELGAYATVPEMSNVGTSVIQTVAHADDPSYGNAXLYVTVDGPEF 208
 QY 184 SYDPQGVKRTLPMMDESETOEELVYVQADMGMGSGSTVTVTLSPDVNPNPKF 243
 DB 209 SEADQGLIRLPLMMDSEAEYHVVVQADMGMGSGSTVTVTLSPDVNPNPKF 268
 QY 244 POSLYQSVETAGPGLTVGRLLRAQDPDLGNALMAVSIIDEGSEAFSITDLOGRDL 303
 DB 269 POSLYQSVETAGPGLTVGRLLRAQDPDLGNALMAVSIIDEGSEAFSITDLOGRDL 328
 QY 304 LTVKRPDPESQSRISFVEATNTLIDPAYLRGPFKVAIVRAVQAPPEPAQAY 363
 DB 329 VTKRPVDFETKRAVSLKEANVHIDKFLSNGFKQVTVKLSVEDAPPEFLAPSY 388
 QY 364 HLTVPENKAPGLVGOISADUDSPASPIRYSILPHSDPERCFSIQPEGTIHTAPLDR 423
 DB 389 HTEQENMAAGTVGRVHAKQDPAANSPIRYSIDHTDLDREFTINPEDGFIKTKPLDR 448
 QY 424 EARAHNLTVLATELGMSWGPGRGVPLLVAEWSAPAPQSSPVGSAVGIPOSSAQAS 483
 DB 449 EETAMINISVFAAEI-----NHRQET 470
 QY 484 RYQVAIQCLDENDNAPOLAEPYDFVCDSPAAP---GOLIVIRALDRDEVNSHVSFO 539
 DB 471 KQFVALRVDVNDNAKFAPEEGTICSDHKLASNPPIVVSADDDDTNAGRFFIS 530
 QY 540 GP--LGPDAFTVQDRDLPA-----WFHPLMASASSWHLWPAERGN 581
 DB 531 LPPEIMHNPFTVRDRDNTAGVYARGGFSRQKDFYLLPIVI-----SDGI 579
 QY 582 QPASQKSSSLP-CG-RLPGALPSC 604
 DB 580 PMWSTNTLTIVKCGDVAGALLSC 604

RESULT 8

Q8CTG6 PRELIMINARY; PRT; 796 AA.
 AC Q8CTG6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone:C530015F15 product:cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

Nature 420:563-573(2002).

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=20493974; PubMed=11042159;
Carlini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes";
Genome Res. 10:1617-1630(2000).

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Spinal cord;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaka S., Sasaki N., Carlini P.,
Kono H., Akiyama J., Nishi K., Katsuna T., Tashiro H., Itoh M.,
Suni M., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer";
Genome Res. 10:1757-1771(2000).

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Spinal cord;
Adechi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carlini P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishihara K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Togawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(by similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).

-1- SIMILARITY: Contains 5 cadherin domains.

EMBL: AK049652; BAC33860.1; -

HSSP: P09803; 117W.

MGD: MGI:99217; Cdh11.

GO: GO:0005737; C:cytoplasm; IDA.

GO: GO:0005886; C:plasma membrane; IDA.

InterPro: IPR002126; Cadherin.

InterPro: IPR000233; Cadherin_C-term.

pfam: PF00028; Cadherin_5.

pfam: PF01049; Cadherin_C_1.

PRINTS: PR0205; CADHERIN.

SMART: SM00112; CA_5.

PROSITE: PS00233; CADHERIN_1; 3.

PROSITE: PS50268; CADHERIN_2; 5.

KM Calcium-binding; Cell adhesion; Transmembrane.

SEQUENCE 796 AA; 88126 MW; 71963374B21B329 CRC64;

Query Match 49.0%; Score 1595.5; DB 2; Length 796;
Best Local Similarity 51.6%; Pred. No. 7.6e-91;
Matches 314; Conservative 97; Mismatches 125; Indels 73; Gaps 7;

QY 20 GPALLRRSRWNNQFVIEVAGPEPVYLGKHSVDGEGTKYLLGEGAGTYFVD 79
DB 45 GQVLOKRGKGMWQFVIEVAGPEPVYLGKHSVDGEGTKYLLGEGAGTYFVD 104
QY 80 EATGNHVTSLDREKAYQVYLLAQVADRASNPLPPEPFILIKGQDINDNPPIFLGPY 139
DB 105 DKSGNIHATKTLDRERAPQYTLMAQAVDRQTNRPFLPPEPFILIKVQDINDNPPIFLHELY 164

QY 140 HATVEMSNVGTSTVQTAHADDPVSGNSAKLYTVLTDGLPFPSPVDQGTAVTAPM 199
DB 165 HANVPSRNVGTSTVQTAHADDPVSGNSAKLYTVLTDGLPFPSPVDQGTAVTAPM 224
QY 200 DEETQEEFLVVIQANDMGHMGSLGSGTTLVTLSDVNDNPKPEPOSILQPSVVEIAPG 259
DB 225 DEAEKEHYHVIQANDMGHMGSLGSGTTLVTLSDVNDNPKPEPOSILQPSVVEIAPG 284
QY 260 TLVGLRQADPDLGNALMAVSIIDGEGSEAFSTIDUGSDGLITVRKPLDFDSQSSYS 319
DB 285 EEWGRVKAADPDIGENGLVTNIVDGDIELEFITTDETQDGVKKLPVDFETKAVS 344
QY 320 FFEVATNTLIDPAYLRSGPFVDVAVRVAVDAPEPAFTQAAVHLTPENKAPGLTVGQ 379
DB 345 LKIEANVHIDPKFISNPFQDVTWKISVEDADEPFELAPSTIHEQENAAAGTVGR 404
QY 380 ISALDLPASPIRISILPHSDPERCSIQEESTITPAALDEBARAHNLTVALTELG 439
DB 405 VHAQDPDANSPIRISIDRHTDLRFPFTINDEDFIKTKPLDEBETAMINISVPAE1- 463
QY 440 MSWGGERGVPLVEMGAPAPAPQSPVGSAGVIPQDSSAQASRQVAVIOTLENDNAP 499
DB 464 -----HNKQETKVVAIRKVLVDVNDNAP 486
QY 500 QLAEPYDTFVCDSPAAP---GQLIQVTRALDRDEVGSSHVSFGCP--LGPDAFTVQDN 553
DB 487 KFAAYEGFICSDHPKALSNOPIVTVASADQDDTANGPRTIFELPPEIMHNPFTVVDN 546
QY 554 RDLPA-----WPHPLMASASSLHMPAPERGNQPSQGSSTLP-CG- 595
DB 547 RDNHGVYARRGGRSRQKQDLYLLPIVI-----SDGGLPMSSTVITLTIKVC 595
QY 596 RLPGALPSC 604
DB 596 DVNGALLSC 604

RESULT 9

ID 093264 PRELIMINARY; PRT; 794 AA.

AC 093264;

DT 01-NOV-1998 (TREMBlrel. 08. Created)

DT 01-NOV-1998 (TREMBlrel. 08. Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26. Last annotation update)

DE Cadherin precursor.

GN Name=Xcad-11;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_Taxid=8355;

RN [1]

RP SEQUENCE FROM N.A.

RP TISSUE=Zygote;

RX MEDLINE=98202517; PubMed=9533956;

RA Hadeball B., Borchers A., Wedlich D.;
"Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
signal";
Mech. Dev. 72:101-113(1998).

RL -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(by similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).

CC -1- SIMILARITY: Contains 5 cadherin domains.

EMBL: AF002983; AAC28073.1; -

HSSP: P09803; 117W.

GO: GO:0016020; C:membrane; IEA.

GO: GO:0005509; F:calcium ion binding; IEA.

GO: GO:0007156; F:homophilic cell adhesion; IEA.

InterPro: IPR002126; Cadherin.

InterPro: IPR000233; Cadherin_C-term.

pfam: PF00028; Cadherin_5.

pfam: PF01049; Cadherin_C_1.

PRINTS: PR0205; CADHERIN.

DR SMART; SMO0112; CA: 5
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 potential.
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEA719DB CRC64;
 Query Match 48.6%; Score 1582.5; DB 2; Length 794;
 Best Local Similarity 50.4%; Pred. No. 4,9e-90;
 Matches 310; Conservative 97; Mismatches 133; Indels 75; Gaps 5;
 QY 20 GPALLRTRSRWVWNOFVIEEYAGEPEVLLIGKLSHDVDRGEGRTKYLTLTGEGAGTVFVID 79
 DB 45 GQVLRHRSKRGWVWNOFVIEEYAGEPEVLLIGKLSHDVDRGEGRTKYLTLTGEGAGTVFVID 104
 QY 80 EATGNHVTKSLDREKAYVLLAQAVDRAASNPPEPSEFTIKGQDINDNPFIFLPGY 139
 DB 105 DKSGNHATKTLDEEERAYTLMAQAVDRETNKPLEPSEFTIKGQDINDNPFIFLPHENY 164
 QY 140 HATVPEMSNVGTSVIQVTAHDADDPYGSNAKLVYTLTDLGPFPSVDPQGVVRAIPNN 199
 DB 165 HANVPEMSNVGTSVIQVTAHDADDPYGSNAKLVYTLTDLGPFPSVDPQGVVRAIPNN 224
 QY 200 DRETQEEFLVYIAQDMGGMGSLGSGTIVYTLSDVNDNPKPQSGLYQFVVEYAGPG 259
 DB 225 DRAKEEYHVYIAQDMGGMGSLGSGTIVYTLSDVNDNPKPQSGLYQFVVEYAGPG 284
 QY 260 TLVGRLAQDPDLGNALMAYSITLDGEGSEAFSITDLOGRDGLTVRKPLDESGRSYS 319
 DB 285 EEVERIRAKDPDIEGNGIKRILEGDAEFETAYTQEGVAKKVVADYEIKKYS 344
 QY 320 FRVEATLTLLDPAALRGRPFEDVAVRVAQDAEPPEAFQAAYHLLVPEKKAQGLTVGO 379
 DB 345 MKVAANVHIDPRRLSGRPFEDTATKISVEDPEPEPIFERSTYLLVEYNAASDVTYGR 404
 QY 380 ISAADLSPASPIRYSITLPSDPERCFSIQPEEETITAAPLDREAAANLTVLATELG 439
 DB 405 VHAQDPAAANSPIRYSIDRHTDLDRPFSINPEDVITKTKGLDREESPMENISIAIEV- 463
 QY 440 WSWGPERGWVLLVAEMSAPAPQSRPVSAGVIGPQSSAQSARVOVAIQTLDENDAP 499
 DB 464 -----HNRIHERVVALKVLDKDNAP 486
 QY 500 QLAPEYDTFVCDAAFGQLIQVIRALDRDEVGNSSHVSFGQP--LQPDANFTVQDNEL 556
 DB 487 EFAKPEYAFVCEANPINOEFITITAVVKDPTANLRLFFSPPEIVHPNPFITIDREDN 546
 QY 557 PA-----WFHPLMASASSWHPAPR-----GNPQASQ 586
 DB 547 TASIRVGRGVFSRKKQDIYLVIVISDGS---PMSSTVTLTVRISCSNDSQSLSCH 602
 QY 587 GKSSSLPCGRLLPGAL 601
 DB 603 AEPQSLNGLSTGAL 617
 RESULT 10
 CADB CHICK STANDARD; PRT; 792 AA.
 AC 093319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 NCBI_Taxid=9031;
 RN [1]

RC STRAIN-White leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thiery J.P.,
 RA Kotelnitsky V., Majesky M.W.,
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media";
 RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-stb.ch).
 CC EMBL; AF053342; AAC33675.1; -
 DR HSSP; P09803; 117W.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C_term.
 DR Pfam; PFO0028; Cadherin_5.
 DR Pfam; PFO1049; Cadherin_C/1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA: 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSMEM 614 634 Potential.
 FT DOMAIN 635 792 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3488C6E06731AB CRC64;
 Query Match 47.8%; Score 1558; DB 1; Length 792;
 Best Local Similarity 55.0%; Pred. No. 1.6e-88;
 Matches 296; Conservative 86; Mismatches 116; Indels 40; Gaps 2;
 QY 20 GPALLRTRSRWVWNOFVIEEYAGEPEVLLIGKLSHDVDRGEGRTKYLTLTGEGAGTVFVID 79
 DB 45 GQVLRHRSKRGWVWNOFVIEEYAGEPEVLLIGKLSHDVDRGEGRTKYLTLTGEGAGTVFVID 104
 QY 80 EATGNHVTKSLDREKAYVLLAQAVDRAASNPPEPSEFTIKGQDINDNPFIFLPGY 139
 DB 105 DKSGNHATKTLDEEERAYTLMAQAVDRETNKPLEPSEFTIKGQDINDNPFIFLPHENY 164
 QY 140 HATVPEMSNVGTSVIQVTAHDADDPYGSNAKLVYTLTDLGPFPSVDPQGVVRAIPNN 199
 DB 165 HANVPEMSNVGTSVIQVTAHDADDPYGSNAKLVYTLTDLGPFPSVDPQGVVRAIPNN 224
 QY 200 DRETQEEFLVYIAQDMGGMGSLGSGTIVYTLSDVNDNPKPQSGLYQFVVEYAGPG 259
 DB 225 DRAKEEYHVYIAQDMGGMGSLGSGTIVYTLSDVNDNPKPQSGLYQFVVEYAGPG 284
 QY 260 TLVGRLAQDPDLGNALMAYSITLDGEGSEAFSITDLOGRDGLTVRKPLDESGRSYS 319
 DB 285 EEVERIRAKDPDIEGNGIKRILEGDAEFETAYTQEGVAKKVVADYEIKKYS 344

QY 320 FRVETNTLLDPAVLRGEPKDVASVAVODAPAPFOTAAVHLTPENKAPGLNGQ 379
 DB 345 LKVEANVHIDPKISNGPFDYTVKIVTEDADEPVPFKPSTIFEVQNSAGVVGK 404
 QY 380 ISAADLDSAPSPIRYSILPHSDPERCSIQPEEGTHTAAPLDREARAWNTLVATLGL 439
 DB 405 VHAADPPAANSAIRYSIDRHIDLERFTYFTINADGNITIALDREELAMNISVPAVEV 463
 QY 440 WSKPEEGWVPLVLAEMSAPAPQSPGSAVCIPODSSAQSRVVAIQTIDENDNAP 499
 DB 464 -----HKHQGQAKVPAVKVVDVNDAP 486
 QY 500 QLAPEYDTFVCDSPAAPQILQIVIRALDRDEVGNSHVSFGCP--LIGDANFTVQDRD 555
 DB 487 KFAAAYEAFVCEMNRNSNQFTTISADKXDSANGPRITFPLPEIITHNPFSLRDND 544
 RESULT 11
 Q8C449 PRELIMINARY; PRT; 716 AA.
 ID Q8C449;
 AC Q8C449;
 DT 01-MAR-2003 (Tremblrel, 23, Created)
 DT 01-MAR-2003 (Tremblrel, 28, Last annotation update)
 DT 01-OCT-2004 (Tremblrel, 28, Last annotation update)
 DB Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: C630002D14 product: cadherin 8, full insert sequence (Cdh8 protein).
 DB Name=Cdh8;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium.
 RA RIKEN FANTOM Consortium.
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20489374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20350913; PubMed=1076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Komoto H., Akiyama J., Nishii K., Katsunai T., Taisho H., Itoh M., Saito N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Aichi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P., Fukuda S., Furuta M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirokane T., Horii F., Imotani K., Ishii Y., Itoh M., Kageura I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Komoto H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiyaki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeya Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marsters K., Parker A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Ueda T.B., Yoshizaki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 DR EMBL; AK083092; BAC38758.1; -;
 DR EMBL; BC057581; AAH57581.1; -;
 DR HSP; P15116; INCT.
 DR MGD; MGI:107434; Cdh8.
 DR GO; GO:0016020; C:membrane; IEA;
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;
 QY Query March 47.1%; Score 1536.5; DB 2; Length 716;
 Best Local Similarity 48.1%; Pred. No. 31e-87;
 Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;
 23 LKTRRSWVWNPVIEEYAGBPVLIGLHSDVDGEGRTKXLLTGAGATVVIDEAT 82

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|||||
Db LSRKRGVWVWVQFVLEFSGPEPLVGRHTDLDPSGKIKYILSDGAGTIFQINDIT 115
QY 83 GNHYTKSLDREKQVYLLAQAVDRASNRPLEPSEFIITGQDINNPFPIGPYHAT 142
Db 116 GDIAIKRLDREKAEYLLTAQAVDFETNKPPESEFIITKQDINNAPFELNGPYHAT 175
QY 143 VPMSNVGTSTVYQVTAHDADDPGYSNAXLYVTLADGPPFSVPOTGVATAPNDRE 202
Db 176 VPMSILGTSTVNTATADDPYVNSAKLYVSLLEGPPYSIPEPAILIKTALPNMDRE 235
QY 203 TQEEFLVYIQAKDMGKMGKLSGSTTYYTLSDVNDNPKFPQSLYQPSVETATGPGLTV 262
Db 236 AKBEVLVYIQAKDMGKMGKLSGSTTYYTLSDVNDNPKFPQSLYHFSVPEDVLTGTAI 295
QY 263 GRLRAODPDLGNALMAVSIIDGEGSEAFSISTDLQGRDGLTVRKPDPSQSRYSFRV 322
Db 296 GRVAKANDDIGNAOSYVLIIDGDTALFEITSDAQADGVIRLRKPDDETKKSTYLV 355
QY 323 EATNTLIDPAYLRQPFKDVASVRYVQADAPPAFTQAAHYLTVPENKAPGLTVQOISA 382
Db 356 EAAIHIDPFRSSRQPFKDTATVKIVEDADEPVSFPTVLLFVHNAALNSVIGQVTA 415
QY 383 ADLDSAPPIRYSLIPHSDEPERCSIQPEBGTHTAALDREARAHNTVLTATELGMSW 442
Db 416 RDPDITSSPIRFSIDRHTDLERQFINADSKITLAPLDRSLVWHNTITITATEI 471
QY 443 GPERGVPPLVLAEMWAPAPAPQSPVGSAGVIGIPDSSAQASVQVAYIQTLDENDAPOLA 502
Db 472 -----RMSQISRVPAIKVLVDVNDAPFA 497
QY 503 EPYDTFVCDASAPGGLIQTALDRDEVNGSHVSFOGCLPGD---ANFTVQDNRD--- 555
Db 498 SEYEAFLECNKRGQVITQVAMKDDPKNGHF--FLYSLLPEWVNNPFITIKKEDNSL 555
QY 556 -----LPWFHPLMLMASASWLMHMPAERGNOPASQGSSSL-PCG-RLPGA 600
Db 556 SILAKHNGFRKQGEVYLLPIVI-----SDSGNPPLSSSTLTITIRVCGSGNDGV 604
QY 601 LPSCQ-----LPGLI---PALGIYVC 618
Db 605 VQSCNVEAYVLPILGSMGALIALIAC 630

RESULT 12
AAH57581 PRELIMINARY; PRT, 716 AA.
ID AAH57581;
AC AAH57581;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCB1_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA [1]

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skislow U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC057581, AAH57581.1, -
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 47.1%; Score 1536.5; DB 2; Length 716;
Best Local Similarity 48.1%; Pred. No. 3,1e-87;
Matches 301; Conservative 109; Mismatches 135; Indels 81; Gaps 9;

QY 23 LRTRRSWVWVQFVLEEYAGPEFVILGKLSHDVDRGEGRTYLLTGAGTVFVIDAT 82
Db 56 LSRKRGVWVWVQFVLEFSGPEPLVGRHTDLDPSGKIKYILSDGAGTIFQINDIT 115
QY 83 GNHYTKSLDREKQVYLLAQAVDRASNRPLEPSEFIITGQDINNPFPIGPYHAT 142
Db 116 GDIAIKRLDREKAEYLLTAQAVDFETNKPPESEFIITKQDINNAPFELNGPYHAT 175
QY 143 VPMSNVGTSTVYQVTAHDADDPGYSNAXLYVTLADGPPFSVPOTGVATAPNDRE 202
Db 176 VPMSILGTSTVNTATADDPYVNSAKLYVSLLEGQYFSEIPEPAILIKTALPNMDRE 235
QY 203 TQEEFLVYIQAKDMGKMGKLSGSTTYYTLSDVNDNPKFPQSLYQPSVETATGPGLTV 262
Db 236 AKBEVLVYIQAKDMGKMGKLSGSTTYYTLSDVNDNPKFPQSLYHFSVPEDVLTGTAI 295
QY 263 GRLAODPDLGNALMAVSIIDGEGSEAFSISTDLQGRDGLTVRKPDPSQSRYSFRV 322
Db 296 GRVAKANDDIGNAOSYVLIIDGDTALFEITSDAQADGVIRLRKPDDETKKSTYLV 355
QY 323 EATNTLIDPAYLRQPFKDVASVRYVQADAPPAFTQAAHYLTVPENKAPGLTVQOISA 382
Db 356 EAAIHIDPFRSSRQPFKDTATVKIVEDADEPVSFPTVLLFVHNAALNSVIGQVTA 415
QY 383 ADLDSAPPIRYSLIPHSDEPERCSIQPEBGTHTAALDREARAHNTVLTATELGMSW 442
Db 416 RDPDITSSPIRFSIDRHTDLERQFINADSKITLAPLDRSLVWHNTITITATEI 471
QY 443 GPERGVPPLVLAEMWAPAPAPQSPVGSAGVIGIPDSSAQASVQVAYIQTLDENDAPOLA 502
Db 472 -----RMSQISRVPAIKVLVDVNDAPFA 497
QY 503 EPYDTFVCDASAPGGLIQTALDRDEVNGSHVSFOGCLPGD---ANFTVQDNRD--- 555
Db 498 SEYEAFLECNKRGQVITQVAMKDDPKNGHF--FLYSLLPEWVNNPFITIKKEDNSL 555
QY 556 -----LPWFHPLMLMASASWLMHMPAERGNOPASQGSSSL-PCG-RLPGA 600
Db 556 SILAKHNGFRKQGEVYLLPIVI-----SDSGNPPLSSSTLTITIRVCGSGNDGV 604
QY 601 LPSCQ-----LPGLI---PALGIYVC 618
Db 605 VQSCNVEAYVLPILGSMGALIALIAC 630

RESULT 13
CADD_HUMAN STANDARD; PRT, 799 AA.
ID CADD_HUMAN;
AC P55286; Q9UBI2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Cadherin-8 precursor.
CX NCB1_TaxID=10090;
RX [1]

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OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed:10861224;
 RA Shimoyama Y., Teujimoto G., Kitajima M., Natori M.,
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins."
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Heilmark R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.,
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue."
 RL Cell Regul. 2:261-270(1991).
 CC -1 FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1 SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL, custodian
 CC of the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AB035305; BA87419.1; -
 DR EMBL: L34060; AAA35628.1; ALT_INTT.
 DR HSBP: P09803; 117W.
 DR GeneW: HGNC:1767; CDH8.
 DR MIM: 603008; -
 DR GO: GO:0007155; P:cell adhesion; TAS.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR Pfam: PF000028; Cadherin; 5.
 DR Pfam: PF01049; Cadherin_C; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SMO0112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM Transmembrane.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Extracellular (Potential).
 FT DOMAIN 643 799 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 643 799 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.

FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 554 554 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
 FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
 SQ SEQUENCE 799 AA; 88253 MW; 981198860396A0A CRC64;
 Query Match 47.1%; Score 1536.5; DB 1; Length 799;
 Best Local Similarity 47.9%; Pred. No. 3.6e-87;
 Matches 300; Conservative 111; Mismatches 134; Indels 81; Gaps 9;
 QY 23 LLTRRSWVWVNFVIEEYACPEVYLGKHSVDVREGRTKYLITGEGATVFVIDEAT 82
 DB 56 LRSKRGVWVWVNFVIEEYACPEVYLGKHSVDVREGRTKYLITGEGATVFVIDEAT 115
 QY 83 GNHHTKSLDPEEKQVYLLAQAVIDRASNRLPEPSSFTIKGQINNPFPFPGPHAT 142
 DB 116 GDHAIKLDPEEKQVYLLAQAVIDRASNRLPEPSSFTIKGQINNPFPFPGPHAT 175
 QY 143 VPEMSNVGTSVIOVTAHDADDPYGSNAKLYVTVLDGLPFPSVDPQTGVRTALPNNDRE 202
 DB 176 VPEMSILGTSVNTVATDADDPYGSNAKLYVTVLDGLPFPSVDPQTGVRTALPNNDRE 235
 QY 203 TOEFVTVIOAKDNGKMGSGSTTVTVLSDVNDNPKRPGSLYQPSVETKGPGLV 262
 DB 236 AKBEVLVIOAKDNGKMGSGSTTVTVLSDVNDNPKRPGSLYQPSVETKGPGLV 295
 QY 263 GLRQADPDLDNLMAYSLIDGEGSEAFSTLDQGRDGLTVRKPLDFESQSYGFRV 322
 DB 296 GRVANNDDIDENNQSSVDIIDGDTALFETSAQAQDGIIRKRLDDETKSYLVK 355
 QY 323 EATNTLIDPAYLRGPFQDVASVNAVQADAPPEPAFTQAAHYLTVPENKAPGLVQISA 382
 DB 356 EAAVNHIDPRSGGPFQDTATKIVEDADEPVPFSPITLVEHNAALNSVIGQVTA 415
 QY 383 ADLSPASPIRYSILPHSDPERCFSDPEEGTHTAALPDEBARWNLVATLQMSW 442
 DB 416 RDPDITSPPIRPSIDREHDLERQINADDKITLAPLDELSWNNITITAIET 471
 QY 443 GPERGWVLLVAEWSAPAPAPQSPVGSANGIPDSSAQAQRYOVAIQTLDENADPQLA 502
 DB 472 -----RNHSQISRVVAIKVLDVNDNADEFA 497
 QY 503 EPIPTFVCDAAAPGOLIOVTRALDRDYGNSHVSFGPLGPD-----ANFTVQDNRD 555
 DB 498 SEYEAFLCENKPGQVQVQVAMKDDPKNGHY--FLYSLPEVNNPNFTIKNEPNSL 555
 QY 556 -----LPWFHPLMASASSWLTWMPAERGNQPSAQSGKSSL-PCG-RLPGA 600
 DB 556 SILAKHNGFNKQKQEVLLPIL-----SDSGNPPLSSTLITRVCCSNDGV 604
 QY 601 LPSCQ-----LPGLI---PALGIYLC 618
 DB 605 VQSCNVEAYVLPILSGWALTAIILAC 630
 RESULT 14
 ID PRELIMINARY; PRT; 754 AA.
 AC Q8BRK4;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 DE library, clone:A830083p13 product:cadherin 8, full insert
 DE sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=cortex;
 EX MEDLINE=99279253; PubMed=10349656;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=cortex;
 RC MEDLINE=21085560; PubMed=1121781;
 RX RIKEN FANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=cortex;
 RC The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL Nature 420:563-573(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=cortex;
 RC MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RT Kono H., Okazaki Y., Muramatsu W., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes";
 Genome Res. 10:1617-1630(2000).
 [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=cortex;
 RX MEDLINE=20330913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
 RA Saito N., Ishii Y., Nakamura S., Hatawa M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Washiwagi K.,
 RA Fujiwara S., Inoue K., Togawa K., Izawa M., Ohara E., Matsubiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu W., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer";
 Genome Res. 10:1757-1771(2000).
 [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=cortex;
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Nakazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogaue Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK044046; BAC1751.1; -.
 DR HSSP; P15146; INCT.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005059; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR RefSeq; NP000233; Cadherin_C_term.
 DR RefSeq; NP000233; Cadherin_E

Query Match	Similarity	Score	DB 2;	Length	754;
Best Local	47.9%;	Pred. No. 6e-87;			
Matches	300;	Conservative	110;	Mismatches	135;
				Indels	81;
				Gaps	9;
DR Pfam; PF01049; Cadherin_C/ 1.					
DR PRINTS; PRO0205; CADHERIN.					
DR SMART; SM00112; CA; 5.					
DR PROSITE; PS00233; CADHERIN_1; 3.					
DR PROSITE; PS50268; CADHERIN_2; 5.					
KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.					
SO SEQUENCE 754 AA; 83624 MW; 149GC3C7003F1568 CRC64;					
Query Match	47.0%;	Score	1532.5;	DB 2;	Length 754;
Best Local	47.9%;	Pred. No.	6e-87;		
Matches	300;	Conservative	110;	Mismatches	135;
				Indels	81;
				Gaps	9;
23 LRRRRRWNNQPFVIEEYAGPEFVLGKLSHVDVDRREGKRYLLTJEGAGTAVVIDAT	82				
56 LSRKRWNNQMFVLEEFSGPEFLVGRHTDLDPSGSKRYLLSGAGATTIQINDIT	115				
83 GNHVTSGLDREKRAQVYLLAQAADRAANRLEPSEFIIKGGDINDNPIFLPGRYAT	142				
116 GDHIAIKRLDREKAEYTLTAQAVDFENKRLPEPSEFIIKVDQINDVAFELNGPYAT	175				
143 VPEMSNGTSTVQVTAHDADDPSGNSAKLYTTLVLDGIFPFSVPPQGVATATAPNRE	202				
176 VPEMSIIGTSTVNTATDADDPVGNASKALYSLILEQPYPSIEPETAIKTALAPNRE	235				
203 TOEFELVIAQADKGMGMSGSGTAVVLLSDVNDNPKPPOSILYQSVVETAGPTLV	262				
236 AKELVYVIAQKMGHSGSGSLGTTTLVLLDNDNPKPAQSLYHFSVEDVVLGTAI	295				
263 GLRAQDPDLGDNALMAVSIIDEGSGEAFSISTDLQGRDGLLYTRKPLDPESQBSYFRV	322				
296 GRVANQODIENNAOSSYDIIDGGGTALFELTSDAQADGVIRLRKPLDFETKKSYYLKV	355				
323 EATVTLDPAYLRGPFEDVAVVAQADAPPEPAFTQAAHLTVLPENKAGSLVQGISA	382				
356 EAAIHIDPRSSSGPFKDTATVAVIVEDADPEPFSPTLLVEHMAALNSVIGQVTA	415				
383 ADLDSAPSPTVSYSLPHSPDPERCSIQDEEGTITTAALDSEKAMNLYLATLGLMSW	442				
416 RDPITSSPIRFSIDRHTDLEKQININADDKITLATPLDELSVMAHITITAIETI	471				
443 GPERGWPLVAEWSAPAPAPQSPVGSVAGIPODSSAQAARVQVATQTLDENDAPOLA	502				
472 -----RNSQIRVRVPAIKVLDVNDMAPEFA	497				
503 EPYTTPVCDASAPQQLIQVITALDRDEVGNSHWSPQGLPD-----ANFTVQDNRD	555				
498 SEYAEFLCENKPGRGVQIVTASAMKDPDKNGHF--FLYSLPPEWVNNENFTIKKNDLSL	555				
556 -----LPWFHPLLMASASASWLMHPAPERNGQAPQGSSSL-PCG-RLPGA	600				
556 SILAKHGFNRQKGEVILPVI-----SDSGNPPLSSTITLIRKGGSGNSGV	604				
601 LPSCQ-----LPDGI--PALGIYLC 618					
605 VQSCNVEAYVLPILGSMGALIAIILAC 630					
RESULT 15					
CAD8_RAT	STANDARD.	PRT;	799 AA.		
AC 054800; OS4801;					
DT 16-OCT-2001 (Rel. 40, Created)					
DT 16-OCT-2001 (Rel. 40, Last sequence update)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Cadherin-8 precursor.					
GN Name=Cdh8;					
OS Rattus norvegicus (Rat).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX NCBI_Taxid=10116;					
RN [1]					
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.					
RC TISSUE=Brain					

RX MEDLINE=99190518; PubMed=9521872;
 RA Kido M., Obata S., Tanihara H., Rochelle J.M., Seidlin M.F.,
 RA Taketani S., Suzuki S.T.;
 RT "Molecular properties and chromosomal location of cadherin-8,"
 RL Genomics 48:186-194(1998).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=O54800-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O54800-2; Sequence=VSP_000638, VSP_000639;
 CC -!- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB010436; BAA24452.1; -
 DR EMBL; AB010437; BAA24453.1; -
 DR HSSP; P09803; 117W.
 DR RCD; 69286; Cdh8.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01048; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 643 167 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 514 532 IGVSAADKDDPKNGHFFL -> NISMLILNMFVNCPLV
 N (in isoform 2).
 FT /FTId=VSP_000638.
 FT /FTId=VSP_000639.
 FT /FTId=VSP_000638.
 FT /FTId=VSP_000639.
 FT VARSPPLIC 533 799 Missing (in isoform 2).
 FT /FTId=VSP_000638.
 FT /FTId=VSP_000639.
 SQ SEQUENCE 799 AA; 88332 MW; F01D145R80966CB6 CRC64;
 Query Match 47.08; Score 1530.5; DB 1; Length 799;
 Best Local Similarity 47.93; Pred. No. 8.6e-87;
 Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;
 QY 23 LILTRRSWVWNOFFVLEEVYAPVILIGKLSHSDVDGEGSTKYLITGEGAGTAVFVDEAT 82
 DB 56 LNSKRGWVWNOFFVLEEVYAPVILIGKLSHSDVDGEGSTKYLITGEGAGTAVFVDEAT 115
 QY 83 GNTHVTKSLDREKAKQVLLAQAADRAKRNLEPPSEFTIKGQDINDNPPIPLGPHYAT 142
 DB 116 GDTHAIKRLDREKAKQVLLAQAADRAKRNLEPPSEFTIKGQDINDNPPIPLGPHYAT 175

QY 143 VEMSGNVTGSIQVTAHADDPSYGNSAKLYVTVLDGLPFPSVDPPQGVTAIPNDRE 202
 DB 176 VEMSGNVTGSIQVTAHADDPSYGNSAKLYVTVLDGLPFPSVDPPQGVTAIPNDRE 235
 QY 203 TOEFLLVYIQAQXGNGGGLSGSTTVTVLSDVNDNPKFPQGLYQPSVVEYAGPGLV 262
 DB 236 AAEFLVYIQAQXGNGGGLSGSTTVTVLSDVNDNPKFPQGLYQPSVVEYAGPGLV 295
 QY 263 GILRAQDDPLGDNALMAVSIIDGEGSAFISTLDGGDGLLTVRKPADPFSQSSYSPRV 322
 DB 296 GILRAQDDPLGDNALMAVSIIDGEGSAFISTLDGGDGLLTVRKPADPFSQSSYSPRV 355
 QY 323 EATNTLIDPAYLRGPFKDVASVRVAVQDADEPPAFTQAAVHTVPEKAPGLTVGOISA 382
 DB 356 EATNTLIDPAYLRGPFKDVASVRVAVQDADEPPAFTQAAVHTVPEKAPGLTVGOISA 415
 QY 383 ADLDSAPAPVYSLPHSDPERCSIOPEBGTITTAAPLDEARAHNTVLADELGMSW 442
 DB 416 RDPDITSPVIRSDIRHTDLERQFVNAADGKITLAPDLRELSVWHNISITATEI 471
 QY 443 GPERGVPLLVAEWSAPAPAPQSPVGSVAVGIPDSSAQAASRYOVAIQTLDENDAPOLA 502
 DB 472 GPERGVPLLVAEWSAPAPAPQSPVGSVAVGIPDSSAQAASRYOVAIQTLDENDAPOLA 497
 QY 503 ERYDTFVCDSPAAPGQILQVITALDRDEVGNSSHSFQGPFGPD---ANFTVQDNRD 555
 DB 498 SEYENFLCENKPGQVVIQTVSAMDKDPKNGH--FLYSILPEVYVNNPNTFKKNEENSL 555
 QY 556 -----LPWFHPLMASASASWLMPPAERGNOPASQKSSSL-PCG-RLPGA 600
 DB 556 SILAHNGFNKQKQEVILLPIVI-----SDSGNPLSLSTLITRVCCSNDGV 604
 QY 601 LPSCQ-----LPLGI---PALGIYLC 618
 DB 605 VQSCNVEPYVLPILGSMGALTAIILAC 630

Search completed: December 8, 2004, 10:24:37
 Job time : 250.512 secs

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutic useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the mature human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 620 AA;

Query Match 100.0%; Score 3259; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 3,8e-270;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMGRLLAARARAWASGRHPPALIRTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
DB 1 CMGRLLAARARAWASGRHPPALIRTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
QY 61 GRTKYLITGEGAGTVFVIDENTGNHVTKSIDREKQYVLLAQAVDRASNRPLEPSEF 120
DB 61 GRTKYLITGEGAGTVFVIDENTGNHVTKSIDREKQYVLLAQAVDRASNRPLEPSEF 120
QY 121 IIKQDINDNPPILPGYHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVTLDGL 180
DB 121 IIKQDINDNPPILPGYHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVTLDGL 180
QY 181 PFFSVDPQTGVVTRTAIPMDRETOEBFLVVIQAKDMGNGHGLSGSTTVTLSDVNDP 240
DB 181 PFFSVDPQTGVVTRTAIPMDRETOEBFLVVIQAKDMGNGHGLSGSTTVTLSDVNDP 240
QY 241 PKFPQSLYQSFVETAGPGLVGRLLAQPDPDLGNALMAYSILDEGSEAFSISTDLQGR 300
DB 241 PKFPQSLYQSFVETAGPGLVGRLLAQPDPDLGNALMAYSILDEGSEAFSISTDLQGR 300
QY 301 DGILLTVKRLPDFESQSYSRFVEATNTLIDPAYIRKPFQDVASVYAAVDAPPAFTQ 360
DB 301 DGILLTVKRLPDFESQSYSRFVEATNTLIDPAYIRKPFQDVASVYAAVDAPPAFTQ 360
QY 361 AAYHLYTPENKAPETLVQGISAADLDSAPSPIRSIILHSDPERCSIQPEEGTITTAAP 420
DB 361 AAYHLYTPENKAPETLVQGISAADLDSAPSPIRSIILHSDPERCSIQPEEGTITTAAP 420
QY 421 LDRRARAHNLTVLATELGMSWGPBGWVPLVAEMSAAPAPQSPVGSAGVCPDSSA 480
DB 421 LDRRARAHNLTVLATELGMSWGPBGWVPLVAEMSAAPAPQSPVGSAGVCPDSSA 480
QY 481 QASRVOVAIQTLIDENDNAPQIAEYDFTFVCDASAPGQLIIVIRALDRDEVGNSHVSFOG 540
DB 481 QASRVOVAIQTLIDENDNAPQIAEYDFTFVCDASAPGQLIIVIRALDRDEVGNSHVSFOG 540
QY 541 PLGPDANFTVQDNNDLPAMFHPILMASASSWLMWPPAERGNQAPASQKSSSLPCGRLPGA 600
DB 541 PLGPDANFTVQDNNDLPAMFHPILMASASSWLMWPPAERGNQAPASQKSSSLPCGRLPGA 600
QY 601 LPSCQLPLGIPALGIVLCAS 620
DB 601 LPSCQLPLGIPALGIVLCAS 620

RESULT 2
ADD29445
ADD29445 standard; protein; 636 AA.

XX ADD29445;
XX AC
XX 15-JAN-2004 (first entry)
XX Human cadherin-like protein amino acid sequence.
XX

KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.

XX Homo sapiens.

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XX

Key Location/Qualifiers
FT Peptide 1..16
FT /label= Signal_peptide
FT Protein 17..636
FT /label= Mature_human_cadherin-like_protein

US2003144491-A1.

31-JUL-2003.

16-FEB-2001; 2001US-00788051.

03-FEB-2000; 2000US-00456914.

27-APR-2000; 2000US-00560875.

(GODB/) GODBOLE S D.

(KNUC/) KNU C.

(ARTE/) ARTERBURN M C.

(YEUN/) YEUNG G.

(PALE/) PALENCIA S.

(TANG/) TANG Y T.

(LIUC/) LIU C.

(DRMA/) DRMANAC R T.

Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

Lin C, Drmanac RT;

WPI; 2003-829799/77.

N-PsDB; ADD29461, ADD29446.

Novel isolated human secreted cadherin-like polypeptide useful for

treating diseases such as cancers, osteoporosis, Paget's disease,

osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 4; 636p; English.

This invention relates to a novel isolated human secreted cadherin-like

protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their

extracellular region. The extracellular portion mediates homotypic cell-

cell adhesion that is calcium dependent. Modulators of the protein of the

invention may have cytostatic or osteopathic activity. The invention may

allow development of therapeutic useful for the treatment of diseases

such as cancers, osteoporosis, Paget's disease, osteomalacia,

hyperostosis and osteopetrosis. The protein and DNA sequence of the

invention may also be useful as markers for prognosis of metastatic

tumours. The present sequence is that of the human secreted cadherin-like

protein of the invention.

Query Match 100.0%; Score 3259; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 4e-270;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMGRLLAARARAWASGRHPPALIRTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
DB 1 CMGRLLAARARAWASGRHPPALIRTRRSWVWNOFVIEBYAGBEPYLICKLHSDVDGR 60
QY 61 GRTKYLITGEGAGTVFVIDENTGNHVTKSIDREKQYVLLAQAVDRASNRPLEPSEF 120
DB 61 GRTKYLITGEGAGTVFVIDENTGNHVTKSIDREKQYVLLAQAVDRASNRPLEPSEF 120
QY 121 IIKQDINDNPPILPGYHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVTLDGL 180
DB 121 IIKQDINDNPPILPGYHATVEMSNVGTSVIQVTAHADDPSSYNSAKLYTVTLDGL 180

QY 161 PFFSVDPQTGVVRTAIPNMDRETOEBFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 240
Db PFFSVDPQTGVVRTAIPNMDRETOEBFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 256
QY 241 PKFPOSILYQFSVETAGPGLTVGRRAODPDLGNALMAVSTLDEGSEAFSTIDLOCR 300
Db PKFPOSILYQFSVETAGPGLTVGRRAODPDLGNALMAVSTLDEGSEAFSTIDLOCR 316
QY 301 DGLTVRKPLDPEESQSRYSFVEAETNTLIDPAYLRGPFKDVASRVAVODAEPPAFQ 360
Db DGLTVRKPLDPEESQSRYSFVEAETNTLIDPAYLRGPFKDVASRVAVODAEPPAFQ 376
QY 361 AAYHLTVPENKAPGTLVGQISAADLDSPASPIRYSILPHSDPERCFSTIQEEGTHHTAP 420
Db AAYHLTVPENKAPGTLVGQISAADLDSPASPIRYSILPHSDPERCFSTIQEEGTHHTAP 436
QY 421 LDREARAHNLTVALTELQSMGMPERGWPPLVAVEMGAPAAPQSRPVGSAVGIPODSA 480
Db LDREARAHNLTVALTELQSMGMPERGWPPLVAVEMGAPAAPQSRPVGSAVGIPODSA 496
QY 437 LDRBARAHNLTVALTELQSMGMPERGWPPLVAVEMGAPAAPQSRPVGSAVGIPODSA 496
Db 437 LDRBARAHNLTVALTELQSMGMPERGWPPLVAVEMGAPAAPQSRPVGSAVGIPODSA 540
QY 481 QASRVQVAICTLDENDNAPQLAEPYDTFVCDSPAAGQIQTIRALDREDEVGNSHVSFOG 540
Db 497 QASRVQVAICTLDENDNAPQLAEPYDTFVCDSPAAGQIQTIRALDREDEVGNSHVSFOG 556
QY 541 PLGPDANFTVQDNEDLPAMFHPPLMASASSWLMHPAERGNQAPASQKSSSLPCGRLEGA 600
Db 557 PLGPDANFTVQDNEDLPAMFHPPLMASASSWLMHPAERGNQAPASQKSSSLPCGRLEGA 616
QY 601 LPSCQLPLGIPALGIVLCAS 620
Db 617 LPSCQLPLGIPALGIVLCAS 636

RESULT 3
ABBS3296
ID ABBS3296 standard; protein, 781 AA.
XX
AC ABBS3296;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human polypeptide #36.
XX
Human; noctropic; neuroprotective; anticonvulsant; antidepressant;
KM neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
KM antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
KM nephrotoxic; anorectic; cytostatic; vaccine; neurological disease;
KM cardiovascular disease; respiratory disease; liver disease;
KM renal disease; skeletal muscle disease; gastrointestinal disease;
KM placental disease; testicular cancer; male fertility; pancreatic disease.
XX
OS Homo sapiens.
XX
EN WO200181363-A1.
XX
PD 01-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US013360.
XX
PR 27-APR-2000; 2000US-0199963P.
PR 11-MAY-2000; 2000US-0203336P.
PR 25-MAY-2000; 2000US-0207087P.
PR 26-MAY-2000; 2000US-0207346P.
XX
PA (SMIK) SMITHLINE BEECHAM CORP.
PA (SMIK) SMITHLINE BEECHAM PLC.
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kahnack KS;
PI Lai Y, Xie Q;
XX
XX WPI, 2002-041392/05.
DR N-PBDB; ABA90361.

XX
PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
PT and treating diseases associated the polypeptide, e.g. Alzheimer's
PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
XX
PS Claim 1; Page 108-109; 116pp; English.

XX
CC The invention relates to an isolated polypeptide comprising a 277, 480,
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
CC given in the specification. The polypeptides, modulators of the
CC polypeptides and antibodies against the polypeptides are useful for
CC treating diseases such as neurological and psychiatric diseases including
CC Alzheimer's, parapranuclear palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including;
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
CC hepatitis, type II diabetes mellitus, acute tubular necrosis and
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including chorioarcanoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including low ketocidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX
SQ Sequence 781 AA;

Query Match 81.4%; Score 2651.5; DB 5; Length 781;
Best Local Similarity 84.5%; Pred. No. 76-218;

Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAPARAWAGREHPALLTRRSWNNQCFVIEEYAPPEVLIGKLSVDRC 60
Db 17 CMGRLAPARAWAGREHPALLTRRSWNNQCFVIEEYAPPEVLIGKLSVDRC 76
QY 61 GRTKYLITGEGAGTVFIDEATGNHVTSLDREKAQVLLAQVDRASNPPLPPSEF 120
Db 77 GRTKYLITGEGAGTVFIDEATGNHVTSLDREKAQVLLAQVDRASNPPLPPSEF 136
QY 121 IIRKQDINDNPIPLGPHATVPMSNVGTSVIOVTAHADDDPSYSAKLVTVLQ 180
Db 137 IIRKQDINDNPIPLGPHATVPMSNVGTSVIOVTAHADDDPSYSAKLVTVLQ 196
QY 181 PFFSVDPQTGVVRTAIPNMDRETOEBFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 240
Db 197 PFFSVDPQTGVVRTAIPNMDRETOEBFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 256
QY 241 PKFPOSILYQFSVETAGPGLTVGRRAODPDLGNALMAVSTLDEGSEAFSTIDLOCR 300
Db 257 PKFPOSILYQFSVETAGPGLTVGRRAODPDLGNALMAVSTLDEGSEAFSTIDLOCR 316
QY 301 DGLTVRKPLDPEESQSRYSFVEAETNTLIDPAYLRGPFKDVASRVAVODAEPPAFQ 360
Db 317 DGLTVRKPLDPEESQSRYSFVEAETNTLIDPAYLRGPFKDVASRVAVODAEPPAFQ 376
QY 361 AAYHLTVPENKAPGTLVGQISAADLDSPASPIRYSILPHSDPERCFSTIQEEGTHHTAP 420
Db 377 AAYHLTVPENKAPGTLVGQISAADLDSPASPIRYSILPHSDPERCFSTIQEEGTHHTAP 436
QY 421 LDREARAHNLTVALTELQSMGMPERGWPPLVAVEMGAPAAPQSRPVGSAVGIPODSA 480
Db 437 LDREARAHNLTVALTELQSMGMPERGWPPLVAVEMGAPAAPQSRPVGSAVGIPODSA 496
QY 481 QASRVQVAICTLDENDNAPQLAEPYDTFVCDSPAAGQIQTIRALDREDEVGNSHVSFOG 540
Db 497 QASRVQVAICTLDENDNAPQLAEPYDTFVCDSPAAGQIQTIRALDREDEVGNSHVSFOG 556

QY 541 PLGPDANFTVDNRD-----LPA-----WFHPLMASASSMLH--- 573
 DB 519 PLGPDANFTVDNRDGSASLLPSPRPAPPRHAPVLPVIELMDQCPALSSATVTVSVCR 578
 QY 574 -----WPPAERGNQPASQG 587
 DB 579 CQPDGSVASCWPEFAHLSAAGLSTG 602
 RESULT 4
 AAM48736
 ID AAM48736 standard; protein; 781 AA.
 AC AAM48736;
 XX
 XX
 XX 28-MAR-2002 (first entry)
 DE Human cadherin family member 57805 protein SEQ ID NO 2.
 KW Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
 KW antidiabetic; neuroprotective; antiarthritic; antineumatic;
 KW dermatologic; immunosuppressive; antiinflammatory; antiporiatic;
 KW antiasthmatic; antiallergic; antileptotic; haemostatic; antipruritic;
 KW antihypertensive; antiserotoclerotic; cardiant; antiarhythmic;
 KW anorectic; immunomodulatory; vasotropic; virucide; cyostatic; liver;
 KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 KW viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
 KW gene therapy.
 OS Homo sapiens.
 XX
 XX WO200190145-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 18-MAY-2001; 2001WO-US016013.
 XX
 XX 19-MAY-2000; 2000US-0205674P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Curtis RAD;
 XX
 XX WPI; 2002-083082/11.
 DR N-PSDB; ABA96406, ABA96407.
 XX
 XX New human cadherin family protein and polynucleotides, useful for
 PT diagnosing and treating disorders e.g. obstructive jaundice, multiple
 PT sclerosis, encephalomyelitis and atherosclerosis and to identify
 PT modulators of therapeutic use.
 XX
 XX Claim 9; Page 105; 119pp; English.
 XX
 XX The invention relates to human cadherin family polypeptide designated
 CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarthritic, antineumatic, dermatological,
 CC immunosuppressive, antiinflammatory, antiporiatic, antiasthmatic,
 CC antiallergic, antileptotic, haemostatic, antipruritic, antihypertensive,
 CC antiserotoclerotic, cardiant, antiarhythmic, anorectic,
 CC immunomodulatory, vasotropic, virucide, cyostatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy; cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,

CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy
 CC
 CC
 XX
 XX Sequence 781 AA;
 SQ
 Query Match 81.4%; Score 2651.5; DB 5; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRILAPARAWAGREHHPALLTRRSWYVWNGFYVIEEYAGEPYVIGKHSVDVRGE 60
 DB 17 CMGRILAPARAWAGREHHPALLTRRSWYVWNGFYVIEEYAGEPYVIGKHSVDVRGE 76
 QY 61 GRTKYLFGBAGTVFVIDEATGNHWTKSIDREKXQVYLLAQVAPRASRPPEPSEF 120
 DB 77 GRTKYLFGBAGTVFVIDEATGNHWTKSIDREKXQVYLLAQVAPRASRPPEPSEF 136
 QY 121 IIKGQDINDNPIPIPLGPHATVEMSNVGTSVIQTVAHADDDPSYNSAKLYVTVDGL 180
 DB 137 IIKVQDINDNPIPIPLGPHATVEMSNVGTSVIQTVAHADDDPSYNSAKLYVTVDGL 196
 QY 181 PPFSTVDPQTGYVTRAIIPMDRETOEBELVYIQAQDMGKHGSLGSTTVYVTLSDVNDP 240
 DB 197 PPFSTVDPQTGYVTRAIIPMDRETOEBELVYIQAQDMGKHGSLGSTTVYVTLSDVNDP 256
 QY 241 PKFPOSIVQFVETAGTGVGRRLRAODPDLGNALMAYSIIDGESSEAFSISTDQGR 300
 DB 257 PKFPOSIVQFVETAGTGVGRRLRAODPDLGNALMAYSIIDGESSEAFSISTDQGR 316
 QY 301 DGLLTVRKPLDPESQSYSPFEVETNTLIDPAYLRGPFQDVASVAVADAPPPAFQ 360
 DB 317 DGLLTVRKPLDPESQSYSPFEVETNTLIDPAYLRGPFQDVASVAVADAPPPAFQ 376
 QY 361 AAYHLTVENKAPGTLVQGISADLDSPASPIRYSIIPSPDECFISOPEGITHAAP 420
 DB 377 AAYHLTVENKAPGTLVQGISADLDSPASPIRYSIIPSPDECFISOPEGITHAAP 436
 QY 421 LDREARAWHNTLVATELGMSWGERGVPLVLAEMSAAPAPQSPVSGAVGIPODSSA 480
 DB 437 LDREARAWHNTLVATEL-----DSSA 458
 QY 481 QASRVQVALIOTLDENDNAPOLAEYPDFVCDASAPGQLIOVIRALDRDEVGNSSHVSFOG 540
 DB 459 QASRVQVALIOTLDENDNAPOLAEYPDFVCDASAPGQLIOVIRALDRDEVGNSSHVSFOG 518
 QY 541 PLGPDANFTVDNRD-----LPA-----WFHPLMASASSMLH--- 573
 DB 519 PLGPDANFTVDNRDGSASLLPSPRPAPPRHAPVLPVIELMDQCPALSSATVTVSVCR 578
 QY 574 -----WPPAERGNQPASQG 587
 DB 579 CQPDGSVASCWPEFAHLSAAGLSTG 602
 RESULT 5
 ABG34078
 ID ABG34078 standard; protein; 781 AA.
 AC ABG34078;
 XX
 XX 15-JUL-2002 (first entry)
 DE Human Pro peptide #49.
 KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2000224888-A2.

XX 28-MAR-2002.
 PD 29-AUG-2001; 2001WO-US027099.
 XX 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0264421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274393P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282128P.
 PR 04-APR-2001; 2001US-0282198P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI: 2002-362426/39.
 DR N-PSDB; ABR70009.
 XX New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX Claim 11, Fig 98; 218pp; English.
 PS This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention
 XX
 XX Sequence 781 AA;
 SQ

Query Match: 81.4%; Score 2651.5; DB 5; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CNGRLAAPRAVAGSTEHGPAALLTRRSWVNOGFVLEEVAGPEPVVIGLTHSDVDGGE 60
 DB 17 CNGRLAAPRAVAGSTEHGPAALLTRRSWVNOGFVLEEVAGPEPVVIGLTHSDVDGGE 76

QY 61 GRTKYLIGEAGCTVFIDEATGNHVTKSLDREKAQYVLLAQVDRASNRPLEPSEF 120
 DB 77 GRTKYLIGEAGCTVFIDEATGNHVTKSLDREKAQYVLLAQVDRASNRPLEPSEF 136
 QY 121 IIKGODINDNPPIFPLGPGYHATVPMSNVGTSVIGVTAHADDPSSYGNASAKLVYVTDGL 180
 DB 137 IIKGODINDNPPIFPLGPGYHATVPMSNVGTSVIGVTAHADDPSSYGNASAKLVYVTDGL 196
 QY 181 PPFSSVDPQGVVTRTAPMWDRETQEEFLVYVQAKMGGMGLSGSTTVYVTLSDVNDP 240
 DB 197 PPFSSVDPQGVVTRTAPMWDRETQEEFLVYVQAKMGGMGLSGSTTVYVTLSDVNDP 256
 QY 241 PPFSSVDPQGVVTRTAPMWDRETQEEFLVYVQAKMGGMGLSGSTTVYVTLSDVNDP 300
 DB 257 PPFSSVDPQGVVTRTAPMWDRETQEEFLVYVQAKMGGMGLSGSTTVYVTLSDVNDP 316
 QY 301 DGLITVRKPLDPSQSYSEFVEATNTLIDPAYLRGFPKDYASVRYVQADAPPPATQ 360
 DB 317 DGLITVRKPLDPSQSYSEFVEATNTLIDPAYLRGFPKDYASVRYVQADAPPPATQ 376
 QY 361 AAYHLTPENKAPGTLVQGISAADLSPASPIRYSITLHSDPERCFSTIOPEEGTHTAP 420
 DB 377 AAYHLTPENKAPGTLVQGISAADLSPASPIRYSITLHSDPERCFSTIOPEEGTHTAP 436
 QY 421 LDREARAMNLTVLATELGMSWGPGRGVVLLVAEWSAPADPPORSYVGSAYGIPQDSA 480
 DB 437 LDREARAMNLTVLATELGMSWGPGRGVVLLVAEWSAPADPPORSYVGSAYGIPQDSA 496
 QY 481 QASRVQVATQTDENDNAPOLAEPTDYCDSAABGCLQVTRALDREVGSSHYVSG 540
 DB 499 QASRVQVATQTDENDNAPOLAEPTDYCDSAABGCLQVTRALDREVGSSHYVSG 518
 QY 541 PLGPDANFTVQDNRD-----LPA-----WFPLMASASSWLH--- 573
 DB 519 PLGPDANFTVQDNRDSSASLLPSRAPPRHAPVYLPIELMDMGQALSTATVTVSVCR 578
 QY 574 -----WPAERGNQPASOG 587
 DB 579 COPDGSVASCWPEAHLSAAGLSTG 602
 RESULT 6
 ABR40114
 ID ABR40114 standard; protein; 781 AA.
 AC ABR40114;
 XX
 DT 04-JUL-2003 (first entry)
 DE Human cell adhesion and extracellular matrix protein, CADECW-11.
 XX
 KW Human; anti-HIV; anti-allergic; cerebroprotective; anti-parkinsonian;
 KW anticonvulsant; nootropic; neuroprotective; immunosuppressive;
 KW dermatological; anti-inflammatory; cyostatic; antiarteriosclerotic;
 KW gene therapy; cell adhesion; extracellular matrix; CADPCM;
 KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
 KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
 KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
 KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 EN W02003027230-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024649.
 XX
 PR 03-AUG-2001; 2001US-0309964P.
 PR 03-AUG-2001; 2001US-0310119P.
 PR 17-AUG-2001; 2001US-0313091P.
 PR 31-AUG-2001; 2001US-0316771P.

07-SEP-2001; 2001US-0317896P.
 PR 21-SEP-2001; 2001US-0324761P.
 PR 05-OCT-2001; 2001US-0324760P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Burford N, Warren BA, Duggan BM, Mason EM, Richardson TW, Yue H;
 PI Forsythe JF, Elliott VS, Griffin JA, Gorvad AE, Azimzal Y,
 PI Kallik DA, Xu Y, Honcheil CD, Baughn MR, Gietzen KJ, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
 XX
 DR WPI: 2003-354645/33.
 DR N-PSDB: ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 PS Claim 1; Page 192-194; 234pp; English.
 XX
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 XX
 SQ Sequence 781 AA:
 Query Match 81.4%; Score 2651.5; DB 6; Length 781;
 Best Local Similarity 84.5%; Pred. No. 76-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRILAPADAMAGSRHHPGALLRTRSWNNQFVIEEYAGPEPLICKLHSDVDGRG 60
 DB 17 CMGRILAPADAMAGSRHHPGALLRTRSWNNQFVIEEYAGPEPLICKLHSDVDGRG 76
 QY 61 GRTYLLTGAGAGVFIYDEATGNIHTKSLDREKQAYVLLAQAVDRASNPRLPEPSEF 120
 DB 77 GRTYLLTGAGAGVFIYDEATGNIHTKSLDREKQAYVLLAQAVDRASNPRLPEPSEF 136
 QY 121 IIRGODINDNPPIPLGPYHATVPENSVGTSVIQTVAHDADDPVGNKAKVYTVLDDG 180
 DB 137 IIRGODINDNPPIPLGPYHATVPENSVGTSVIQTVAHDADDPVGNKAKVYTVLDDG 196
 QY 181 PFESVDPQTGVVTAIPNMDRETOEELVVIQAKDWGNGHSGSTTVVTLSDVDNDP 240
 DB 197 PFESVDPQTGVVTAIPNMDRETOEELVVIQAKDWGNGHSGSTTVVTLSDVDNDP 256
 QY 241 PKFQSLYQFSVYVETAPGTLVGRILRQDPLDGNLMAVSIIDGGSEAFSISTDLQR 300
 DB 257 PKFQSLYQFSVYVETAPGTLVGRILRQDPLDGNLMAVSIIDGGSEAFSISTDLQR 316
 QY 301 DGLITVAKPLDFESQRSYFRVEATNTLIDPAVLRGPFEDVAVVAQDAPEPAFTQ 360
 DB 317 DGLITVAKPLDFESQRSYFRVEATNTLIDPAVLRGPFEDVAVVAQDAPEPAFTQ 376
 QY 361 AAHHLTVENKARGLTVGQISADLSPASPPIRYSLIHPSDPRCSIOPEBCTITTAAP 420
 DB 377 AAHHLTVENKARGLTVGQISADLSPASPPIRYSLIHPSDPRCSIOPEBCTITTAAP 436
 QY 421 LDSEARAHNLTVLATELGMWGPBERGWPLVAEWSAPAPQSPVGSAGVIGODSSA 480
 DB 437 LDSEARAHNLTVLATELGMWGPBERGWPLVAEWSAPAPQSPVGSAGVIGODSSA 480
 DSA 458

QY 481 QASRYOVAIQTLDENDNAPQALAEPYDTFVCSAARGQILQYTRALDRDENSSHSVSG 540
 DB 459 QASRYOVAIQTLDENDNAPQALAEPYDTFVCSAARGQILQYTRALDRDENSSHSVSG 518
 QY 541 PLGPDANFTVQDNRD-----LPA-----WHEPLMASASSWTH--- 573
 DB 519 PLGPDANFTVQDNRGSGASLLPSRPARPRHAPVPIELMDQGPALSSATATVSVCR 578
 QY 574 -----WPPARGNOPASQG 587
 DB 579 COPDGSVASCWEALHSAAGLSTG 602
 RESULT 7
 ID ADA01366 standard, protein, 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 PR 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurey AL, Smith V, Stephan JP, Watanabe CK, Wood WJ, Zhang Z,
 PI Fong S;
 XX
 DR WPI: 2003-625484/59.
 DR N-PSDB: ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a

medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

Sequence 781 AA:

Query Match 81.4%; Score 2651.5; DB 6; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 CMGRLAAPARAWAGSREHGPALIRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 60
DB 17 CMGRLAAPARAWAGSREHGPALIRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 76
QY 61 GRTKYVLLTGBGAGTVFVIDEATGNIHVTKSLDREERKQYVLLAQAVDRASNPLEPSEF 120
DB 77 GRTKYVLLTGBGAGTVFVIDEATGNIHVTKSLDREERKQYVLLAQAVDRASNPLEPSEF 136
QY 121 IIKGQDINDNPPIPLGPGYHATVPEMSNVGTSVIOVTAHADDPDSYGSATLVYTVLDGL 180
DB 137 IIKGQDINDNPPIPLGPGYHATVPEMSNVGTSVIOVTAHADDPDSYGSATLVYTVLDGL 196
QY 181 PPFISVDPTGTVRTAIPNNDRBTQEEFLVITQAKDMGSHMGSLSGSTTVYTVLSDVNDP 240
DB 197 PPFISVDPTGTVRTAIPNNDRBTQEEFLVITQAKDMGSHMGSLSGSTTVYTVLSDVNDP 256
QY 241 PKFPOSILQFSVETWAGPGLVGRRAQDPDLGNALMAYSIILGEGSEAFSISTDQGR 300
DB 257 PKFPOSILQFSVETWAGPGLVGRRAQDPDLGNALMAYSIILGEGSEAFSISTDQGR 316
QY 301 DGLTVRRKPLDFESGSGYSFVEATNTLLIDPAYLRGPGKQVAVRVAVQDAPSPAPFTQ 360
DB 317 DGLTVRRKPLDFESGSGYSFVEATNTLLIDPAYLRGPGKQVAVRVAVQDAPSPAPFTQ 376
QY 361 AAHYHTVPEKRAPGLTVGOISAADLDSBASPRTYSIILPHSPBECFSGIOPEEGTHTAP 420
DB 377 AAHYHTVPEKRAPGLTVGOISAADLDSBASPRTYSIILPHSPBECFSGIOPEEGTHTAP 436
QY 421 LDREARAHNLTVLATELGWSMGPGRGVPLLVAVWSAPAAPQPSPVGASAVGIPDSSA 480
DB 437 LDREARAHNLTVLATELGWSMGPGRGVPLLVAVWSAPAAPQPSPVGASAVGIPDSSA 498
QY 441 QASRQVAVIQLTLDENDNAPQLAEPYDTVCDSAPAGQIIQVIRALDREVNSSSHVFEQG 540
DB 459 QASRQVAVIQLTLDENDNAPQLAEPYDTVCDSAPAGQIIQVIRALDREVNSSSHVFEQG 518
QY 541 PLGEPANFTVQDNRD-----LPA-----WFPHLMASASSMLH--- 573
DB 519 PLGEPANFTVQDNRDGASALLPSRAPPRHAPYIVFELMDWQGPALSSATYTVGCR 578
QY 574 -----WPPAERGNQPASQG 587
DB 579 CQPDGVSASCPWEAHLASAALSTG 602

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RESULT 8

ADA43795
ID ADA43795 standard; protein; 781 AA.

ADA43795;

20-NOV-2003 (first entry)

Human secreted/transmembrane polypeptide PRO34009.

Human; PRO; secreted protein; transmembrane protein;
endothelial cell tube formation; chondrocyte cell differentiation;
microvascular endothelial cell; tumour; lung tumour; colon tumour;
breast tumour; prostate tumour; rectal tumour; kidney tumour;
liver tumour; cytostatic; vaccine.

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XX Homo sapiens.
OS US2003064474-A1.
PN 03-APR-2003.
PD 16-SEP-2002; 2002US-00245859.
PF 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
PA (GENENTECH INC.
PI Baker KP, Eaton DL, Filvaroff E, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2003-60567/57.
DR N-PDB; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 11; Fig 98; 308bp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO1275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SO Sequence 781 AA:

```

Query Match 81.4%; Score 2651.5; DB 6; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 CMGRLAAPARAWAGSREHGPALIRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 60
DB 17 CMGRLAAPARAWAGSREHGPALIRTRRSWVMNQFVIEEYAGEPVLIGKLSVDVDRGE 76
QY 61 GRTKYVLLTGBGAGTVFVIDEATGNIHVTKSLDREERKQYVLLAQAVDRASNPLEPSEF 120
DB 77 GRTKYVLLTGBGAGTVFVIDEATGNIHVTKSLDREERKQYVLLAQAVDRASNPLEPSEF 136

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QY 121 IIKGQDINDNPPILPLGPGYHATVEMSNVGTSVIQTVAHADDDPSYGNSAKLYTVTLVLDGL 180
 DB 137 IIKVQDINDNPPILPLGPGYHATVEMSNVGTSVIQTVAHADDDPSYGNSAKLYTVTLVLDGL 186
 QY 181 PFFSVDPQTGVVRAIPMMDETOEELVVIQAQDMGCHGSGSTTVTVTLSDVNDP 240
 DB 197 PFFSVDPQTGVVRAIPMMDETOEELVVIQAQDMGCHGSGSTTVTVTLSDVNDP 256
 QY 241 PKFPOSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 300
 DB 257 PKFPOSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 316
 QY 301 DGLITVRKPLDPEQORSYSPRVENATNTLIDPAYLRGPPQDVASVYAVQDAPPPAFTQ 360
 DB 317 DGLITVRKPLDPEQORSYSPRVENATNTLIDPAYLRGPPQDVASVYAVQDAPPPAFTQ 376
 QY 361 AAYHLTVENKAPGTLVGOISAADLSPASPIRYSIIPHSDEPRCSIOPEEGTITPAAP 420
 DB 377 AAYHLTVENKAPGTLVGOISAADLSPASPIRYSIIPHSDEPRCSIOPEEGTITPAAP 436
 QY 421 LDREARAWHNTLTATELIGMSWGERGVPLVLAEMSAAPAPQPSFVGSAGIPODSSA 480
 DB 437 LDREARAWHNTLTATELIGMSWGERGVPLVLAEMSAAPAPQPSFVGSAGIPODSSA 488
 QY 481 QASRVOVAIOTLDENDNAPOLAEEDYDFVCDASAPQGLIQVIRALDRDEYGNSSHYSPQG 540
 DB 459 QASRVOVAIOTLDENDNAPOLAEEDYDFVCDASAPQGLIQVIRALDRDEYGNSSHYSPQG 518
 QY 541 PLGPDANFTVDND-----LPA-----WFHPLMASASSWLH--- 573
 DB 519 PLGPDANFTVDNDGASALLPSPRAPPRHAPYLVPIELMDGQAPLSTATVTVSVCR 578
 QY 574 -----WPPAERGNQSPASQ 587
 DB 579 CQPDGVSVAACWPEAHLSAAGLSTG 602

RESULT 9
 ADA43563
 ID ADA43563 standard; protein: 781 AA.
 XX
 AC ADA43563;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KM Human; PRO; secreted protein; transmembrane protein;
 KM endothelial cell tube formation; chondrocyte cell differentiation;
 KM microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KM breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KM liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 FN US2003073196-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 18-SEP-2002; 2002US-00246210.
 XX
 PR 04-APR-2001; 2001US-02821999.
 PR 28-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DU, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX
 XX WPI; 2003-743814/70.

DR N-PSDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acid sequences deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acid encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as
 CC a hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 XX Sequence 781 AA;
 XX
 Query Match 81.4%; Score 2651.5; DB 6; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRLAIPARAWAGSRHHPGALIRTRSWWNOFFVIEEYAGEPYVIGKLSHDVDRGE 60
 DB 17 CMGRLAIPARAWAGSRHHPGALIRTRSWWNOFFVIEEYAGEPYVIGKLSHDVDRGE 76
 QY 61 GRTYLLTGEGAGVAFIDEATGNVHTKSLDREKQVYLLAQAVRASNPPEPSEF 120
 DB 77 GRTYLLTGEGAGVAFIDEATGNVHTKSLDREKQVYLLAQAVRASNPPEPSEF 136
 QY 121 IIKGQDINDNPPILPLGPGYHATVEMSNVGTSVIQTVAHADDDPSYGNSAKLYTVTLVLDGL 180
 DB 137 IIKVQDINDNPPILPLGPGYHATVEMSNVGTSVIQTVAHADDDPSYGNSAKLYTVTLVLDGL 186
 QY 181 PFFSVDPQTGVVRAIPMMDETOEELVVIQAQDMGCHGSGSTTVTVTLSDVNDP 240
 DB 197 PFFSVDPQTGVVRAIPMMDETOEELVVIQAQDMGCHGSGSTTVTVTLSDVNDP 256
 QY 241 PKFPOSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 300
 DB 257 PKFPOSLYQFSVETAGPGLVGRRAQDDPDLGNALMAYSIIDGSESAFSTIDLOGR 316
 QY 301 DGLITVRKPLDPEQORSYSPRVENATNTLIDPAYLRGPPQDVASVYAVQDAPPPAFTQ 360
 DB 317 DGLITVRKPLDPEQORSYSPRVENATNTLIDPAYLRGPPQDVASVYAVQDAPPPAFTQ 376
 QY 361 AAYHLTVENKAPGTLVGOISAADLSPASPIRYSIIPHSDEPRCSIOPEEGTITPAAP 420

Db 377 AAYHLTPENKAPGTLVGQISADLDSPPASPIRYSILPHSDPERCFSIQPEEGTHTAP 436
 QY 421 LDRERAMHNLTVLATELGMKSGPERGWPVLVAMENSAAPAPQPSRVSGAVGIPDDSSA 480
 Db 437 LDRERAMHNLTVLATEL-----DSSA 458
 QY 481 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 540
 Db 459 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 518
 QY 541 PLGPDANFTVQDNRD-----LPA-----WFHPLMASASSWLH--- 573
 Db 519 PLGPDANFTVQDNRDGASALLPSRPAPPRHAPYLVPIELMDWGQPALSTATVTVSVCR 578
 QY 574 -----WPPAERGNOPASOG 587
 Db 579 CQPDGVSASCPWPAHLSAAGLSTG 602

RESULT 10

ADA01238
 ID ADA01238 standard; protein; 781 AA.

AC ADA01238;

DT 06-NOV-2003 (first entry)

DE Human PRO polypeptide #49.

XX Human; PRO, secreted polypeptide; transmembrane polypeptide;

XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;

XX cancer; lung; colon; breast; prostate; rectum; kidney; liver;

XX microvascular endothelial cell; endothelial cell tube formation.

OS Homo sapiens.

XX US2003068782-A1.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245851.

XX 27-APR-1999; 99US-0131271P.

XX 29-OCT-1999; 99US-0162506P.

XX 02-DEC-1999; 99MO-05028551.

XX 29-AUG-2001; 2001MO-05027099.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,

XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,

XX Fong S;

XX WPI; 2003-625487/59.

XX N-PESDB; ADA01237.

XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the

XX preparation of a medicament for treating a condition responsive to PRO

XX polypeptide, and as therapeutic agents e.g. vaccines.

CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.

XX Sequence 781 AA;

SQ Query Match 81.4%; Score 2651.5; DB 6; Length 781;

Best Local Similarity 84.5%; Pred. No. 7e-218;

Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAWAGSRHPPALTRRSWNNQFVEEYAGPEPVILGKLSVDVDRGE 60
 Db 17 CMGRLAAPARAWAGSRHPPALTRRSWNNQFVEEYAGPEPVILGKLSVDVDRGE 76
 QY 61 GRTKYLLTGEAGTGFVIDEATGNHVTKSLDREKAQVYLLAQAVDRAVDRASNPPLPPESEF 120
 Db 77 GRTKYLLTGEAGTGFVIDEATGNHVTKSLDREKAQVYLLAQAVDRAVDRASNPPLPPESEF 136
 QY 121 IIRGQDINNPPFPGPHATVPKMSNGTGVIVQVTAHDADDPGKNGAKIVTVYLDL 180
 Db 137 IIRGQDINNPPFPGPHATVPKMSNGTGVIVQVTAHDADDPGKNGAKIVTVYLDL 196
 QY 181 PFFSVPOGIVRTAIPMDRETOEFLVIOAKMGHMGSLGSGTIVTVLSDVNDP 240
 Db 197 PFFSVPOGIVRTAIPMDRETOEFLVIOAKMGHMGSLGSGTIVTVLSDVNDP 256
 QY 241 PKFPGSLVQPSVETAGPGTIVGRRLAOPDIDGNALMAYSLIDGSEAFSISTDLQGR 300
 Db 257 PKFPGSLVQPSVETAGPGTIVGRRLAOPDIDGNALMAYSLIDGSEAFSISTDLQGR 316
 QY 301 DGLITRKLPDESQSFVFEATNTLIDPAYLRGPFKDVAVVAQDAPEPPAFIQ 360
 Db 317 DGLITRKLPDESQSFVFEATNTLIDPAYLRGPFKDVAVVAQDAPEPPAFIQ 376
 QY 361 AAYHLTPENKAPGTLVGQISADLDSPPASPIRYSILPHSDPERCFSIQPEEGTHTAP 420
 Db 377 AAYHLTPENKAPGTLVGQISADLDSPPASPIRYSILPHSDPERCFSIQPEEGTHTAP 436
 QY 421 LDRERAMHNLTVLATELGMKSGPERGWPVLVAMENSAAPAPQPSRVSGAVGIPDDSSA 480
 Db 437 LDRERAMHNLTVLATEL-----DSSA 458
 QY 481 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 540
 Db 459 QASRVQVAIQTLDDENNAPQLAEPYDTFVCDSPAAPGQLIQVIRALDRDEVGNSHVSFOG 518
 QY 541 PLGPDANFTVQDNRD-----LPA-----WFHPLMASASSWLH--- 573
 Db 519 PLGPDANFTVQDNRDGASALLPSRPAPPRHAPYLVPIELMDWGQPALSTATVTVSVCR 578
 QY 574 -----WPPAERGNOPASOG 587
 Db 579 CQPDGVSASCPWPAHLSAAGLSTG 602

RESULT 11

ADA01122
 ID ADA01122 standard; protein; 781 AA.

AC ADA01122;

DT 06-NOV-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO, secreted protein; transmembrane protein;

QY 1 CMGR LAAPARA WAGSREHPG PALLTRRSWVNQFVIEEYAGPEPVLIGKLHSDVDRGE 60

Db	17	CMGLIAPAPAAACSGREHPGEPALLRTRRSKMMNQFVLEIYAGPEPVLIGKLHSDVDGE	76
QY	61	GRITKYLITGSGAGTVFVIDEATGNIHVTSLDREEKAQYVLLAQA VDRASNRPLEPSEF	120
Db	77	GRITKYLITGSGAGTVFVIDEATGNIHVTSLDREEKAQYVLLAQA VDRASNRPLEPSEF	130
QY	121	IIKKQDINDNPPILFPLGPHATVPENSNNGTSIVQYTHADADDPVSGSAKLVTVLDGL	180
Db	137	IIKKQDINDNPPILFPLGPHATVPENSNNGTSIVQYTHADADDPVSGSAKLVTVLDGL	190
QY	181	PFPSVDPQTGVVTALIPMDRETQEEFLVIOAKMGCMGGLSGSTTVTTLSDVNDP	240
Db	197	PFPSVDPQTGVVTALIPMDRETQEEFLVIOAKMGCMGGLSGSTTVTTLSDVNDP	250
QY	241	PKPQSIYQSVVETAGPGTIVGRSLAODPDUGNALMAYSTLDEGSEAFSISTDLOGR	300
Db	257	PKPQSIYQSVVETAGPGTIVGRSLAODPDUGNALMAYSTLDEGSEAFSISTDLOGR	310
QY	301	DGLITVKKPLDPFESQSSYFRVYATNTLLDPAVYLRGPKQVASYRAVADAPPEPAFTQ	360
Db	317	DGLITVKKPLDPFESQSSYFRVYATNTLLDPAVYLRGPKQVASYRAVADAPPEPAFTQ	370
QY	361	AAVHLIVPENKAPGTLVGGIISAADLSDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAP	420
Db	377	AAVHLIVPENKAPGTLVGGIISAADLSDSPASPIRYSILPHSDPERCFSTIQPEEGTHTAP	430
QY	421	LDRBARAHNLITVALTELGMGSMGPERGWPVLLVAMSAAPAPQKSPVGSAGVGIPOSSA	480
Db	437	LDRBARAHNLITVALTELGMGSMGPERGWPVLLVAMSAAPAPQKSPVGSAGVGIPOSSA	490
QY	481	QASRVQVALITTDENNANPOLAEPYDTFVCSNAAGQLIOVIRALDRDEVGSSHVSFOG	540
Db	499	QASRVQVALITTDENNANPOLAEPYDTFVCSNAAGQLIOVIRALDRDEVGSSHVSFOG	510
QY	541	PLPGDANFTVQDNRD-----LPA-----WHPILMASASSMLH---573	600
Db	519	PLPGDANFTVQDNRDSSASLLPSPRAPPRAHPLYPIELMDWQGPALSTATVIVSCR	578
QY	574	-----WPPAERGNQPASQG 587	
Db	579	CPDPGVSASCPBAHLASAAGLSTG 602	

RESULT 12

ADA43679

ADA43679 standard; protein; 781 AA.

ADA43679;

AC

AD

20-NOV-2003 (first entry)

Human secreted/transmembrane polypeptide PRO34009.

Human; PRO; secreted protein; transmembrane protein; endothelial cell tube formation; chondrocyte cell differentiation; microvascular endothelial cell; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; kidney tumour; liver tumour; cytoslastic; vaccine.

Homo sapiens.

US2003073190-A1.

17-APR-2003.

09-SEP-2002; 2002US-00238283.

01-JUL-1998; 98US-0091358P.

02-JUL-1999; 99WO-US012282.

20-JUL-1999; 99US-0144758P.

28-JUL-1999; 99US-0146222P.

25-AUG-1999; 99US-00380137.

30-MAR-2000; 2000MO-US008439.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gunney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 WI WPI; 2003-585304/55.
 DR N-PSDB; ADA43678.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO2183, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 PT
 PS Claim 11; Fig 98; 352pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO2183 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 XX
 SQ Sequence 781 AA;
 Query Match: 81.4%; Score 2651.5; DB 7; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;
 QY 1 CMGRLLAARAWAGSREHGPALLTRRSWNNQFVIEEYAGPEPVILGKLSHDVDRGE 60
 DB 17 CMGRLLAARAWAGSREHGPALLTRRSWNNQFVIEEYAGPEPVILGKLSHDVDRGE 76
 QY 61 GRTKYLILGEGAGTGVFVDEATGNTHTKSLDREKAYVLLAQAQVDSNRPLEPPEEF 120
 DB 77 GRTKYLILGEGAGTGVFVDEATGNTHTKSLDREKAYVLLAQAQVDSNRPLEPPEEF 136
 QY 121 IIKGODINDNPPIPLGPHATVPMSNVGTSVIGVTAHDADDPSSYGSANKLVTVLDGL 180
 DB 137 IIKVQDINDNPPIPLGPHATVPMSNVGTSVIGVTAHDADDPSSYGSANKLVTVLDGL 196
 QY 181 PPSVDPTQGVVTRTALPMDRSTQEEFLVIVIAKMGHMGGLSSTVTVTLISVNNP 240

DB 197 PFFSVDPQTQGVVTRTALPMDRETOEEFLVIVIAKMGHMGGLSSTVTVTLISVDNDP 256
 QY 241 PFFSVDPQTQGVVTRTALPMDRETOEEFLVIVIAKMGHMGGLSSTVTVTLISVDNDP 300
 DB 257 PFFSVDPQTQGVVTRTALPMDRETOEEFLVIVIAKMGHMGGLSSTVTVTLISVDNDP 316
 QY 301 DELLTVRKLDPESQSRYSFVEATNTLIDPAYIRGCFKQVAVYVAVQADPEPAPQ 360
 DB 317 DELLTVRKLDPESQSRYSFVEATNTLIDPAYIRGCFKQVAVYVAVQADPEPAPQ 376
 QY 361 AAYHLTVENKAPGLTVQISAADLSPASPIRYSILPHSPERCFSLQPEEGTHTAP 420
 DB 377 AAYHLTVENKAPGLTVQISAADLSPASPIRYSILPHSPERCFSLQPEEGTHTAP 436
 QY 421 LDREARAHNLTVLATLGLWMSGPERGWVPLLVAMSAPAAPQSPVSAVGIPOSSA 480
 DB 437 LDREARAHNLTVLATLGLWMSGPERGWVPLLVAMSAPAAPQSPVSAVGIPOSSA 496
 QY 481 QASRYQVAIQITDENNDNAQOLAEPTVFCDSAPAGQILQVIRALDREYNSHVSFQ 540
 DB 499 QASRYQVAIQITDENNDNAQOLAEPTVFCDSAPAGQILQVIRALDREYNSHVSFQ 518
 QY 541 PLGPDANFTVQDNRD-----LFA-----WFHPLMASASSWLA--- 573
 DB 519 PLGPDANFTVQDNRDGASALLPSRPAPRHAPVLPVLEWMDWGQFALSTATVSVCR 578
 QY 574 -----WPARSGNOPASQ 587
 DB 579 CQPDGVSASCPWEAHLISAAGLSTG 602
 RESULT 13
 ID ADA06941 standard; protein; 781 AA.
 ID ADA06941;
 AC ADA06941;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW bone disorder; cartilage disorder; sports injury; proteoglycan;
 KW cartilage; sports-related joint problem; articular cartilage defect;
 KW osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder;
 KW thalassemia; immune system cell infiltration; cancer; vulvectomy;
 KW anti-nausea; osteopathic; antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003066781-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245771.
 XX
 PR 03-AUG-1999; 99US-0146843P.
 PR 15-MAY-2000; 2000MO-US013358.
 PR 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gunney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 WI WPI; 2003-625486/59.
 DR N-PSDB; ADA06940.
 XX

PT Novel secreted and transmembrane polypeptides, PRO polypeptides useful
PT for stimulating proliferation or differentiation of chondrocyte cells and
PT inducing endothelial cell tube formation.

XX Claim 11; Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptide or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating various bone and/or cartilage disorders
CC such as sports injuries and arthritis. PRO polypeptides which stimulate
CC the release of proteoglycans from cartilage are useful for treating
CC sports-related joint problems, articular cartilage defects,
CC osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful
CC for treating various mammalian haemoglobin-associated disorders such as
CC various thalassemias and conditions which may benefit from enhanced
CC local immune system cell infiltration. This sequence represents a human
CC PRO polypeptide of the invention.

SO Sequence 781 AA:

Query Match 81.4%; Score 2651.5; DB 7; Length 781;
Best Local Similarity 84.5%; Pred. No. 7e-218;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGSLAAPAMAGSREHPALLRTBRVWVNOFPIEYVAPREVLIGKHSVDREE 60
DB 17 CMGSLAAPAMAGSREHPALLRTBRVWVNOFPIEYVAPREVLIGKHSVDREE 76
QY 61 GRITYLLTGAGCTFVIDBATGNHVTSLDREKAQVYLAQAVDRASNPLEPPSEF 120
DB 77 GRITYLLTGAGCTFVIDBATGNHVTSLDREKAQVYLAQAVDRASNPLEPPSEF 136
QY 121 IINGODINDNPPFPIGPRVATPEMSNGTSTVYTADHDDPSYGNAAKIVYVLDGL 180
DB 137 IIXQDINDNPPFPIGPRVATPEMSNGTSTVYTADHDDPSYGNAAKIVYVLDGL 196
QY 181 PFSVDPQTSVGTALPNMDRETQBEFLVVIQAKDMGMMGSGSTVTVTLSDVNDP 240
DB 197 PFSVDPQTSVGTALPNMDRETQBEFLVVIQAKDMGMMGSGSTVTVTLSDVNDP 256
QY 241 PKFPQSLYQSVVETAGPGLVGRLAQDPDLGNALMAYSLIDGSGEAFSITDLCGR 300
DB 257 PKFPQSLYQSVVETAGPGLVGRLAQDPDLGNALMAYSLIDGSGEAFSITDLCGR 316
QY 301 DGLITVRKPLDFESQSYSRFVEATNTLIDPATLRGPRDVAASVAVQADAPPEPAFTQ 360
DB 317 DGLITVRKPLDFESQSYSRFVEATNTLIDPATLRGPRDVAASVAVQADAPPEPAFTQ 376
QY 361 AAHHLVPEKAGTIVGQISADLDSAPSPRYSILPHSDPERCFSTIQEBEGTHTAP 420
DB 377 AAHHLVPEKAGTIVGQISADLDSAPSPRYSILPHSDPERCFSTIQEBEGTHTAP 436
QY 421 LDREAAHNLIVLATELGWSMGPGRGWPLVLAEMSAAPAPQSPVGSANGIQDSSA 480
DB 437 LDREAAHNLIVLATELGWSMGPGRGWPLVLAEMSAAPAPQSPVGSANGIQDSSA 498
QY 481 QASRVOVAIQTLDENNDNAPQLAEPYDTFVCDASAPQQLIQVIRALDRDEVGNSHVSFQG 540

DB 459 QASRVOVAIQTLDENNDNAPQLAEPYDTFVCDASAPQQLIQVIRALDRDEVGNSHVSFQG 518
QY 541 PLGPDANFTVQDNRRGASLLPSPRAPPRAPIVPIELMDWGPALSTATVTVSVCR 573
DB 519 PLGPDANFTVQDNRRGASLLPSPRAPPRAPIVPIELMDWGPALSTATVTVSVCR 578
QY 574 -----WPPARGNQPASQ 587
DB 579 COPDGSVASCPDEALISAAGLSTG 602

RESULT 14
ADA08429
ID ADA08429 standard; protein, 781 AA.

AC ADA08429;
DT 06-NOV-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO34009.
XX osteopathic; anti-rheumatic; antiarthritic; gene therapy;
KW cell proliferation stimulator;
KW chondrocyte cell differentiation stimulator;
KW secreted and transmembrane protein; PRO; human; PRO1213; PRO20080;
KW PRO1213; human microvascular endothelial cell proliferation; PRO6071;
KW PRO4487; PRO6006; PRO240; PRO256; PRO1002; PRO4316; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; tissue typing.

OS Homo sapiens.
PN US2003068783-A1.
PD 10-APR-2003.

PF 16-SEP-2002; 2002US-00245883.
PR 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.

PA (GETH) GENENTECH INC.

PI Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WT, Zhang Z,
PI Fong S;
DR MPI; 2003-625488/59.
DR N-PSDB; ADA08428.

PT Novel isolated PRO1313, PRO20080 or PRO2183 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.

PS Claim 11; Fig 98; 308pp; English.

CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080,
CC or PRO2183 polypeptide is useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487, or PRO6006
CC polypeptide is useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides such as PRO240, PRO256,
CC PRO699, PRO1002, PRO4316, etc., are useful for detecting the presence of
CC tumour in a mammal which involves comparing the level of expression of
CC the above mentioned polypeptides in a test sample of cells taken from the
CC mammal, and a control sample of normal cells of the same cell type, where
CC a higher level of expression of the PRO polypeptide in the test sample as

Query Match 81.4%; Score 2651.5; DB 7; Length 781;
 Best Local Similarity 84.5%; Pred. No. 7e-218;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

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DB	77	GRTKYLITGSGAGTVFVIDEATGNIVHTKSLDREKAYVLLAQAVDRASNRPLEPSEF	136
QY	121	IKKODINDNPPIFPLGPHATVPEMGNVGTSVIQTAAHADDPSYGNSAKLYTVLDGL	180
DB	137	IKKODINDNPPIFPLGPHATVPEMGNVGTSVIQTAAHADDPSYGNSAKLYTVLDGL	196
QY	181	PEFSYDPTQGVYRTAIPMDRETOEELVVIQAKDMGSHMGSLGSLTTLVTLSDVNDP	240
DB	197	PEFSYDPTQGVYRTAIPMDRETOEELVVIQAKDMGSHMGSLGSLTTLVTLSDVNDP	256
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DB	257	PKFPOSILYQFSVETAGGTLVGRRAQDPDLGNALMAYSILDGEGSEAFSISTDLQGR	316
QY	301	DGLLTVRKPLDFESQSYSEFEATNTLIDPAYLRGPFKDVASVRVAVODAPEPPAFTQ	360
DB	317	DGLLTVRKPLDFESQSYSEFEATNTLIDPAYLRGPFKDVASVRVAVODAPEPPAFTQ	376
QY	361	AAHILTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFISIQPEEGTIHTAAP	420
DB	377	AAHILTVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFISIQPEEGTIHTAAP	436
QY	421	LDRERAMHNLTVLATELGMSWGPGRGVPLVAVEMSAAPAPQRPVSAGVIGQDSSA	480
DB	437	LDRERAMHNLTVLATELGMSWGPGRGVPLVAVEMSAAPAPQRPVSAGVIGQDSSA	458
QY	481	QASRYQVAIOTLDENDNAPQIAEPIYDTFVCDASAPGQLIQVIRALDRDEVGNSSHYVFOG	540
DB	459	QASRYQVAIOTLDENDNAPQIAEPIYDTFVCDASAPGQLIQVIRALDRDEVGNSSHYVFOG	518
QY	541	PLGPDANFTVQDNRD-----LPA-----WFHPLMASASSWLH---	573
DB	519	PLGPDANFTVQDNRDGASLLPSRPAFRHAPYLVFIELMDWGQPALSTATVTSVGR	578
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DB	579	CQPDGVSVCWCPFAHLISAAGLSTG	602

Search completed: December 8, 2004, 10:13:04
 Job time : 257.564 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 633.542 Seconds
(Without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-7
Perfect score: 3259
Sequence: 1 CMGRAPARAWAGSEHFG.....LPSCQPLGIPALGIVLCAS 620

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3259	100.0	620	10	US-09-788-051-7
2	3259	100.0	636	10	US-09-788-051-4
3	2651.5	81.4	781	9	US-09-860-866-2
4	2651.5	81.4	781	14	US-10-245-752-98
5	2651.5	81.4	781	14	US-10-245-559-98
6	2651.5	81.4	781	14	US-10-245-103-98
7	2651.5	81.4	781	14	US-10-245-107-98
8	2651.5	81.4	781	14	US-10-245-143-98
9	2651.5	81.4	781	14	US-10-245-771-98
10	2651.5	81.4	781	14	US-10-245-851-98
11	2651.5	81.4	781	14	US-10-245-883-98
12	2651.5	81.4	781	14	US-10-237-535-98

14	2651.5	81.4	781	14	US-10-238-283-98	Sequence 98, Appl
15	2651.5	81.4	781	14	US-10-238-370-98	Sequence 98, Appl
16	2651.5	81.4	781	14	US-10-245-055-98	Sequence 98, Appl
17	2651.5	81.4	781	14	US-10-245-147-98	Sequence 98, Appl
18	2651.5	81.4	781	14	US-10-245-730-98	Sequence 98, Appl
19	2651.5	81.4	781	14	US-10-245-739-98	Sequence 98, Appl
20	2651.5	81.4	781	14	US-10-246-210-98	Sequence 98, Appl
21	2651.5	81.4	781	14	US-10-239-196-98	Sequence 98, Appl
22	2651.5	81.4	781	14	US-10-243-024-98	Sequence 98, Appl
23	2651.5	81.4	781	14	US-10-243-409-98	Sequence 98, Appl
24	2651.5	81.4	781	14	US-10-245-821-98	Sequence 98, Appl
25	2651.5	81.4	781	14	US-10-245-880-98	Sequence 98, Appl
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27	2651.5	81.4	781	14	US-10-243-095-98	Sequence 98, Appl
28	2651.5	81.4	781	14	US-10-245-185-98	Sequence 98, Appl
29	2651.5	81.4	781	14	US-10-245-427-98	Sequence 98, Appl
30	2651.5	81.4	781	14	US-10-245-473-98	Sequence 98, Appl
31	2651.5	81.4	781	14	US-10-245-770-98	Sequence 98, Appl
32	2651.5	81.4	781	14	US-10-245-877-98	Sequence 98, Appl
33	2651.5	81.4	781	14	US-10-246-976-98	Sequence 98, Appl
34	2651.5	81.4	781	14	US-10-243-320-98	Sequence 98, Appl
35	2651.5	81.4	781	14	US-10-162-435-13	Sequence 19, Appl
36	2651.5	81.4	781	14	US-10-242-743-98	Sequence 98, Appl
37	2651.5	81.4	781	14	US-10-237-636-98	Sequence 98, Appl
38	2651.5	81.4	781	14	US-10-238-325-98	Sequence 98, Appl
39	2651.5	81.4	781	14	US-10-238-346-98	Sequence 98, Appl
40	2651.5	81.4	781	14	US-10-238-411-98	Sequence 98, Appl
41	2651.5	81.4	781	14	US-10-243-124-98	Sequence 98, Appl
42	2651.5	81.4	781	14	US-10-243-425-98	Sequence 98, Appl
43	2651.5	81.4	781	14	US-10-243-446-98	Sequence 98, Appl
44	2651.5	81.4	781	14	US-10-245-874-98	Sequence 98, Appl
45	2651.5	81.4	781	14	US-10-245-874-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yennu, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radole T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-051-7

Query Match 100.0%; Score 3259; DB 10; Length 620;

Best Local Similarity 100.0%; Pred. No. 8.3e-233; Indels 0; Gaps 0;

Matches 620; Conservative 0; Mismatches 0; US-09-788-051-7

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 Db 121 IIKGODINDNPIIFPLGPHATVPEMSVNGSVQVTAHDAADDSYGNASAKLYTVTLVLDGL 180
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 Db 181 PFFSVDPQTGVVTRTAIPMDRETOEEFLVVIQAADMGGHGGLSGSTTVTLSDVNDP 240
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 Db 601 LPSCQLPLGIPALGIVLCAS 620
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 RESULT 2
 US-09-788-051-4
 ; Sequence 4, Application US/09788051
 ; Publication No. US20030144491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Godbole, Shubhada D
 ; APPLICANT: Kuo, Chiaoyn
 ; APPLICANT: Ateeburn, Matthew C
 ; APPLICANT: Yeung, George
 ; APPLICANT: Palencia, Servando
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenchua
 ; APPLICANT: Dramac, Radoje T
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
 ; FILE REFERENCE: HYS-39
 ; CURRENT APPLICATION NUMBER: US/09/788,051
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: US 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-788-051-4

Query Match 100.0%; Score 3259; DB 10; Length 636;
 Best Local Similarity 100.0%; Pred. No. 8,7e-233;
 Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 17 CMGRILAAPARAWAGSRREHPGALLTRRSWVWNOFVIEEYAGEPVLIGKLSVDVDRGE 76
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 Db 77 GRTKYLITGEGAGTVFVIDEATGNIHVTKSLDREKQAYVLLAQAVIDRASNRPLEPSEF 136
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 QY 601 LPSCQLPLGIPALGIVLCAS 620
 Db 617 LPSCQLPLGIPALGIVLCAS 636
 RESULT 3
 US-09-860-868-2
 ; Sequence 2, Application US/09860868
 ; Patent No. US20020076757A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Roy A. J.
 ; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
 ; FILE REFERENCE: 10448-050001
 ; CURRENT APPLICATION NUMBER: US/09/860,868
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: 60/205,674
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-860-868-2
 Query Match 81.4%; Score 2651.5; DB 9; Length 781;
 Best Local Similarity 84.5%; Pred. No. 1.3e-187;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

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DB 579 QCPDGSVASCWPEAHLSAAGLSTG 602

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RESULT 4

US-10-245-752-98

Sequence 98, Application US/10245752
 Publication No. US20030064473A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Bacon, Dan
 APPLICANT: Filvarciff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Phillippe
 APPLICANT: Watande, Collin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3630RJC66
 CURRENT APPLICATION NUMBER: US/10/245,752
 CURRENT FILING DATE: 2002-09-16
 PRIOR APPLICATION NUMBER: 10/197942
 PRIOR FILING DATE: 2002-07-18
 PRIOR APPLICATION NUMBER: 60/059114
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/063046

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; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-752-98

```

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
 Best Local Similarity 84.5%; Pred. No. 1.3e-187;
 Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

```

QY 1 CMGRLAAPARAWAGSRHHPGALLTRRSWVWNOFFVIEEYAGPEPVILIGKLSVDVDRGE 60
DB 17 CMGRLAAPARAWAGSRHHPGALLTRRSWVWNOFFVIEEYAGPEPVILIGKLSVDVDRGE 76
QY 61 GRTKYLLTGEAGTAVFVIDEATGNHVTKSLDREKAQVYLLAQAVDRASNRPLEPSEF 120
DB 77 GRTKYLLTGEAGTAVFVIDEATGNHVTKSLDREKAQVYLLAQAVDRASNRPLEPSEF 136
QY 121 IIKGQDINDNPPFPELGPYHATVPEMSNVGTSVIOVTAHADDPSSYNSAKLYVTVLDGL 180
DB 137 IIKVQDINDNPPFPELGPYHATVPEMSNVGTSVIOVTAHADDPSSYNSAKLYVTVLDGL 196
QY 181 PFEVSVDQGTGVRTAIPNDRETQEEFLVYIOAKDMGHWGGLSGSTTVTLSDVNDNF 240
DB 197 PFEVSVDQGTGVRTAIPNDRETQEEFLVYIOAKDMGHWGGLSGSTTVTLSDVNDNF 256
QY 241 PKFQSLYQFSVETAGPGLVGRLAQDDPDLGNALMAYSILDGSESAFSTIDLOQR 300
DB 257 PKFQSLYQFSVETAGPGLVGRLAQDDPDLGNALMAYSILDGSESAFSTIDLOQR 316
QY 301 DGLITVRKPLDPESSQSYSEFVEATNTLIDPAYLRGPFXDVASVRVAQDAPEPAFTQ 360
DB 317 DGLITVRKPLDPESSQSYSEFVEATNTLIDPAYLRGPFXDVASVRVAQDAPEPAFTQ 376
QY 361 AAYHLYVPENKAPGTLVQISADLDSBPASPIRYSILPHSDPERCFSIOPEEGTHTAAP 420
DB 377 AAYHLYVPENKAPGTLVQISADLDSBPASPIRYSILPHSDPERCFSIOPEEGTHTAAP 436
QY 421 LDREARAHNLTYLATELGMSWGPBGWVPLVAVMSAARPPQSRPVSAAGIPODSSA 480
DB 437 LDREARAHNLTYLATELGMSWGPBGWVPLVAVMSAARPPQSRPVSAAGIPODSSA 496
QY 481 QASRVOVAIOTLDENNAPOLAEPYDTFVCDSPAAGOLIQTIRALDRDEVGNSSHVSFOG 540
DB 499 QASRVOVAIOTLDENNAPOLAEPYDTFVCDSPAAGOLIQTIRALDRDEVGNSSHVSFOG 558
QY 541 PLGPDANFTVQDNRD-----LPA-----WFHPLMASASMLH--- 573
DB 519 PLGPDANFTVQDNRDGSASLLPSRPAPRHAPVPLVIELMDWQPALSTATVTVSVCR 578
QY 574 -----WPPAERGNOPASOG 587
DB 579 QCPDGSVASCWPEAHLSAAGLSTG 602

```

RESULT 5

US-10-245-859-98
; Sequence 98, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Macande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P630R1C78
; CURRENT APPLICATION NUMBER: US/10/245, 859
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/066478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-859-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAPARAMGSRHPPALLRTTRRSWVNOQFVIERHAGPEVLLGKLSHSDVDRGE 60
DB 17 CMGRLAPARAMGSRHPPALLRTTRRSWVNOQFVIERHAGPEVLLGKLSHSDVDRGE 76
QY 61 GRTYVLLTGAGTVEVIDEATGNINHTKSLDREERQAVYLLAQAVDRASNPPLSEPSSEF 120
DB 77 GRTYVLLTGAGTVEVIDEATGNINHTKSLDREERQAVYLLAQAVDRASNPPLSEPSSEF 136
QY 121 IIRGQDINDNPPFPLGPHATVPEMSNGTSTYQTAHADDDPSYGNSAKIYTVVLGDL 180
DB 137 IIRGQDINDNPPFPLGPHATVPEMSNGTSTYQTAHADDDPSYGNSAKIYTVVLGDL 196
QY 181 PFSVDPQTSVATAPNMDRETQEEFLVYIAQKMGHGGISGTTVTTLSDVNDP 240
DB 197 PFSVDPQTSVATAPNMDRETQEEFLVYIAQKMGHGGISGTTVTTLSDVNDP 256
QY 241 PKPFSQSVETVETGPGTLVGRAPQDPDLDGNALMAYSILDGSGSAFISITDLOGR 300
DB 257 PKPFSQSVETVETGPGTLVGRAPQDPDLDGNALMAYSILDGSGSAFISITDLOGR 316

QY 301 DGLTVRKLPDESORSYFRYEATNTLLIDPAYLRSGPFKDVASVAVQADAPPPATQ 360
DB 317 DGLTVRKLPDESORSYFRYEATNTLLIDPAYLRSGPFKDVASVAVQADAPPPATQ 376
QY 361 AAYHLTVENKAPGTLVQOISADIDSPASPIRYSILPHSDPERCFSIQPEEGTHTAP 420
DB 377 AAYHLTVENKAPGTLVQOISADIDSPASPIRYSILPHSDPERCFSIQPEEGTHTAP 436
QY 421 LDREARAWNTLVLTATELGWSGPRGVPPLVAVMSAPAPRQSPVGSVAGLPQSSA 480
DB 437 LDREARAWNTLVLTATELGWSGPRGVPPLVAVMSAPAPRQSPVGSVAGLPQSSA 458
QY 481 QASRVQVALIOTLDENDNAPOLAEPYDFVCDAAFGOLIQVIRALDRDEVGNSSHVSFOG 540
DB 459 QASRVQVALIOTLDENDNAPOLAEPYDFVCDAAFGOLIQVIRALDRDEVGNSSHVSFOG 518
QY 541 PEGPANTVQDNRP-----LPA-----WHPPLMASASMLH--- 573
DB 519 PEGPANTVQDNRGASALLPSRPADPRHAPYLVPIELMDWQOPALSTATVTSYCR 578
QY 574 -----WPPARGNQPASOG 587
DB 579 CQPDGSVASCPPEAHLASAAGLSTG 602

RESULT 6
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Macande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P630R1C112
; CURRENT APPLICATION NUMBER: US/10/245, 103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rapb

Page 5

US-10-245-103-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAWAGSREHPGALLRTRRSVMNQFVIEEYAGPEPVILGKLHSDVDRC 60
DB 17 CMGRLAAPARAWAGSREHPGALLRTRRSVMNQFVIEEYAGPEPVILGKLHSDVDRC 76
QY 61 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREBAQVYLLAQAVDRASNPLEPSEF 120
DB 77 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREBAQVYLLAQAVDRASNPLEPSEF 136
QY 121 IIRKQDINDNPPFLPGYHATVPEMSNGSVIQTADADDPSSYNSAKLYTVLDGL 180
DB 137 IIRKQDINDNPPFLPGYHATVPEMSNGSVIQTADADDPSSYNSAKLYTVLDGL 196
QY 181 PFEVSVDQGTGVRTAIPMDRETOEEFLVVIQAKDGMGMSGLSGSTTVTLSDVNDP 240
DB 197 PFEVSVDQGTGVRTAIPMDRETOEEFLVVIQAKDGMGMSGLSGSTTVTLSDVNDP 256
QY 241 PKFPOSUYOFSVETAGPGLVGRRAODPDLGNALMAYSILDGSEAFSISTDLOGR 300
DB 257 PKFPOSUYOFSVETAGPGLVGRRAODPDLGNALMAYSILDGSEAFSISTDLOGR 316
QY 301 DGLLTVRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVVADAPPEPAFTQ 360
DB 317 DGLLTVRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVVADAPPEPAFTQ 376
QY 361 AAHYLTVPENKAPGTLVGOISAADLDSAPSPRYSILPHSDPERCSIQPEEGTHTAAP 420
DB 377 AAHYLTVPENKAPGTLVGOISAADLDSAPSPRYSILPHSDPERCSIQPEEGTHTAAP 436
QY 421 LDREARAHNLTVLATELGSWGPBERGWPLVAEWSAPAAPQSPVGSAGVIPDSSA 480
DB 437 LDREARAHNLTVLATEL-----DSSA 458
QY 481 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAPQOLIQTIRALDRDEVNSHVSFOG 540
DB 459 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAPQOLIQTIRALDRDEVNSHVSFOG 518
QY 541 PLGPDANFTVQDNRD-----LPA-----WEPFLMASASMLH--- 573
DB 519 PLGPDANFTVQDNRDGASLLPSRPAPRHAAPYVPIELMDWQPALSSATATVYSVCR 578
QY 574 -----WPAERGNQPASOG 587
DB 579 CQPDGVSACWPEALHLSAAGLSTG 602

RESULT 7

US-10-245-107-98
Sequence 98, Application US/10245107
Publication No. US20030068779A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Guiney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Matambe, Collin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C71

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAWAGSREHPGALLRTRRSVMNQFVIEEYAGPEPVILGKLHSDVDRC 60
DB 17 CMGRLAAPARAWAGSREHPGALLRTRRSVMNQFVIEEYAGPEPVILGKLHSDVDRC 76
QY 61 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREBAQVYLLAQAVDRASNPLEPSEF 120
DB 77 GRTKYLLTGEAGATVVIDEATGNHVTKSLDREBAQVYLLAQAVDRASNPLEPSEF 136
QY 121 IIRKQDINDNPPFLPGYHATVPEMSNGSVIQTADADDPSSYNSAKLYTVLDGL 180
DB 137 IIRKQDINDNPPFLPGYHATVPEMSNGSVIQTADADDPSSYNSAKLYTVLDGL 196
QY 181 PFEVSVDQGTGVRTAIPMDRETOEEFLVVIQAKDGMGMSGLSGSTTVTLSDVNDP 240
DB 197 PFEVSVDQGTGVRTAIPMDRETOEEFLVVIQAKDGMGMSGLSGSTTVTLSDVNDP 256
QY 241 PKFPOSUYOFSVETAGPGLVGRRAODPDLGNALMAYSILDGSEAFSISTDLOGR 300
DB 257 PKFPOSUYOFSVETAGPGLVGRRAODPDLGNALMAYSILDGSEAFSISTDLOGR 316
QY 301 DGLLTVRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVVADAPPEPAFTQ 360
DB 317 DGLLTVRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVVADAPPEPAFTQ 376
QY 361 AAHYLTVPENKAPGTLVGOISAADLDSAPSPRYSILPHSDPERCSIQPEEGTHTAAP 420
DB 377 AAHYLTVPENKAPGTLVGOISAADLDSAPSPRYSILPHSDPERCSIQPEEGTHTAAP 436
QY 421 LDREARAHNLTVLATELGSWGPBERGWPLVAEWSAPAAPQSPVGSAGVIPDSSA 480
DB 437 LDREARAHNLTVLATEL-----DSSA 458
QY 481 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAPQOLIQTIRALDRDEVNSHVSFOG 540
DB 459 QASRVQVAIQTLDENDNAPQLAEPYDTFVCDSPAAPQOLIQTIRALDRDEVNSHVSFOG 518
QY 541 PLGPDANFTVQDNRD-----LPA-----WEPFLMASASMLH--- 573
DB 519 PLGPDANFTVQDNRDGASLLPSRPAPRHAAPYVPIELMDWQPALSSATATVYSVCR 578
QY 574 -----WPAERGNQPASOG 587

Db 579 COPDGSVASCWPEAHLSAAGLSTG 602

RESULT 8

US-10-245-143-98

/ Sequence 98, Application US/10245143
/ Publication No. US20030068780A1
/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin

/ APPLICANT: Eaton, Dan

/ APPLICANT: Filvaroff, Ellen

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin

/ APPLICANT: Smith, Victoria

/ APPLICANT: Stephan, Jean-Philippe

/ APPLICANT: Matande, Colin

/ APPLICANT: Wood, William

/ APPLICANT: Zhang, Zemin

/ APPLICANT: Fong, Sherman

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ FILE REFERENCE: P3630R1C90

/ CURRENT FILING DATE: 2002-09-16

/ PRIOR FILING DATE: 2002-07-18

/ PRIOR FILING DATE: 2002-07-18

/ PRIOR FILING DATE: 1997-09-17

/ PRIOR FILING DATE: 1997-10-24

/ PRIOR FILING DATE: 1997-11-10

/ PRIOR FILING DATE: 1998-03-27

/ PRIOR FILING DATE: 1998-05-22

/ PRIOR FILING DATE: 1998-06-02

/ PRIOR FILING DATE: 1998-06-18

/ PRIOR FILING DATE: 1998-06-24

/ PRIOR FILING DATE: 1998-06-25

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 116

/ SEQ ID NO 98

/ LENGTH: 781

/ TYPE: PRT

/ ORGANISM: Homo Sapien

US-10-245-143-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;

Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAMAGSREHPGALLRTRRSVWVWQFVIEVYAGPEVVLIGKLSHVDRE 60
Db 17 CMGRLAAPARAMAGSREHPGALLRTRRSVWVWQFVIEVYAGPEVVLIGKLSHVDRE 76
QY 61 GRKTYLLTGAGTAVVIDAATNIHVTKSLDREKAYQVLLAQAADRASNEPLEPSEF 120
Db 77 GRKTYLLTGAGTAVVIDAATNIHVTKSLDREKAYQVLLAQAADRASNEPLEPSEF 136
QY 121 IIGODINDNPFIFPGPYATVPEMSNGTSTVQVTAHDADDPSSGSAKLVTVLGL 180
Db 137 IIVQDINDNPFIFPGPYATVPEMSNGTSTVQVTAHDADDPSSGSAKLVTVLGL 196
QY 181 PFSVDPQGTGVVTAIPNMDRETQEBFLVVIQAKDGMGAGLSGSTTVTVLSDVDNP 240
Db 197 PFSVDPQGTGVVTAIPNMDRETQEBFLVVIQAKDGMGAGLSGSTTVTVLSDVDNP 256

QY 241 EKPSQVSVSVETVETAGPTVIGRLRADPDLDGNALMAYSLDGESEAFSISTDLOGR 300
Db 257 EKPSQVSVSVETVETAGPTVIGRLRADPDLDGNALMAYSLDGESEAFSISTDLOGR 316
QY 301 DELLTVRKLPDESGRSYFRVEATNTLIDPAYLRGPFKQVASYRVAQDAPPEPPTQ 360
Db 317 DELLTVRKLPDESGRSYFRVEATNTLIDPAYLRGPFKQVASYRVAQDAPPEPPTQ 376
QY 361 AAYHLLTPENKAPGLTVQVQISAAIDSPASPIRYSILHSDPERCFSTQPEEGITHAP 420
Db 377 AAYHLLTPENKAPGLTVQVQISAAIDSPASPIRYSILHSDPERCFSTQPEEGITHAP 436
QY 421 LDREARAHNLTIVLATELGWSGPERGWVPLVWMSAPAPQRPVGSVAVGIPDSSA 480
Db 437 LDREARAHNLTIVLATELGWSGPERGWVPLVWMSAPAPQRPVGSVAVGIPDSSA 458
QY 481 QASRYQVAIQITDENMNPOLAEPIVDTVCSSAPGQILQVIRALDRDEVNSSHVFOG 540
Db 459 QASRYQVAIQITDENMNPOLAEPIVDTVCSSAPGQILQVIRALDRDEVNSSHVFOG 518
QY 541 PLGPANFTVODNRD-----LPA-----WPHPLMASASSMLH--- 573
Db 519 PLGPANFTVODNRDGSALLPSRPAPFRAPVLPVLEMDMQPALSTAITVTSVCR 578
QY 574 -----WPAERGNQPASOG 587
Db 579 COPDGSVASCWPEAHLSAAGLSTG 602

RESULT 9

US-10-245-771-98

/ Sequence 98, Application US/10245771
/ Publication No. US20030068781A1
/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin

/ APPLICANT: Eaton, Dan

/ APPLICANT: Filvaroff, Ellen

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin

/ APPLICANT: Smith, Victoria

/ APPLICANT: Stephan, Jean-Philippe

/ APPLICANT: Matande, Colin

/ APPLICANT: Wood, William

/ APPLICANT: Zhang, Zemin

/ APPLICANT: Fong, Sherman

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ FILE REFERENCE: P3630R1C98

/ CURRENT FILING DATE: 2002-09-16

/ PRIOR FILING DATE: 2002-07-18

/ PRIOR FILING DATE: 2002-07-18

/ PRIOR FILING DATE: 1997-09-17

/ PRIOR FILING DATE: 1997-10-24

/ PRIOR FILING DATE: 1997-11-10

/ PRIOR FILING DATE: 1998-03-27

/ PRIOR FILING DATE: 1998-05-22

/ PRIOR FILING DATE: 1998-06-02

/ PRIOR FILING DATE: 1998-06-18

/ PRIOR FILING DATE: 1998-06-24

/ PRIOR FILING DATE: 1998-06-25

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 116

/ SEQ ID NO 98

/ LENGTH: 781

/ TYPE: PRT

/ ORGANISM: Homo Sapien

US-10-245-771-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;

Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAMAGSREHPGALLRTRRSVWVWQFVIEVYAGPEVVLIGKLSHVDRE 60
Db 17 CMGRLAAPARAMAGSREHPGALLRTRRSVWVWQFVIEVYAGPEVVLIGKLSHVDRE 76
QY 61 GRKTYLLTGAGTAVVIDAATNIHVTKSLDREKAYQVLLAQAADRASNEPLEPSEF 120
Db 77 GRKTYLLTGAGTAVVIDAATNIHVTKSLDREKAYQVLLAQAADRASNEPLEPSEF 136
QY 121 IIGODINDNPFIFPGPYATVPEMSNGTSTVQVTAHDADDPSSGSAKLVTVLGL 180
Db 137 IIVQDINDNPFIFPGPYATVPEMSNGTSTVQVTAHDADDPSSGSAKLVTVLGL 196
QY 181 PFSVDPQGTGVVTAIPNMDRETQEBFLVVIQAKDGMGAGLSGSTTVTVLSDVDNP 240
Db 197 PFSVDPQGTGVVTAIPNMDRETQEBFLVVIQAKDGMGAGLSGSTTVTVLSDVDNP 256

NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo sapien
US-10-245-771-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

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QY 1 CMGLAAPARAWASREHPGALLTRRSWVNOFFVEIYAGEPVLIGKLSHDVDRGE 60
DB 17 CMGLAAPARAWASREHPGALLTRRSWVNOFFVEIYAGEPVLIGKLSHDVDRGE 76
QY 61 GRTKYLLTGBGAGTVFVIDEATGNHVTKSLDREKAQVYLLAQAVDRASNPLEPPSEF 120
DB 77 GRTKYLLTGBGAGTVFVIDEATGNHVTKSLDREKAQVYLLAQAVDRASNPLEPPSEF 136
QY 121 IIKQDINDNPFIFLPGYHATVPEMSNVGTSVIQVTAHADDPSSYNSAKLYVTYLDGL 180
DB 137 IIKQDINDNPFIFLPGYHATVPEMSNVGTSVIQVTAHADDPSSYNSAKLYVTYLDGL 196
QY 181 PFEVSDPOTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTLSDVNDP 240
DB 197 PFEVSDPOTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTLSDVNDP 256
QY 241 PKFPOSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSIIDGSGSAFSTLDLQGR 300
DB 257 PKFPOSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSIIDGSGSAFSTLDLQGR 316
QY 301 DGLLTVRKPLDPEFSQSYSEFRVEATNTLIDPAYLRGPKVDVASVAVQADAPPEPAFTQ 360
DB 317 DGLLTVRKPLDPEFSQSYSEFRVEATNTLIDPAYLRGPKVDVASVAVQADAPPEPAFTQ 376
QY 361 AAYHLTVPENKAPGTLVGOISADLDSAPSPRYSILPHSDPERCSIQPEEGTHTTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISADLDSAPSPRYSILPHSDPERCSIQPEEGTHTTAAP 436
QY 421 LDREARAHNLTIVLATELGMWGPBRGWVPLVAEMSAAPAPQPSVGSANGVIGPOSSA 480
DB 437 LDREARAHNLTIVLATELGMWGPBRGWVPLVAEMSAAPAPQPSVGSANGVIGPOSSA 488
QY 481 QASRVOVAIQTLDENNAPQLAEPYDTFVCDSPAAGQLIQVIRALDDEVGNSSHVSFOG 540
DB 459 QASRVOVAIQTLDENNAPQLAEPYDTFVCDSPAAGQLIQVIRALDDEVGNSSHVSFOG 518
QY 541 PLGPDANFTVQDNRD-----LPA-----WHPPLMASASGMLH--- 573
DB 519 PLGPDANFTVQDNRDNGSASLLPSSRPAPRHAAYPLVPIELMDWQFALSTATVTSVCR 578
QY 574 -----WPAERGNQPAASOG 587
DB 579 CQPDGVSASCMPEAHLSHAAGLSTG 602
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QY 1 CMGLAAPARAWASREHPGALLTRRSWVNOFFVEIYAGEPVLIGKLSHDVDRGE 60
DB 17 CMGLAAPARAWASREHPGALLTRRSWVNOFFVEIYAGEPVLIGKLSHDVDRGE 76
QY 61 GRTKYLLTGBGAGTVFVIDEATGNHVTKSLDREKAQVYLLAQAVDRASNPLEPPSEF 120
DB 77 GRTKYLLTGBGAGTVFVIDEATGNHVTKSLDREKAQVYLLAQAVDRASNPLEPPSEF 136
QY 121 IIKQDINDNPFIFLPGYHATVPEMSNVGTSVIQVTAHADDPSSYNSAKLYVTYLDGL 180
DB 137 IIKQDINDNPFIFLPGYHATVPEMSNVGTSVIQVTAHADDPSSYNSAKLYVTYLDGL 196
QY 181 PFEVSDPOTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTLSDVNDP 240
DB 197 PFEVSDPOTGVVTRTAIPMDRETOEFLVVIQAKMGGMGGLSGSTTVTLSDVNDP 256
QY 241 PKFPOSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSIIDGSGSAFSTLDLQGR 300
DB 257 PKFPOSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSIIDGSGSAFSTLDLQGR 316
QY 301 DGLLTVRKPLDPEFSQSYSEFRVEATNTLIDPAYLRGPKVDVASVAVQADAPPEPAFTQ 360
DB 317 DGLLTVRKPLDPEFSQSYSEFRVEATNTLIDPAYLRGPKVDVASVAVQADAPPEPAFTQ 376
QY 361 AAYHLTVPENKAPGTLVGOISADLDSAPSPRYSILPHSDPERCSIQPEEGTHTTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISADLDSAPSPRYSILPHSDPERCSIQPEEGTHTTAAP 436
QY 421 LDREARAHNLTIVLATELGMWGPBRGWVPLVAEMSAAPAPQPSVGSANGVIGPOSSA 480
DB 437 LDREARAHNLTIVLATELGMWGPBRGWVPLVAEMSAAPAPQPSVGSANGVIGPOSSA 488
QY 481 QASRVOVAIQTLDENNAPQLAEPYDTFVCDSPAAGQLIQVIRALDDEVGNSSHVSFOG 540
DB 459 QASRVOVAIQTLDENNAPQLAEPYDTFVCDSPAAGQLIQVIRALDDEVGNSSHVSFOG 518
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QY 541 PLGPANFTVQDNRD-----LPA-----WFHPLMASASMLH--- 573
DB 519 PLGPANFTVQDNRDGSGSLPLPSRPAPRRAPFLVPLVPLMDWQPALSTIATVTSVCR 578
QY 574 -----WPAERGNQPASOG 587
DB 579 CQPDGVSASCPWEAHLISAAGLSTG 602

RESULT 11
US-10-245-883-98
Sequence 98, Application US/10245883
Publication No. US20030068783A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C70
CURRENT FILING DATE: 1998-06-25
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-883-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1,3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRLAAPARAWAGSRHPPALLRTRRSVWNOQFVIEEYAGPEVVLIGKXHSVDRE 60
DB 17 CMGRLAAPARAWAGSRHPPALLRTRRSVWNOQFVIEEYAGPEVVLIGKXHSVDRE 76
QY 61 GRKTYLLTGGAQTVVIDEATNINHTVKSLSREKAAQVLLAQAADVRAASNPLEPPSEF 120
DB 77 GRKTYLLTGGAQTVVIDEATNINHTVKSLSREKAAQVLLAQAADVRAASNPLEPPSEF 136
QY 121 IIGQDINDNPFIFPLGPYATVPEMSNVTGTSVIOVTADADDPSSGSAKIVYVVLGL 180

DB 137 IIGQDINDNPFIFPLGPYATVPEMSNVTGTSVIOVTADADDPSSGSAKIVYVVLGL 196
QY 181 PFFSVDPQGTGVVRAIIPNNDRETOEEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 240
DB 197 PFFSVDPQGTGVVRAIIPNNDRETOEEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 256
QY 241 PFFSVDPQGTGVVRAIIPNNDRETOEEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 300
DB 257 PFFSVDPQGTGVVRAIIPNNDRETOEEFLVVIQAKMGHMGGLSGSTTVTLSDVNDP 316
QY 301 DGLTVRKPDESGRSYSPVEATNTLIDPAYLRGPFKDVASVRAVQDAPPPAFQ 360
DB 317 DGLTVRKPDESGRSYSPVEATNTLIDPAYLRGPFKDVASVRAVQDAPPPAFQ 376
QY 361 AAYHLLTPENKAPGLVQISAADPSASTIRSLPHSPBECFSTQPEEGTHRAP 420
DB 377 AAYHLLTPENKAPGLVQISAADPSASTIRSLPHSPBECFSTQPEEGTHRAP 436
QY 421 LDREARAHNLTVLATELGMSWGERGWVPLVWMSAPAPFORSPVSAVGIPODSA 480
DB 437 LDREARAHNLTVLATELGMSWGERGWVPLVWMSAPAPFORSPVSAVGIPODSA 498
QY 481 QASRQVVAIQTLDENDNAPQIAEPYDTVCSSAAPGQILQVTRALDRDEVGNSHVSFOG 540
DB 459 QASRQVVAIQTLDENDNAPQIAEPYDTVCSSAAPGQILQVTRALDRDEVGNSHVSFOG 518
QY 541 PLGPANFTVQDNRD-----LPA-----WFHPLMASASMLH--- 573
DB 519 PLGPANFTVQDNRDGSGSLPLPSRPAPRRAPFLVPLVPLMDWQPALSTIATVTSVCR 578
QY 574 -----WPAERGNQPASOG 587
DB 579 CQPDGVSASCPWEAHLISAAGLSTG 602

RESULT 12
US-10-237-535-98
Sequence 98, Application US/10237535
Publication No. US20030073188A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C3
CURRENT FILING DATE: 1998-06-25
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
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PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
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PRIOR FILING DATE: 1999-04-01
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PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
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PRIOR APPLICATION NUMBER: 60/151700
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PRIOR APPLICATION NUMBER: 60/170262
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PRIOR APPLICATION NUMBER: 60/177118
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PRIOR FILING DATE: 2000-02-02
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PRIOR APPLICATION NUMBER: 60/187202
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PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
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PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
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PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/180997
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PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 2001-08-06

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PRIORITY APPLICATION NUMBER: 09/927796
PRIORITY FILING DATE: 2001-08-09
PRIORITY APPLICATION NUMBER: 09/929404
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PRIORITY APPLICATION NUMBER: 09/931836
PRIORITY FILING DATE: 2001-08-16
PRIORITY APPLICATION NUMBER: 09/941992
PRIORITY FILING DATE: 2001-08-28
PRIORITY APPLICATION NUMBER: 09/946374
PRIORITY FILING DATE: 2001-09-04
PRIORITY APPLICATION NUMBER: 10/001054
PRIORITY FILING DATE: 2001-11-30
PRIORITY APPLICATION NUMBER: 10/025866
PRIORITY FILING DATE: 2002-01-15
PRIORITY APPLICATION NUMBER: 10/081056
PRIORITY FILING DATE: 2002-02-20
PRIORITY APPLICATION NUMBER: 10/119480
PRIORITY FILING DATE: 2002-04-09

Query Match      81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRAPARAWAGSREHPGALLIRTRSWVWNOFVIEYAGEPVILGKLSVDVRCGE 60
DB 17 CMGRAPARAWAGSREHPGALLIRTRSWVWNOFVIEYAGEPVILGKLSVDVRCGE 76
QY 61 GRTKYLITGEGAGTVFVDEATGNHYTKSLDREKAOYLLAQAVDRASNRPLPSPSEF 120
DB 77 GRTKYLITGEGAGTVFVDEATGNHYTKSLDREKAOYLLAQAVDRASNRPLPSPSEF 136
QY 121 IIKQDINDNPPILPGLPYHATVEMSNVGTSVIQTVAHADDDPSYNSAKLYVTVLDGL 180
DB 137 IIKQDINDNPPILPGLPYHATVEMSNVGTSVIQTVAHADDDPSYNSAKLYVTVLDGL 196
QY 181 PEFVDPQTGVVTAIRNMRERTEEFVYVQAQDMGNGHGLSGSTTVTVLSDVNDP 240
DB 197 PEFVDPQTGVVTAIRNMRERTEEFVYVQAQDMGNGHGLSGSTTVTVLSDVNDP 256
QY 241 PKFQOSLYQSVSVETAGPGLVGRIRAOQDPLDGNALMAVSIIDGESSEAFSISTDLOGR 300
DB 257 PKFQOSLYQSVSVETAGPGLVGRIRAOQDPLDGNALMAVSIIDGESSEAFSISTDLOGR 316
QY 301 DGLITVKKPLDFESQRSYSTRVEXTNTLIDPAYLRGPFVDVASVRYAVODAPPEPAFTQ 360
DB 317 DGLITVKKPLDFESQRSYSTRVEXTNTLIDPAYLRGPFVDVASVRYAVODAPPEPAFTQ 376
QY 361 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRYSIIPHSDBPRCFSIQPEEGTITTAAP 420
DB 377 AAYHLTVPENKAPGTLVGOISAADLDSAPSPIRYSIIPHSDBPRCFSIQPEEGTITTAAP 436
QY 421 LDRPARAHNLTVALTELGMWGBERGWPVLVAEMSAAPAPQORSFVGSAGVIGPODSSA 480
DB 437 LDRPARAHNLTVALTELGMWGBERGWPVLVAEMSAAPAPQORSFVGSAGVIGPODSSA 496
QY 481 QASVVOVAIOITLNDNDNAPOLARBYDTFVCDSSAPQOLIOVTRALDRDVGNSHVSFOG 540
DB 499 QASVVOVAIOITLNDNDNAPOLARBYDTFVCDSSAPQOLIOVTRALDRDVGNSHVSFOG 518
QY 541 PLGPDANFTVQDNND-----LPA-----WFHPLMASASWHL----- 573
DB 519 PLGPDANFTVQDNNDGASALLPSRPARPRHAPYVLIELMDWGQALSTATVTVSVOR 578
QY 574 -----WPPARENGNPSAG 587
DB 579 CQPDGVSACMFEAHLASAAGLSTG 602

RESULT 13
US-10-238-183-98
; Sequence 98, Application US/10238183
; Publication No. US20030073183A1
; GENERAL INFORMATION:
```

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APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanabe, Collin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Ford, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3650R1C11
CURRENT FILING DATE: 2002-09-09
PRIORITY APPLICATION NUMBER: 10/197942
PRIORITY FILING DATE: 2002-07-18
PRIORITY APPLICATION NUMBER: 60/059114
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/063046
PRIORITY FILING DATE: 1997-10-24
PRIORITY APPLICATION NUMBER: 60/065027
PRIORITY FILING DATE: 1997-11-10
PRIORITY APPLICATION NUMBER: 60/079689
PRIORITY FILING DATE: 1998-03-27
PRIORITY APPLICATION NUMBER: 60/086478
PRIORITY FILING DATE: 1998-05-22
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PRIORITY FILING DATE: 1998-06-02
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PRIORITY FILING DATE: 1998-06-18
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PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090689
PRIORITY FILING DATE: 1998-06-25
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PRIORITY APPLICATION NUMBER: 60/091978
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PRIORITY APPLICATION NUMBER: 60/135729
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PRIORITY FILING DATE: 1999-05-25
PRIORITY APPLICATION NUMBER: 60/138385
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PRIORITY FILING DATE: 1999-06-22
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PRIOR FILING DATE: 2000-07-13
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PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1.3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

1 CWGRLLAPARAWAGSEHGPALILTRRSWVWVNFVIEEYAGPEVLLIGKLSVDVDRGE 60
17 CWGRLLAPARAWAGSEHGPALILTRRSWVWVNFVIEEYAGPEVLLIGKLSVDVDRGE 76
61 GRTKYLITGEGAGTAVVIDEATGNHVTSLDREERAOVYLLAAQAVDRASNRPLEPSEF 120
77 GRTKYLITGEGAGTAVVIDEATGNHVTSLDREERAOVYLLAAQAVDRASNRPLEPSEF 136
121 IIRGODINDNPIFFPLGPYHATVPKSNVGTSVIQTVAHDADDPSTGNSAKLYTYLVDGI 180
137 IIRGODINDNPIFFPLGPYHATVPKSNVGTSVIQTVAHDADDPSTGNSAKLYTYLVDGI 196
181 PFTSVDPQGVVATTAIPNMDRETOEERLVVIAQKDXGSHMGSLGSGSTTYTTLSPVNDNP 240
197 PFTSVDPQGVVATTAIPNMDRETOEERLVVIAQKDXGSHMGSLGSGSTTYTTLSPVNDNP 256
241 PKFPOSIVQPSVETAGPGLTVGLRLAODPDLDGNALMAYSIUDGSESAFISITDLOGR 300

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; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-98
Query Match      81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1,3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Db      257 PKFPOSILYQFSVETAGPGLVGRRAQDPDLGNALMAYSILDEGESEAFSISTDIQGR 316
;
Qy      301 DGLLTVRKPLDPESESRSYFRVEATNTLIDPAYLRGPFKQVAVRVAVODAPPEPFTQ 360
;
Db      317 DGLLTVRKPLDPESESRSYFRVEATNTLIDPAYLRGPFKQVAVRVAVODAPPEPFTQ 376
;
Qy      361 AAYHLTVPENKAPGTLVQISAADLSPASPIRYSILPHSDPEECFSIQPEEGTHTAAP 420
;
Db      377 AAYHLTVPENKAPGTLVQISAADLSPASPIRYSILPHSDPEECFSIQPEEGTHTAAP 436
;
Qy      421 LDREARAHMNTLVATLTELGMWGPGRGVPLLVAMWAPAPPRRSVGSVGVLPQSSA 480
;
Db      437 LDREARAHMNTLVATLTELGMWGPGRGVPLLVAMWAPAPPRRSVGSVGVLPQSSA 458
;
Qy      481 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAPGQLIYIRALDRDEVGNSSHVSPQG 540
;
Db      459 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAPGQLIYIRALDRDEVGNSSHVSPQG 518
;
Qy      541 PLGPANTVQDND-----LPA-----WHPILMASASGWLH--- 573
;
Db      519 PLGPANTVQDNDNDGASLLPLPSRPAPPRHAPYLVPIELMDWGQPALSTATVTVSVCR 578
;
Qy      574 -----WPPARGNQAPASQG 587
;
Db      579 CQPGGSVASCWPEAHLSAAGLSTG 602

RESULT 14
US-10-238-283-98
; Sequence 98, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238,283
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98

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; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-98
Query Match      81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1,3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

Qy      1 CMGRILAAPRAAAGREHGPALNTRRSWNNQFVEEYAGPPVYIGLHSDVDGE 60
;
Db      17 CMGRILAAPRAAAGREHGPALNTRRSWNNQFVEEYAGPPVYIGLHSDVDGE 76
;
Qy      61 GRTKYLTLGEGAGTFFVIDEATGNHVTKSIDREKAQYVLLAQRASNRPLEPSEF 120
;
Db      77 GRTKYLTLGEGAGTFFVIDEATGNHVTKSIDREKAQYVLLAQRASNRPLEPSEF 136
;
Qy      121 IIKGQDINDNPFIFPLGTYHATVPEMSVNGSVIQTVAHDADDPSYGNASALVTVVDGL 180
;
Db      137 IIKQDINDNPFIFPLGTYHATVPEMSVNGSVIQTVAHDADDPSYGNASALVTVVDGL 196
;
Qy      181 PFFSVDPQTGVVTRTAPNMDBRETOEEFLVVIQAKDMGSGMGLSGSTTVTVTLSDVNDP 240
;
Db      197 PFFSVDPQTGVVTRTAPNMDBRETOEEFLVVIQAKDMGSGMGLSGSTTVTVTLSDVNDP 256
;
Qy      241 PKFPOSILYQFSVETAGPGLVGRRAQDPDLGNALMAYSILDEGESEAFSISTDIQGR 300
;
Db      257 PKFPOSILYQFSVETAGPGLVGRRAQDPDLGNALMAYSILDEGESEAFSISTDIQGR 316
;
Qy      301 DGLLTVRKPLDPESESRSYFRVEATNTLIDPAYLRGPFKQVAVRVAVODAPPEPFTQ 360
;
Db      317 DGLLTVRKPLDPESESRSYFRVEATNTLIDPAYLRGPFKQVAVRVAVODAPPEPFTQ 376
;
Qy      361 AAYHLTVPENKAPGTLVQISAADLSPASPIRYSILPHSDPEECFSIQPEEGTHTAAP 420
;
Db      377 AAYHLTVPENKAPGTLVQISAADLSPASPIRYSILPHSDPEECFSIQPEEGTHTAAP 436
;
Qy      421 LDREARAHMNTLVATLTELGMWGPGRGVPLLVAMWAPAPPRRSVGSVGVLPQSSA 480
;
Db      437 LDREARAHMNTLVATLTELGMWGPGRGVPLLVAMWAPAPPRRSVGSVGVLPQSSA 458
;
Qy      481 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAPGQLIYIRALDRDEVGNSSHVSPQG 540
;
Db      459 QASRYOVAIQTLDENDNAPOLAEPYDTFVCDSPAAPGQLIYIRALDRDEVGNSSHVSPQG 518
;
Qy      541 PLGPANTVQDND-----LPA-----WHPILMASASGWLH--- 573
;
Db      519 PLGPANTVQDNDNDGASLLPLPSRPAPPRHAPYLVPIELMDWGQPALSTATVTVSVCR 578
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;
Db      579 CQPGGSVASCWPEAHLSAAGLSTG 602

RESULT 15
US-10-238-370-98
; Sequence 98, Application US/10238370
; Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME

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FILE REFERENCE: P3630R1C10
CURRENT APPLICATION NUMBER: us/10/238,370
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-238-370-98

Query Match 81.4%; Score 2651.5; DB 14; Length 781;
Best Local Similarity 84.5%; Pred. No. 1,3e-187;
Matches 527; Conservative 5; Mismatches 17; Indels 75; Gaps 4;

QY 1 CMGRAPARAWAGREHHPGALLTRRSWVWNOFPVIEEYAGPEPVILGKHSVDVNGE 60
DB 17 CMGRAPARAWAGREHHPGALLTRRSWVWNOFPVIEEYAGPEPVILGKHSVDVNGE 76
QY 61 GRTXYLLTGEAGTGVIDEATGNHVTKSLDREKQAYVLLAQVDRASNRPLEPSEF 120
DB 77 GRTXYLLTGEAGTGVIDEATGNHVTKSLDREKQAYVLLAQVDRASNRPLEPSEF 136
QY 121 IIKGODINDNPIEPLGPHATVPMSVGTSVIOVTAHDADDP8YGSATLYTVLDGL 180
DB 137 IIKVODINDNPIEPLGPHATVPMSVGTSVIOVTAHDADDP8YGSATLYTVLDGL 196
QY 181 PFFSVDPQGVVTRTAIPNMDRETOEFLVIOAKMGHMGGLSGTIVTVLSDVNDP 240
DB 197 PFFSVDPQGVVTRTAIPNMDRETOEFLVIOAKMGHMGGLSGTIVTVLSDVNDP 256
QY 241 PFFSVDPQGVVTRTAIPNMDRETOEFLVIOAKMGHMGGLSGTIVTVLSDVNDP 300
DB 257 PFFSVDPQGVVTRTAIPNMDRETOEFLVIOAKMGHMGGLSGTIVTVLSDVNDP 316
QY 301 DELTAVRKPLDFESORSYFRVEATNTLIDPAYLRGPFKDVASVRAVODAPPEPAFTQ 360
DB 317 DELTAVRKPLDFESORSYFRVEATNTLIDPAYLRGPFKDVASVRAVODAPPEPAFTQ 376
QY 361 AAYHATVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAP 420
DB 377 AAYHATVPENKAPGTLVQGISAADLSPASPIRYSILPHSDPERCFSTIQPEEGTHTAAP 436
QY 421 LDREARAWNTLVLTALTELGSWNGPERGWPLVAEWSAPAAPPGQSPVGSAGVIGQDSSA 480
DB 437 LDREARAWNTLVLTALTELGSWNGPERGWPLVAEWSAPAAPPGQSPVGSAGVIGQDSSA 458
QY 481 QASRVQVAIQTLDENNDAPQLAEPYDTFVCD5AAPGQLIQVIRALDRDEVANS5HVSFG 540

DB 519 PLGPDANFTVQDNRDGASLLP8RPAPPRAPFVILVPIELMDKQOPALSSATATVTSVCR 578
QY 574 -----WPAERGNQPASOG 587
DB 579 QPDGVSASCPWEAHL5AAGLSTG 602
Search completed: December 8, 2004, 11:34:28
Job time : 635.542 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 73.9315 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-7

Perfect score: 3259

Sequence: 1 CMGRLLAPARAWAGSRHFG.....LPSCQLPLGIPALGIVLCAS 620

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfltest.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1607	49.3	693	2	US-08-738-349-6
2	1607	49.3	693	2	US-09-919-497-55
3	1607	49.3	796	2	US-08-738-349-4
4	1602	49.2	796	1	US-08-188-228-58
5	1602	49.2	796	1	US-08-332-643-52
6	1602	49.2	796	1	US-08-332-638-58
7	1602	49.2	796	4	US-09-654-328-2
8	1596	49.0	796	2	US-08-738-349-2
9	1530.5	47.0	799	1	US-08-188-228-42
10	1530.5	47.0	799	1	US-08-332-638-42
11	1529.5	46.9	793	1	US-08-188-228-54
12	1529.5	46.9	793	1	US-08-332-643-48
13	1529.5	46.9	793	1	US-08-332-638-54
14	1493	45.8	615	2	US-08-738-349-12
15	1468	45.0	532	1	US-08-188-228-44
16	1468	45.0	532	1	US-08-332-638-44
17	1365.5	41.9	794	1	US-08-188-228-60
18	1365.5	41.9	794	1	US-08-332-643-54
19	1365.5	41.9	794	1	US-08-332-638-60
20	1136.5	34.9	653	1	US-08-188-228-46
21	1136.5	34.9	653	1	US-08-332-638-46
22	933.5	28.6	780	1	US-08-188-228-50
23	933.5	28.6	780	1	US-08-332-643-44
24	933.5	28.6	780	1	US-08-332-638-50
25	596	18.3	506	4	US-09-417-039-11
26	591	18.1	913	2	US-08-474-067-6

28	591	18.1	913	2	US-08-472-481-5	Sequence 5, Appl
29	586	18.0	837	2	US-08-474-067-7	Sequence 7, Appl
30	586	18.0	837	2	US-08-474-068A-7	Sequence 7, Appl
31	586	18.0	837	2	US-08-472-481-6	Sequence 6, Appl
32	580.5	17.8	555	2	US-08-453-702A-98	Sequence 98, Appl
33	576	17.7	556	1	US-07-998-003A-98	Sequence 98, Appl
34	576	17.7	556	1	US-08-453-274B-98	Sequence 98, Appl
35	576	17.7	556	1	US-08-453-695A-98	Sequence 98, Appl
36	576	17.7	556	1	US-08-268-161A-98	Sequence 98, Appl
37	576	17.7	556	3	US-09-099-635-98	Sequence 98, Appl
38	574.5	17.6	712	2	US-08-474-067-2	Sequence 2, Appl
39	574.5	17.6	712	2	US-08-474-067-5	Sequence 5, Appl
40	574.5	17.6	712	2	US-08-474-068A-2	Sequence 2, Appl
41	574.5	17.6	712	2	US-08-474-068A-5	Sequence 5, Appl
42	574.5	17.6	712	2	US-08-472-481-2	Sequence 2, Appl
43	574.5	17.6	717	2	US-08-474-067-4	Sequence 4, Appl
44	574.5	17.6	717	2	US-08-474-068A-4	Sequence 4, Appl
45	574.5	17.6	717	2	US-08-472-481-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shunji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 49.3%; Score 1607; DB 2; Length 693;
Best Local Similarity 50.5%; Pred. No. 2,2e-137;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

QY 1 CMGRLA-----APAR-----AMAGSRE--HGPALLATRRSWWNQFVIEEYAGPEPV 47
DB 13 CLGMCHSHAFAPBERGHLRPSFHGHKEKGEQVLRQSKGWMNQFVIEEYTGDPV 72
QY 48 LIGKLSHDVDRGEGRKTXLLTGEAGTVFVIDEAGNTHVTKSLDREKKAQVYLLAQAVD 107
DB 73 LVGRHSDIDSDGNIKTILSGEAGTIFVIDDSGNHAKTLDREERQYTLMAQAVD 132
QY 108 RASNPPLPPEPSEFIIKQDINDNPIFLGPYHATVPEMSVNGSVIQTVAHADDDPYG 167
DB 133 RDTNRPFLPPEPSEFIIKQDINDNPIFLGPYHATVPEMSVNGSVIQTVAHADDDPYG 192
QY 168 NSAKLVYTVLIDLPFFSVDPQTVGVRATAPMNDRETOEPEFLVVIQAKDMGSHMGLSGST 227
DB 193 NSAKLVYTVLIDLPFFSVDPQTVGVRATAPMNDRETOEPEFLVVIQAKDMGSHMGLSGST 252
QY 228 TVTVTLSDVNDNPPKPFPOSIVQSVSEAAVGEVGRYKADPDIGENGLVTYNIIVDGDG 287
DB 253 KVTITLTVNDNPPKPFPOSIVQSVSEAAVGEVGRYKADPDIGENGLVTYNIIVDGDG 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEQSRSYFVEATNTLIDPAYLRGPFKDVASVRY 347
DB 313 MESEFITTDETOEGVILKKEPVDETRKRAVSLVKEANVHIIDPKFISNGPFKDVTVKI 372
QY 348 AVQDAPEPFAFTQAAVHLTVPENKAPGTLVQGISAADLSPASIRYSILPHSDPERCF 407
DB 373 AVEDADEPMPFLAPSYIHEVOENAAAGTVGRVHAKDPDANSPIRISIDRHTDLDRPFT 432
QY 408 IOPEEGTHTAAPLDREARAHNTLVATLGLMNGWGERGVPLLVAMGAPAPQORSP 467
DB 433 INPDGFIKTKPDLREBTALNITVPAELI----- 463
QY 468 VGSAGVIGPOSSAQSRYOVAIOTLDENDNAPQLAEPYDFVCD-----AAPQOLIQVIR 523
DB 464 -----HNRHQAAPVPAIRVLDVNDNAKFAAPYEGFICSDQTKPLSNQPIVTIS 514
QY 524 ALDRDEVGNSSHVSPQGP--LGPDAFTVQDNRLPA-----WFHPLIM 565
DB 515 ADDKDDTANGPRPFLSPELIIHNPNFTVRDNRNTAGVYARRGFSRQKODLYLPIVI 574
QY 566 ASASSWLMHPPAERGNQPAQKSSLP-CG-RLPGLPSC 604
DB 575 -----SDGIPPMSTNTLTITKVCQDVNGALLSC 604

RESULT 2
US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773863
GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 49.3%; Score 1607; DB 4; Length 693;
Best Local Similarity 50.5%; Pred. No. 2,2e-137;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

QY 1 CMGRLA-----APAR-----AMAGSRE--HGPALLATRRSWWNQFVIEEYAGPEPV 47
DB 13 CLGMCHSHAFAPBERGHLRPSFHGHKEKGEQVLRQSKGWMNQFVIEEYTGDPV 72
QY 48 LIGKLSHDVDRGEGRKTXLLTGEAGTVFVIDEAGNTHVTKSLDREKKAQVYLLAQAVD 107
DB 73 LVGRHSDIDSDGNIKTILSGEAGTIFVIDDSGNHAKTLDREERQYTLMAQAVD 132
QY 108 RASNPPLPPEPSEFIIKQDINDNPIFLGPYHATVPEMSVNGSVIQTVAHADDDPYG 167
DB 133 RDTNRPFLPPEPSEFIIKQDINDNPIFLGPYHATVPEMSVNGSVIQTVAHADDDPYG 192
QY 168 NSAKLVYTVLIDLPFFSVDPQTVGVRATAPMNDRETOEPEFLVVIQAKDMGSHMGLSGST 227
DB 193 NSAKLVYTVLIDLPFFSVDPQTVGVRATAPMNDRETOEPEFLVVIQAKDMGSHMGLSGST 252
QY 228 TVTVTLSDVNDNPPKPFPOSIVQSVSEAAVGEVGRYKADPDIGENGLVTYNIIVDGDG 287
DB 253 KVTITLTVNDNPPKPFPOSIVQSVSEAAVGEVGRYKADPDIGENGLVTYNIIVDGDG 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEQSRSYFVEATNTLIDPAYLRGPFKDVASVRY 347
DB 313 MESEFITTDETOEGVILKKEPVDETRKRAVSLVKEANVHIIDPKFISNGPFKDVTVKI 372
QY 348 AVQDAPEPFAFTQAAVHLTVPENKAPGTLVQGISAADLSPASIRYSILPHSDPERCF 407
DB 373 AVEDADEPMPFLAPSYIHEVOENAAAGTVGRVHAKDPDANSPIRISIDRHTDLDRPFT 432
QY 408 IOPEEGTHTAAPLDREARAHNTLVATLGLMNGWGERGVPLLVAMGAPAPQORSP 467
DB 433 INPDGFIKTKPDLREBTALNITVPAELI----- 463
QY 468 VGSAGVIGPOSSAQSRYOVAIOTLDENDNAPQLAEPYDFVCD-----AAPQOLIQVIR 523
DB 464 -----HNRHQAAPVPAIRVLDVNDNAKFAAPYEGFICSDQTKPLSNQPIVTIS 514
QY 524 ALDRDEVGNSSHVSPQGP--LGPDAFTVQDNRLPA-----WFHPLIM 565
DB 515 ADDKDDTANGPRPFLSPELIIHNPNFTVRDNRNTAGVYARRGFSRQKODLYLPIVI 574
QY 566 ASASSWLMHPPAERGNQPAQKSSLP-CG-RLPGLPSC 604
DB 575 -----SDGIPPMSTNTLTITKVCQDVNGALLSC 604

RESULT 3
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sumao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rai

Page 3

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.123-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 49.3%; Score 1607; DB 2; Length 796;
Best Local Similarity 50.5%; Pred. No. 2.8e-137;
Matches 324; Conservative 98; Mismatches 133; Indels 86; Gaps 10;

1 CWRGLA-----APAR-----AMAGSRF--HGPALLTRRSKVMNQFVIEEYAGPEV 47
13 CLGMLCHSHAFAPERRGHLRPSFHGHEKKGQVLRKSGVMNQFVIEEYAGPEV 72
48 LIGLHSDVDREGGRKYLITGEGAGTVFIDEATGNINHTKSLDREKAQVYLLAQAVD 107
73 LVGRHSDIDSGDNKIKYLSGEGAGTIFVIDKSGNINHTKSLDREKAQVYLLAQAVD 132
108 RASNRPLEPPESEFIKGGDINDNPPFLPGPHYATVPMSNVGTSVYQVTAHADADPSYG 167
133 RDTNRPLEPPESEFIKGGDINDNPPFLPGPHYATVPMSNVGTSVYQVTAHADADPSYG 192
168 NSAKLVYTVLDGPEFSVDPQTGVRTAIPNMDREKKEEFLVYQAKDGMGSHGSLGSGT 227
193 NSAKLVYTVLDGPEFSVDPQTGVRTAIPNMDREKKEEFLVYQAKDGMGSHGSLGSGT 252
228 TVTTLSDVNDNPPKPEPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDGE 287
253 KVTITLTDVNDNPPKPEPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDGE 312
288 SEAFSISTDLQGDGLTVRKPLDPESQRSYFRVEATNTLIDPAYLRGPFKDVASVY 347
313 MESFEITTDYETQEGVILKKEVPDFTETRAVSLKEANVHIDPKFISNGPFKDTVTAKI 372
348 AVQDPEPPAFAQAAYHLLTPENKAPGTLVQGISADLSDSPASPIRYSILHSDPERCF 407
373 AVEDDEPPEMFLAPYIHEVQENAAAGTVGRVAKDPAANSPIRYSIDHIDLDLFT 432
408 IQPEEGTHTAALPDRERAMENLTVLATELGMSNGPERGWPLIVAEWSAPAAPQSRP 467
433 INPEDGFIKTKPLDREETAMLNTVFAAEI----- 463
468 VGSAGIIPQDSSAQSRVQVAILCTLDENDNAPOLAEPTDFVQDS---AAPGLIQVIR 523
494 -----HNHQAQKVPVALRVLDVNDNAKFPAPYEGFICSDQTKPSNPIVITIS 514
524 ALDRDEVGNSSHVSEFGP--LGPANFTVQDNRLPA-----WHPILM 565
545 ADDKODTANGPRFISLPEIITHNPNFTVRDNRDNTAGVYARAGGFSKODLYLLPIVI 574
566 ASASSMLWHPARERGNQAPASQKSSSLP-CG-RLEGALPSC 604
575 -----SDGGLPMSSTNLTITKVCQCDVAGALLSC 604

RESULT 4
US-08-188-228-58

Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Boston
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 49.2%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 7.9e-137;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

1 CWRGLA-----APAR-----AMAGSRF--HGPALLTRRSKVMNQFVIEEYAGPEV 47
13 CLGMLCHSHAFAPERRGHLRPSFHGHEKKGQVLRKSGVMNQFVIEEYAGPEV 72
48 LIGLHSDVDREGGRKYLITGEGAGTVFIDEATGNINHTKSLDREKAQVYLLAQAVD 107
73 LVGRHSDIDSGDNKIKYLSGEGAGTIFVIDKSGNINHTKSLDREKAQVYLLAQAVD 132
108 RASNRPLEPPESEFIKGGDINDNPPFLPGPHYATVPMSNVGTSVYQVTAHADADPSYG 167
133 RDTNRPLEPPESEFIKGGDINDNPPFLPGPHYATVPMSNVGTSVYQVTAHADADPSYG 192
168 NSAKLVYTVLDGPEFSVDPQTGVRTAIPNMDREKKEEFLVYQAKDGMGSHGSLGSGT 227
193 NSAKLVYTVLDGPEFSVDPQTGVRTAIPNMDREKKEEFLVYQAKDGMGSHGSLGSGT 252
228 TVTTLSDVNDNPPKPEPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDGE 287
253 KVTITLTDVNDNPPKPEPQSLYQFSVETAGPGLVGRRAQDPDLGNALMAYSLDGE 312
288 SEAFSISTDLQGDGLTVRKPLDPESQRSYFRVEATNTLIDPAYLRGPFKDVASVY 347
313 MESFEITTDYETQEGVILKKEVPDFTETRAVSLKEANVHIDPKFISNGPFKDTVTAKI 372

DQ 1 CMGRLA-----APAR-----AWAGSKE--HGCPALLTRRSWVNNQFFVIEEYAGEPPV 4
 ||| :|| | || ||
D5 13 CLGMLCHSAFAPERSGHLRPSFGHHEKKGEGQLTRSKRGVMNQGFFVIEEYTGPDVP 72

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,466
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 49.2%; Score 1602; DB 1; Length 796;
Best Local Similarity 50.4%; Pred. No. 7,9e-137;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

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QY 1 CMGRLA-----APAR-----AMAGSR--HPGPAALTRRSVMNQFVIEYAGPEV 47
DB 13 CLGMLCHSHAFAPERRGHLRPSFHGHKEKKGQVLOQSKRGVMNQFVIEYAGPEV 72
QY 48 LIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTXSLDREKAQYVLLAQA 107
DB 73 LVGRHSDDIDSGDGNIKYILSGEGAGTIFVIDKSGNTHATKTLDRERAAQYTLMAQAV 132
QY 108 RASNRPLEPSEFEIIGKODINDNPIFLPGYHATVPMSVNGTSTVQTVAHADDDPSYG 167
DB 133 RDNRLPEPSEFEIIVQDINDNPEFLHETTHANVPERSVNGTSTVQTVAHADDDPSYG 192
QY 168 NSAKLVYTLVDGLPEFSVDPQTGVVTAIPNMDRETOEFLVVIQAKDMGSMGSLGST 227
DB 193 NSAKLVYTLVDGLPEFSVDPQTGVVTAIPNMDRETOEFLVVIQAKDMGSMGSLGST 252
QY 228 TVTVTLSDVNDNPPKPPQSLYQFSVETAGPGLVGRADPDLDGNALMAYSILDEG 287
DB 253 KVTITLVDNDNPPKPPQSLYQFSVETAGPGLVGRADPDLDGNALMAYSILDEG 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEQSRSYFVEATNTLIDPAYLRGPFKDVASVY 347
DB 313 MESFEITTDYETQESVILKPKVPDEFETERAYSLKVEAAVHIDPKFISNGPFKDVYVXI 372
QY 348 AVQDAPEPPATQAAYHLTVPENKAPGLVQGISAADLSPASIRISILPHSPERCS 407
DB 373 SVEADPEPPATQAAYHLTVPENKAPGLVQGISAADLSPASIRISILPHSPERCS 432
QY 408 IOPEEGTHTAALDREARAHNLTATLTELQMSWGPGRGWPLVAEWSAPAPQPSR 467
DB 433 INPEEGTHTAALDREARAHNLTATLTELQMSWGPGRGWPLVAEWSAPAPQPSR 463
QY 468 VGSAGVIFQDSSAQSRVQVAIQTLDENDNAQALAEPTVTCDS---AAPGLQIVR 523
DB 464 VGSAGVIFQDSSAQSRVQVAIQTLDENDNAQALAEPTVTCDS---AAPGLQIVR 514
QY 524 ALDREVGNSHVSFGP--LGPDAFTVQDNRLDPA-----WFHPLM 565
DB 515 ADDKDDTANGPRFTISLPPEIITHNPFYTRDNRDNTAGVYARRGGFSRQKODLYLLPIVI 574
QY 566 ASASSWLHWPAPERGQNPASQGSKSLP-CG-RLPGLPSC 604
DB 575 ASASSWLHWPAPERGQNPASQGSKSLP-CG-RLPGLPSC 604
```

RESULT 7
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
of Inflammatory Disease Using Cadherin-11 Modulating Agents

FILE REFERENCE: B0801/7187/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 49.2%; Score 1602; DB 4; Length 796;
Best Local Similarity 50.4%; Pred. No. 7,9e-137;
Matches 323; Conservative 98; Mismatches 134; Indels 86; Gaps 10;

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QY 1 CMGRLA-----APAR-----AMAGSR--HPGPAALTRRSVMNQFVIEYAGPEV 47
DB 13 CLGMLCHSHAFAPERRGHLRPSFHGHKEKKGQVLOQSKRGVMNQFVIEYAGPEV 72
QY 48 LIGKLSHDVDRGEGRTKYLITGEGAGTVFIDEATGNHVTXSLDREKAQYVLLAQA 107
DB 73 LVGRHSDDIDSGDGNIKYILSGEGAGTIFVIDKSGNTHATKTLDRERAAQYTLMAQAV 132
QY 108 RASNRPLEPSEFEIIGKODINDNPIFLPGYHATVPMSVNGTSTVQTVAHADDDPSYG 167
DB 133 RDNRLPEPSEFEIIVQDINDNPEFLHETTHANVPERSVNGTSTVQTVAHADDDPSYG 192
QY 168 NSAKLVYTLVDGLPEFSVDPQTGVVTAIPNMDRETOEFLVVIQAKDMGSMGSLGST 227
DB 193 NSAKLVYTLVDGLPEFSVDPQTGVVTAIPNMDRETOEFLVVIQAKDMGSMGSLGST 252
QY 228 TVTVTLSDVNDNPPKPPQSLYQFSVETAGPGLVGRADPDLDGNALMAYSILDEG 287
DB 253 KVTITLVDNDNPPKPPQSLYQFSVETAGPGLVGRADPDLDGNALMAYSILDEG 312
QY 288 SEAFSISTDLQGRDGLTVRKPLDPEQSRSYFVEATNTLIDPAYLRGPFKDVASVY 347
DB 313 MESFEITTDYETQESVILKPKVPDEFETERAYSLKVEAAVHIDPKFISNGPFKDVYVXI 372
QY 348 AVQDAPEPPATQAAYHLTVPENKAPGLVQGISAADLSPASIRISILPHSPERCS 407
DB 373 SVEADPEPPATQAAYHLTVPENKAPGLVQGISAADLSPASIRISILPHSPERCS 432
QY 408 IOPEEGTHTAALDREARAHNLTATLTELQMSWGPGRGWPLVAEWSAPAPQPSR 467
DB 433 INPEEGTHTAALDREARAHNLTATLTELQMSWGPGRGWPLVAEWSAPAPQPSR 463
QY 468 VGSAGVIFQDSSAQSRVQVAIQTLDENDNAQALAEPTVTCDS---AAPGLQIVR 523
DB 464 VGSAGVIFQDSSAQSRVQVAIQTLDENDNAQALAEPTVTCDS---AAPGLQIVR 514
QY 524 ALDREVGNSHVSFGP--LGPDAFTVQDNRLDPA-----WFHPLM 565
DB 515 ADDKDDTANGPRFTISLPPEIITHNPFYTRDNRDNTAGVYARRGGFSRQKODLYLLPIVI 574
QY 566 ASASSWLHWPAPERGQNPASQGSKSLP-CG-RLPGLPSC 604
DB 575 ASASSWLHWPAPERGQNPASQGSKSLP-CG-RLPGLPSC 604
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RESULT 8
US-08-738-349-2
Sequence 2, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawasaki, Shinji
APPLICANT: Tsujimura, Akiyoshi

```

APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1223-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match
Best Local Similarity 49.0%; Score 1596; DB 2; Length 796;
Matches 317; Conservative 97; Mismatches 127; Indels 84; Gaps 8;

QY 15 SREHP-----GPAALLTRRSWVWNOQFVIEBYEAPPEVLIGKLSHDYDRGEGRT 63
DB 29 SHLPSPFHGHEKKEQGVLORSKRGWVWNOQFVIEBYETGPDVILVGRHSIDSDGNI 88
QY 64 KYLLTGGAGTVFVIDATGNIHTKSLDREKAKQVYLLAQVDRASNRLPEPSEFTIK 123
DB 89 KYILSGGAGTIFVIDKSGNIHATKTLDEERAKQYLLMAQAVDRITNRLPEPSEFTIK 148
QY 124 QGDINDNPPIPLGPGYHATVPENMNGSVIQTVAHDADDPSSYNSAKLVYTVLDELPPFF 183
DB 149 VQDINDNPPELHITIANVPENNGSVIQTVAHDADDPPTGNSAKLVYSLDEQPIYF 208
QY 184 SVDPQTEGVTALTNMDREFLOEFLVYIAKMGHNGGLSGSTTVYVTLSDVNDNPKYF 243
DB 209 SVEAQOTGIITFALPNMDREKKEHYVYIAKMGHNGGLSGSTTVYVTLSDVNDNPKYF 268
QY 244 POSLYGSVYETAGPGTLVGRRLRAODPDLGDNALMAYSLIDGSGSEAFSISTDLOGRDL 303
DB 269 POSLYGMSVSEANPGEVEGRVAKADPDIGENGLVYINIVDGGGIELFELITDYEQDVY 328
QY 304 LTVRKLDPESQRSYFRVATNTLLIDPAYLRGPFKDVASVAVAVQDAEPPAFTQAAV 363
DB 329 VKLKKPVPDFETKRAYSIKIEANVHIDPKFISNGPFDQTVYKISVEDADEPMPFAPSY 388
QY 364 HLTVBEKAPGTLVGOISADLDSPASPIRYSLTSPSDPERCSIQPEEGTITTAAPLR 423
DB 389 IHEVQENAAAGTVGVGRHAKDPDANSPIRYSIDRHTDLPFTINPEDEFTIKTPXLR 448

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QY 424 EAPAHNLTVALTEIGMSWGPGRGVNPLVAMSNAPAPPOKSPVGNVGIPODSSAQS 483
DB 449 ESTAMINISVFAET-----HNRQET 470
QY 484 RVQVALIQTLDENDNAPQLAEPYDFVCDAAPE-----GQLIYIRALDRDEGNSSHSFQ 539
DB 471 KVPVAILRVLDVNDAPKRAPEYEGICESDHPKLSNPPIYTVAGADQDDIAPNPPRIFS 530
QY 540 GP-LGPDANFTVQDNRDLPA-----WFHPLMASASSWILHMPAERGN 581
DB 531 LPPEIMHNPNFTVRNDRNTAGVVARRGFSRQKDFYILPIVI-----SDGGI 579
QY 582 OPASQKSSLP-CG-RUGALPSC 604
DB 580 PPMSTNTLITIKCCGVNGALLSC 604

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match
Best Local Similarity 47.0%; Score 1530.5; DB 1; Length 799;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;

QY 23 LLRTSRWVWNOQFVIEBYEAPPEVLIGKLSHDYDRGEGRTKYLLTGGAGTVFVIDEAT 82
DB 56 LNRSGGWNWNOQFVIEBYEAPPEVLIGKLSHDYDRGEGRTKYLLTGGAGTVFVIDEAT 115
QY 83 GNIHVTSLDREKAKQVYLLAQAVDRASNRLPEPSEFTIKQGDINDNPPIPLGPGYHAT 142

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116 GDIHAIKRLDREKAEYTLTAQAVDMETNKPDPSEFIITKVQDINNAPFNGPHYAT 175
143 VPEMSNGTSTVITQVTAHDADDPSTGNSAKLYVTLDGLPFPSVDPOGTGVRTAIPNMRE 202
176 VPEMSITIGSTVNTATADDDPVYGNASAKLYVSIIEGQYFPISEPTAIIKTALPNNDR 235
203 TOSEFLVVIQAKMGKHGSGSTVTVLTSDVNDNPKPKPQSLYQFSVETAPGTLV 262
236 AKERYLVVIQAKMGKHGSGSTVTVLTSDVNDNPKPKPQSLYQFSVETAPGTLV 295
263 GRLLAQPDPDLGNALMAYSLIDGSGSEAFSISTDLQGRDGLTVRKPLDFESQSYSEFV 322
296 GRVAKNDQDIGNAQSVDIIDGGDTALFEITSDAQADGVIRLRKPLDEFETKSYTLKV 355
323 EANTVLIDPAYLRGPFEDVASVRVAVQDAPPEPAFOAHLVPEPKAPGLTVQOISA 382
356 EAAHNIHIDPRFSGRPFEDTATVKI VEDADEPVPFSSPTVLLSEHNAALNSVIGQVTA 415
383 ADLSPASPIRYSILPHSDPERCFESIQPEEGTHTAAPLDREARAHNLTVALTELGMSW 442
416 RDPITSSPIRFSIDRHTDLERQFNINADGKITLATPDLRELISVWHNISITATEI 471
443 GPERGWVPLVAEMSAAPAPQSPVGSVAVGIPODSSAQASRVQVAIQTLDENDNAQOLA 502
472 -----RMSQISRVPAIKVLDVNDNAEFA 497
503 EPYDTFVCDASAPGOLIOVIRALDRDEVGNSHVSFOGAPGPD---ANFTVQDNRD--- 555
498 SEYEAFLCENGRPGQVITQVSAMDKDPKNGHF--FLYSLLEPMANNPFTIKKEDNLS 555
556 -----LPWFHPLLMASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 600
556 SILAKENGFNROKQEVYLLPIVI-----SDSGNPPLSSTLTITRVCGCSNDGV 604
601 LPSCQ-----LPLGI---PALGIYLC 618
605 VQSCNVEAYVPLIGLSMGALITALLAC 630

RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302

```

```

REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 47.0%; Score 1530.5; DB 1; Length 799;
Best Local Similarity 47.9%; Pred. No. 2,6e-130;
Matches 300; Conservative 110; Mismatches 135; Indels 81; Gaps 9;

23 LKTRRSWVWQPFYIEYAGRPVILGKLSHDVDRGEGRTXYLLTGAGGVFIYDEAT 82
56 LKRSKGMWVWQPFYIEYAGRPVILGKLSHDVDRGEGRTXYLLTGAGGVFIYDEAT 115
83 GNHTYKSLDREKAEYTLTAQAVDMETNKPDPSEFIITKVQDINNAPFNGPHYAT 142
116 GDIHAIKRLDREKAEYTLTAQAVDMETNKPDPSEFIITKVQDINNAPFNGPHYAT 175
143 VPEMSNGTSTVITQVTAHDADDPSTGNSAKLYVTLDGLPFPSVDPOGTGVRTAIPNMRE 202
176 VPEMSITIGSTVNTATADDDPVYGNASAKLYVSIIEGQYFPISEPTAIIKTALPNNDR 235
203 TOSEFLVVIQAKMGKHGSGSTVTVLTSDVNDNPKPKPQSLYQFSVETAPGTLV 262
236 AKERYLVVIQAKMGKHGSGSTVTVLTSDVNDNPKPKPQSLYQFSVETAPGTLV 295
263 GRLLAQPDPDLGNALMAYSLIDGSGSEAFSISTDLQGRDGLTVRKPLDFESQSYSEFV 322
296 GRVAKNDQDIGNAQSVDIIDGGDTALFEITSDAQADGVIRLRKPLDEFETKSYTLKV 355
323 EANTVLIDPAYLRGPFEDVASVRVAVQDAPPEPAFOAHLVPEPKAPGLTVQOISA 382
356 EAAHNIHIDPRFSGRPFEDTATVKI VEDADEPVPFSSPTVLLSEHNAALNSVIGQVTA 415
383 ADLSPASPIRYSILPHSDPERCFESIQPEEGTHTAAPLDREARAHNLTVALTELGMSW 442
416 RDPITSSPIRFSIDRHTDLERQFNINADGKITLATPDLRELISVWHNISITATEI 471
443 GPERGWVPLVAEMSAAPAPQSPVGSVAVGIPODSSAQASRVQVAIQTLDENDNAQOLA 502
472 -----RMSQISRVPAIKVLDVNDNAEFA 497
503 EPYDTFVCDASAPGOLIOVIRALDRDEVGNSHVSFOGAPGPD---ANFTVQDNRD--- 555
498 SEYEAFLCENGRPGQVITQVSAMDKDPKNGHF--FLYSLLEPMANNPFTIKKEDNLS 555
556 -----LPWFHPLLMASASSWLHMPAERGNOPASQKSSSL-PCG-RLPGA 600
556 SILAKENGFNROKQEVYLLPIVI-----SDSGNPPLSSTLTITRVCGCSNDGV 604
601 LPSCQ-----LPLGI---PALGIYLC 618
605 VQSCNVEAYVPLIGLSMGALITALLAC 630

RESULT 11
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302

```

STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 46.9%; Score 1529.5; DE 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 3.1e-130;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

23 LLRTRRSMWNQFVIEEYAGPEPVILGKHSVDNREGSKYLLTGEAGTYFVDEAT 82
49 LNRKRGWVNMQFVLEFSGPEPILVGRHTLDLPSSKIKYILSGDAGTIFQINDVT 108
83 GNIHVTSLDREKAQYVLLAQAADVRASNPLEPPSEFIKQDINDNPPIPLGPHAT 142
109 GDIAIKRLDREKAEYTLTAQAADVDMETSKLEPPSEFIKQDINDNPEFLNGPYHAT 168
143 VPMSNVTGVTIQTADDDPSYNSAKLVYTVLDGLPFFSVDPQTGVRTAIPNMDRE 202
169 VPMSILGTSTVNTATDADDPYNSAKLVYSILGQPYFSIEPETAIITKIALPNMDRE 228
203 TOEEFLVIOAKMGHMGSLGSTVTVTLSDVNDNPKFPOSTLYQFSVETAGGTLV 262
229 AKELYLVIAQKMGHSGSLGSTTTLTVLTDVNDNPKFQSLVHFVPELVGTAL 288
263 GRAPADPDLDNNALNAYSLDGBGEAFSISTDLQGRDGLTVRKLDPFESORSYFRV 322
289 GRVANKQDIDGENAOSYDIIDSDGTALFEITSDAQAODGIIRLRKPLFEETKSYTLMD 348
323 EATYLLDPAVLRGPKDVAAYVAVQADPEPPAFTQAAYHLTVENKAPGLVQISA 382
349 EAANVHTDPRFSGRGPDKTATYKIVVEDADPEPVSSPYLLLENNALNSVIGQVTA 408
409 RDPDITSSPIRFSIDRTDLEQFINADGKITLTPLDRELNVNHTIATET----- 464
443 GPERGWVPLVAEMSAAPAPQSPVGSANGIPQDSSAQASRQVAILQLDENDAPOLA 502
465 -----RNSQISRPVPAIKVLVDNDADEPA 490
503 EPYDFTVCDSAPAGQLQVIRALDRBVGNSHVSFQGLGPD---ANFTVQDNRD--- 555

DB 491 SEYEAFLENGKRGVIOVTSAMDQDPKNCHY--FLYSLLPEWNNPFIKXNEDNSL 548
QY 556 -----LPAFHPILIMASASWMLWMPAERGNQAPASQKSSL-PCG-RLPGA 600
DB 549 SLLAHNGNPKQKQEVILLPIII-----SDSGNPPLSSTITLITVCCGSNDV 597
QY 601 LPSCQ-----LPLGI--PALGIYLC 618
DB 598 VQSCVNEAVVPLGISMALIAIILAC 623

RESULT 12
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 46.9%; Score 1529.5; DE 1; Length 793;
Best Local Similarity 47.8%; Pred. No. 3.1e-130;
Matches 299; Conservative 111; Mismatches 135; Indels 81; Gaps 9;

23 LLRTRRSMWNQFVIEEYAGPEPVILGKHSVDNREGSKYLLTGEAGTYFVDEAT 82
49 LNRKRGWVNMQFVLEFSGPEPILVGRHTLDLPSSKIKYILSGDAGTIFQINDVT 108
83 GNIHVTSLDREKAQYVLLAQAADVRASNPLEPPSEFIKQDINDNPPIPLGPHAT 142
109 GDIAIKRLDREKAEYTLTAQAADVDMETSKLEPPSEFIKQDINDNPEFLNGPYHAT 168
143 VPMSNVTGVTIQTADDDPSYNSAKLVYTVLDGLPFFSVDPQTGVRTAIPNMDRE 202
169 VPMSILGTSTVNTATDADDPYNSAKLVYSILGQPYFSIEPETAIITKIALPNMDRE 228

STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/738,349
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/364,439
 FILING DATE:
 APPLICATION NUMBER: US 08/112,061
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. P.
 REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 02481.1323-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 615 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-738-349-12

Query Match 45.8%; Score 1493; DB 2; Length 615;
 Best Local Similarity 50.9%; Pred. No. 4,4e-127;
 Matches 308; Conservative 92; Mismatches 123; Indels 82; Gaps 15;

20 GPALLRRRWVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 79
 39 GGVVQRKRGWVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 98
 80 EATGNIVTKSLDREERAGVYLAQAVDRASNPPLPSPFFIKGGINDPPIFLGY 139
 99 DKSINIAKTLDREERAGVYLAQAVDRASNPPLPSPFFIKGGINDPPIFLGY 157
 140 HATVPKSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLGLPFSVDPQTGVVTAIPM 199
 158 HANVPKSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLGLPFSVDPQTGVVTAIPM 217
 200 DRETOEFLVYIAKMGVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 259
 218 DREKEEYVYIAKMGVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 276
 260 TLVGRLLAODPDLDGNALMAYSILDEGESEAFSITDLQGRDGLTVRKPLDPESQSYS 319
 277 EGVGRVAKXDPDLDGNALMAYSILDEGESEAFSITDLQGRDGLTVRKPLDPESQSYS 332
 320 FRVATNTLLDPAYLRGPRKDVASRVANQDAPPEPAFTQAAYHILTEENKAPFTLVGQ 379
 333 LK-EAANVHIDPFKISNGPKDVTYKI-VEDADEPMLAPBYIHEVENMAAGTVGR 390
 380 ISADJDSPPSPRYSLIPHSDEPCFSIQPEEGITHTAAPLDREARAFNLTVALTEIG 439
 391 VHAQDPDANSP-RYSIDRHTDLPFTINPEDGFIKTKPLDRETAFLNI-VFAAEI- 448
 440 WMSGPERGWVPLVAEKSAAPAPQASVGSANGIQDSSAQASRVQVALIQLDENDNP 499
 449 -----HNRHQEKVPAIRVLVDVNDNP 470
 500 QLAEPYDFVCDAAFGQLIQTIRALDRDEGVNSHVSFGPFGPD---ANFTVQDNRDL 556
 471 KFAAPRGFTICSDKXSNQ-PIVTSADDDDDIANGPFITSLP--PEIHNPNTVQDNRDN 527
 557 PA-----WFHPLMASASSWLMHPAERGNQASQKSSSLP-CG-RLPG 599

DB 528 TAGVYARRGFSRQKODYLLPIVI-----SDGIDPMSSTNTLTKVCGCDVNG 576
 QY 600 ALPSC 604
 DB 577 ALLSC 581

RESULT 15
 US-08-188-228-44
 Sequence 44, Application US/08188228
 Patent No. 5597725
 GENERAL INFORMATION:
 APPLICANT: Suzuki, Shintaro
 TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bortun
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/188,228
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,460
 FILING DATE: 19 APR 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/872,643
 FILING DATE: 17 APR 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5597725 and, Grete E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31340
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 532 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-188-228-44

Query Match 45.0%; Score 1468; DB 1; Length 532;
 Best Local Similarity 54.6%; Pred. No. 6,5e-125;
 Matches 271; Conservative 89; Mismatches 98; Indels 38; Gaps 1;

23 LLTRRSWVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 82
 56 LNRKRGWVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 115
 83 GNIVTKSLDREERAGVYLAQAVDRASNPPLPSPFFIKGGINDPPIFLGYHAT 142
 116 GDIAIRKLDREERAGVYLAQAVDRASNPPLPSPFFIKGGINDPPIFLGYHAT 175
 143 VPMSNVGTSVIQTVAHDADDPYSGNSAKLVYTVLGLPFSVDPQTGVVTAIPM 202
 176 VPEMSILGTSTVNTVAIDADDPYSGNSAKLVYTVLGLPFSVDPQTGVVTAIPM 235
 203 TQEEFLVYIAKMGVWVNFVIEEYAGPEVYLGLKHSVDVREGGTYLITGEAGTVFVID 262

Wed Dec 8 11:46:33 2004

us-09-788-051-7.rat

Page 11

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Db 236 AKERYLVVIOAKDMGSHSGGIGTTLTVLTVLVNDNPKFAQSLYHPSVPEDEVILGTAI 295
QY 263 GRLRQDPDLGDNALMAYSLIDGEGSEAFSISTDLQGRDGLTVRKPLDFESQSRYSFRV 322
Db 296 GRVXANDODIGENAOSSYDITIDGDTALFELTSDAQOQDGVIRLRKPLDFETKKSITLKV 355
QY 323 EATNTLIDPAYLRGPFKQVAVRVAVODAPPEPPAFTQAAVHLYPENKAPGTLVQISA 382
Db 356 EAANHIDPFRSGRGPFKDTATVKIIVEDADEPPFSSPTLYLEVHENAALNSVIGQVTA 415
QY 383 ADLSPASPIRYSILPHSDPERCFISOPEEGTIHTAAPLDREARAHNLTVLATELGMSW 442
Db 416 RDPDITSSPIRFSIDRHTDLERQENINADDKITLATPLDRELsvMINISITATEI----- 471
QY 443 GPERGWVPLVAEWSAPAPQORSPVGSVGIPODSSAQASRVQVAIQTLDENNDAPOLA 502
Db 472 -----RNHSQISRVPAIKVLDVNDNAPEFA 497
QY 503 EPYDTFVCGDSAPQOL 518
Db 498 SEYBAFLCENGKPGQV 513
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Search completed: December 8, 2004, 10:01:12
Job time : 76.9315 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 3.88194 Seconds
(without alignments)

1189.717 Million cell updates/sec

Title: US-09-788-051-8

Perfect score: 259
Sequence: 1 PSEPIKQDINDNPPIFPL.....EMSNVGTSVIQTADADDP 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 segs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR.79.*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	73.0	796	2 A38992	cadherin 11 precu
2	187	72.2	796	2 I48277	cadherin-11 - mus
3	187	72.2	796	2 I48556	cadherin-11 - mus
4	187	72.2	796	2 A53584	OB-cadherin precu
5	186	71.8	793	2 D38992	cadherin 8 - huma
6	177	68.3	790	2 G02678	cadherin-14 - huma
7	172	66.4	785	2 I50180	cadherin-7 - chick
8	171	66.0	790	2 I51638	F-cadherin - Afri
9	166	64.1	790	2 I37016	cadherin-6 - huma
10	164	63.3	789	2 I52701	K-cadherin - rat
11	162	62.5	794	2 I50178	cadherin-6B - chlc
12	162	62.5	794	2 I59372	cadherin 12 - huma
13	144	55.6	784	1 ITHUC5	cadherin 5 precu
14	141	46.7	871	2 S47518	cadherin - African
15	111	42.9	713	2 B38992	cadherin 13 precu
16	106	40.9	712	1 IUMSC1	T-cadherin precu
17	106	40.9	717	2 I51206	T-cadherin 2 - chi
18	106	40.9	877	1 IUBOCN	N-cadherin precu
19	106	40.9	906	1 ITHUCN	cadherin 2 precu
20	106	40.9	912	1 ITHUCN	N-cadherin precu
21	106	40.9	1043	1 ITHUC1	desmoglein 1 precu
22	106	40.9	1049	1 ITHUC1	cadherin-related t
23	106	40.9	5147	1 IUFFRM	MEG1 protein - ra
24	104	40.2	4351	2 T00252	DN-cadherin - frui
25	103	39.8	3097	2 T00021	N-cadherin precu
26	102	39.4	906	1 IUMSCN	N-cadherin 2 precu
27	100	38.6	906	1 IUXLC2	desmocollin - bovi
28	99	38.2	896	2 I45858	desmocollin 1b pre
29	98	37.8	732	1 IUCRCH	B-cadherin precu

30	98	37.8	847	1 ITHUD8	desmocollin 3b pre
31	98	37.8	901	1 ITHUDA	desmocollin 3a pre
32	98	37.8	1117	2 S38673	desmoglein 2 - hum
33	97	37.5	809	1 ITHODD	desmocollin 2b pre
34	97	37.5	863	1 ITHODC	desmocollin 2a pre
35	96	37.1	905	1 ITHYCL	N-cadherin 1 precu
36	95	36.7	770	2 B48910	desmocollin 1b pre
37	95	36.7	824	2 A48910	desmocollin 1a pre
38	95	36.7	840	2 I37281	Dscib precursor -
39	95	36.7	894	2 I37282	hypothetical prote
40	94	36.3	2610	2 T20968	cadherin 1 precu
41	93	35.9	882	1 ITHUCE	N-cadherin precu
42	92	35.5	783	2 I50116	desmocollin 1a - b
43	91	35.1	761	1 ITHODE	desmocollin 1b pre
44	91	35.1	832	2 S55396	desmocollin 1b pre
45	91	35.1	839	1 ITHODF	desmocollin 1b pre

ALIGNMENTS

RESULT 1

A38992
cadherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul., 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DDSD
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:U34056; NID:9506403; PIDN:AAA35622.1; PID:950640
C/Genetics:
A/Gene: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
A/Map position: 16q22.1-16q22.1
C/Suprafamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/271-383/Domain: cadherin repeat homology <CR3>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 73.0%; Score 189; DB 2; Length 796;
Best Local Similarity 79.2%; Pred. No. 3; 8e-16;

Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Db 142 PSEPIKQDINDNPPIFPLGPHATVPEMSNVGTSVIQTADADDP 48
142 PSEPIKQDINDNPPIFPLHETHTANVPERSNVGTSVIQTADADDP 189

RESULT 2

I48277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48277
R/Hoffmann, I.; Balling, R.
Dev. Biol., 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: I48277; MUID:95269886; PMID:7750649
A/Accession: I48277
A/Status: preliminary; translated from GB/EMBL/DDSD
A/Molecule type: mRNA
A/Residues: 1-796 <RHS>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:9666
C/Genetics:

A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 72.2%; Score 187; DB 2; Length 796;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGPYHATVPEMSNVGTSVIGVTAHDADDP 48
DB 142 PSEFIKQDINDNPPFLHETIHANVPERSNVGTSVIGVTAHDADDP 189

RESULT 3

A:Gene: cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49556

R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: I49556; MUID:95263887; PMID:7750650
A:Accession: I49556

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-796 <RES>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:G994774; PIDN:BA06730.1; PID:G974191
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 72.2%; Score 187; DB 2; Length 796;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGPYHATVPEMSNVGTSVIGVTAHDADDP 48
DB 142 PSEFIKQDINDNPPFLHETIHANVPERSNVGTSVIGVTAHDADDP 189

RESULT 4

A:Gene: cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584

R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Xudo, A.; Amano, E.
J. Biol. Chem. 269, 12092-12098, 1994
A:Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584; MUID:94216322; PMID:8163513
A:Accession: A53584

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:G994774; PIDN:BA06730.1; PID:G994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
F:162-268/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:162-268/Domain: cadherin repeat homology <CR4>

Query Match
Best Local Similarity 72.2%; Score 187; DB 2; Length 796;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGPYHATVPEMSNVGTSVIGVTAHDADDP 48
DB 142 PSEFIKQDINDNPPFLHETIHANVPERSNVGTSVIGVTAHDADDP 189

RESULT 5
D38992
cadherin 8 - human

C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992

R:Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous

A:Reference number: S24305; MUID:91283540; PMID:2055658

A:Accession: D38992

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <SUZ>

A:Cross-references: GB:U34060; NID:G506411; PIDN:AAA35628.1; PID:G506412

C:Gene: GDB:CDH8

C:Accession: GDB:5822911

A:Cross-references: GDB:5822911

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: calcium binding; cell adhesion; duplication

F:163-269/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 71.8%; Score 186; DB 2; Length 793;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGPYHATVPEMSNVGTSVIGVTAHDADDP 48
DB 143 PSEFIKQDINDNPPFLHETIHANVPERSNVGTSVIGVTAHDADDP 190

RESULT 6

G02678

cadherin-14 - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C:Accession: G02678

R:Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.

submitted to the EMBL Data Library, May 1996

A:Reference number: H01584

A:Accession: G02678

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-790 <SHI>

A:Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:G1389852; PIDN:AA02933.1; PID:G13

C:Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 68.3%; Score 177; DB 2; Length 790;
Matches 36; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 SEFIKQDINDNPPFLPGPYHATVPEMSNVGTSVIGVTAHDADDP 48
DB 143 SEFIKQDINDNPPFLHETIHANVPERSNVGTSVIGVTAHDADDP 189

RESULT 7

I50180

cadherin-7 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C:Accession: I50180

R:Nakagawa, S.; Takeichi, M.

Development 121, 1321-1332, 1995

A:Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-spec

A:Reference number: I50178; MUID:95309115; PMID:7540531

A:Accession: I50180

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-785 <NAK>

A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:G868000; PIDN:BA07721.1; PID:G868001

C:Superfamily: cadherin; cadherin repeat homology

F:156-262/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 66.4%; Score 172; DB 2; Length 785;

Best Local Similarity 76.6%; Pred. No. 5.8e-14;
Matches 36; Conservative 2; Mismatches 9; Indels 0; Gaps 0

Qy 2 SEFIKGGDINDNPETPLGPHYATVPMSNVGSVIQVTAHDADD 48
|||:||||| ||| |||:||||| |||
Db 137 SEFVIKIQDINDNPKFLDGPYTAGVEMSPVGISVQVTAIDADD 183

RESULT 8
I51638

C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A>Title: Xenopus P-cadherin, a novel member of the cadherin family of cell adhesion mole
A:Reference number: I51638; PMID:1496627
A:Accession: I51638
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ESP>
A:Cross-references: UNIPROT:091838; EMBL:X85330; NID:G854634; PIDN:CAA59679.1; PID:G854634
C:Superfamily: cadherin, cadherin repeat homology
F:161-267//Domain: cadherin repeat homology <CR2>

Query Match	66.0%	Score 171	DB 2;	Length 790;
Best Local Similarity	74.5%	Pred. No	7.9e-14;	
Matches 35;	Conservative	4;	Mismatches 8;	Indels 0;
				Gaps 0;

```

QY      2 SEFIKQDINDNPFIFPLGYPHATVPEMSNVGTSVIQVTAHADDP 48
      |||:|||||:|||||:|||||
DB     142 SEFIKVIQDINDNEPKFLDGPYASVPEMSPVGTSIIQVSATADDDP 18

```

RESULT 5

cadherin-6 - human
 C.Species: Homo sapiens (man)
 C.Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C.Accession: I37016
 R.Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitaajima, M.; Hirohashi, S.
 Cancer Res. 55, 2206-2211, 1995
 A>Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the E
 A.Reference number: I37016; M01D:95562134; PMID:7745525
 A.Accession: I37016
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-790 <RES>
 A.Cross-references: UNIPROT:P55285; GB:DJ1784; NID:G974184; PIDN:BAA06562.1; PID:G974184E
 C.Gene: CDB:CDH6
 A.Gene: CDB:CDH6
 A.Cross-references: GDB:S822908
 C.Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match	64.1 %	Score 166;	DB 2;	Length 790;
Similarity	74.5 %	Pred. No. 3.5e-13;		
Best Local	35;	Mismatches 10;	Indels 0;	Gaps 0;
Matches				

```
QY      2 SEFIKGGDINDNPPIEPLGPHATVPENMSNGTSVIQVTAHDADDP 48
      ||||| ||||| ||||| :||| :||| |||||
Db      143 SEFIKIHNDINDNEPIFTKEVYATATVPENMSDVGTFVQVYATATDADDP 189
```

RESULT 10

X-cadherin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I52701
R/Xiang, Y.Y.; Tanaka, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, T.
FEBS Lett 1994

A:Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
A:Reference number: 152701; PMID:94283827; PMID:81867093
A:Accession: 152701

A1status: preliminary; A1molecule type: mRNA; A1cross-references: UNIPROT:P55280; GB:D25290; NID:g435460; PIDN:BA06975.1; PID:g435461

A/gene: NCAD
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match	63.3%	Score 164	DB 2	length 789
Best Local Similarity	72.3%	Pred. No.	6.3e-13	
Matches 34	Conservative 3	Mismatches 10	Indels 0	Gaps 0

```

Qy      2 SEFIITKODINDNPIPIPLGIPYHATVPKMSNVGTSVIQVTAHADDP 48
          |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db     143 SEFIITKIHINDNEPIFTKDYVYATVPKEMADVGTFVQVATATADDP 188
          |||||  |||||  |||||  |||||  |||||  |||||  |||||

```

RESULT 11

C:Species: Gallus gallus (chicken)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I50178
R:Nakagawa, S.; Takeichi, M.
A:Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-specific
A:Reference number: I50178; MUID:95309115; PMID:754053.
A:Accession: I50178
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-790 <NA>
A:Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA00720.1; PID:9867999
C:Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match	62.5%	Score 162;	DB 2;	Length 790;
Best Local Similarity	68.1%;	Pred. No. 1.1e-12;		
Matches 32; Conservative	6;	Mismatches 9;	Indels 0;	Gaps 0

```
OY      2 SEFIKGGQDINDNDPPIFPLGPGHYHAYPEMSNVGTSTVQTATHADDDPP 48
        |||||   ||||| : ::|||::||| :||| | ||||
DB     143 SEFIKIHDINDNEPMFTKDYNASIPEMSDVGTFVVQVTATDADDP 189
```

RESULT 12

cadherin 12 -human
 N/Alternate names: Br-cadherin
 C/Species: Homo sapiens (man)
 C/Date: 31-May-1996 #sequence revision 31-May-1996 #text_change 03-Jul-2004
 C/Accession: I59372
 R/Selly, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
 A>Title: Expressed cadherin pseudogenes are localized to the critical region of the sp1
 A/Reference number: I59372; MUID:95249541; PMID:7731968
 A/Accession: I59372
 A>Status: nucleic acid sequence not shown; translated from GB/EMBL
 A:Molecule type: mRNA
 A/Residues: 1-794 <RES>
 A/Cross-references: UNIPROT:P55289; GB:I33477; NID:G793942; PIDN:AA84853.1; PID:G793942
 C/Genetics:

F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <INT>

Query Match 62.5%; Score 162; DB 2; Length 794;
Best Local Similarity 74.5%; Pred. No. 1,1e-12;
Matches 35; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 2 SEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 48
DB 144 SEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 190

RESULT 13

10HUC5

cadherin 5 precursor - human

N/Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: S49893; S24305; A43418

R/Reviewer: F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamg

Submitted to the EMBL Data Library, June 1994

A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov

A/Reference number: S49893

A/Accession: S49893

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-784

A/Cross-references: UNIPROT:P3151; EMBL:X79981; NID:G599833; PIDN:CAA56306.1; PID:G5998

R/Suzuki, S.; Sano, K.; Tanhara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: S24305

A/Molecule type: mRNA

A/Residues: 5-516, 'I', 518-784 <SU2>

A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CAA42468.1; PID:G29593

R/Lampunant, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Houen, G.; Ruco,

J. Cell Biol. 118, 1511-1522, 1992

A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts

A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418

A/Molecule type: protein

A/Residues: 48-60, 'X', '62', 'X', '64', '108-116', 'X', '118-133', '237-238', 'X', '240', 'X', '242-252', 'X', '254-

A/Experimental source: cultured endothelial cells

A/Note: sequence extracted from NCBI backbone (NCBI:113040, NCBI:113045, NCBI:113047,

C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t

C/Genetics:

A/Genes: GDB:CDH5

A/Cross-references: GDB:134230; OMIM:601120

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-47/Domain: propeptide #status predicted <PRO>

F:48-784/Product: cadherin 5 #status predicted <MAT>

F:48-593/Domain: extracellular #status predicted <EXT>

F:50-151/Domain: cadherin repeat homology <CR1>

F:154-258/Domain: cadherin repeat homology <CR2>

F:261-372/Domain: cadherin repeat homology <CR3>

F:375-479/Domain: cadherin repeat homology <CR4>

F:481-587/Domain: cadherin repeat homology <CR5>

F:594-620/Domain: transmembrane #status predicted <TM>

F:621-784/Domain: intracellular #status predicted <INT>

F:736-753/Region: serine-rich

F:61,112,157,362,442,523,535/Binding site: carbonylate (Asn) (covalent) #status predict

Query Match 55.6%; Score 144; DB 1; Length 784;

Best Local Similarity 62.5%; Pred. No. 2.4e-10;

Matches 30; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 48

DB 134 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 181

RESULT 14

S47518

cadherin - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999

C/Accession: S47518

R/Tool: O.; Fujii, G.; Tashiro, K.; Shikawa, K.

Biochim. Biophys. Acta 1219, 121-128, 1994

A/Title: Molecular cloning of cDNA for XTCAD-1, a novel Xenopus cadherin, and its expe

A/Reference number: S47518; MUID:94368839; PMID:8086449

A/Accession: S47518

A/Molecule type: mRNA

A/Residues: 1-871 <TCO>

C/Superfamily: cadherin; cadherin repeat homology

F:151-256/Domain: cadherin repeat homology <CR1>

Query Match 46.7%; Score 121; DB 2; Length 871;

Best Local Similarity 53.2%; Pred. No. 2.5e-07;

Matches 25; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 47

DB 239 PSEFIKQDINDNDPPIPLGPHATVPMSNVGTSTVQVTAHDADD 265

RESULT 15

B38992

cadherin 13 precursor - human

N/Alternate names: H-cadherin; T-cadherin

C/Species: Homo sapiens (man)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: B38992; G02676

R/Suzuki, S.; Sano, K.; Tanhara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: B38992

A/Molecule type: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-713 <SU2>

A/Cross-references: UNIPROT:P55290; GB:L34058; NID:G506407; PIDN:AAA35624.1; PID:G506408

R/Lee, S.W.

Submitted to the EMBL Data Library, May 1996

A/Reference number: H01582

A/Accession: G02676

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-713 <LSE>

A/Cross-references: EMBL:U59288; NID:G1381789; PIDN:AA18911.1; PID:G1381790

A/Genetics:

A/Genes: GDB:CDH13

A/Cross-references: GDB:5822917; OMIM:601364

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: blocked carboxyl end; calcium binding; cell adhesion; duplication; glycoprot

F:1-32/Domain: signal sequence #status predicted <SIG>

F:23-138/Domain: amino-terminal propeptide #status predicted <PRO>

F:139-693/Product: cadherin 13 #status predicted <MAT>

F:141-245/Domain: cadherin repeat homology <CR1>

F:248-363/Domain: cadherin repeat homology <CR2>

F:366-477/Domain: cadherin repeat homology <CR3>

F:480-585/Domain: cadherin repeat homology <CR4>

F:586-681/Domain: cadherin repeat homology <CR5>

F:694-712/Domain: carboxyl-terminal propeptide #status predicted <CPR>

F:732,500,530,638,671/Binding site: carbonylate (Asn) (covalent) #status predicted

F:693/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match 42.9%; Score 111; DB 2; Length 713;

Best Local Similarity 54.2%; Pred. No. 3.8e-06;

Matches 26; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

Wed Dec 8 11:46:36 2004

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Page 5

Qy 1 PSEFIKGDINDNPPPIPLGPHYHATVEMSNVGTSTVQVTAHDADDP 48
| : | | | | : : : : | | | |
Db 230 PLEVIVIDQ--NDNRPIFREGPYIGHVMEGSPGTITVMTATFADADDP 275

Search completed: December 8, 2004, 10:27:05
Job time : 3.88194 secs

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DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Thyroid;
RA Niimiya K., Magatsuuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Futaya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nagagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isegai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 cadherin domains.
CC EMBL; AK057922; BABY1613.1; -
DR HSSP; E12830; 106S.
DR GeneW; HGNC:14265; CDH24.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00205; CADHERIN.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS0268; CADHERIN_2; 4.
KW Calcium, Calcium-binding
SQ SEQUENCE 493 Aa; 3310DF63AP09C1E CXC64;

Query Match 96.5%; Score 250; DB 2; Length 493;
Best Local Similarity 97.9%; Pred. No. 2e-22;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 PSEFIKQDINDNPRIPLGPRATVEMNNGSVQVTAHADDP 48
Dd 133 PSEFIKQDINDNPRIPLGPRATVEMNNGSVQVTAHADDP 180
|||||

RESULT 3
CADO_HUMAN STANDARD. PRT; 819 AA.
ID CADO_HUMAN
AC Q86UF0; Q86UP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ833/PRO34009).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP CAENININS.
RA MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA Katsiaz B., Nieman M.T., Wheelock M.J., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
II cadherin";
RT J. Biol. Chem. 278:27513-27519 (2003).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA MEDLINE=22687296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen Y., Chow B., Chui C., Crowley C., Currell B., Daniel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Lido D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehgagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vardieri R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansuta D.,
RA Yi S., Yu G., Yuan J., Zhang W., Zhang Z., Goddard A., Wood W.I.,

RA	Godowak P., Gray A.
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
RL	Bioinformatics assessment."/
RN	Genome Res. 13:2265-2270(2003).
RP	[3]
RC	SEQUENCE FROM N.A. (ISOFORM 3).
RD	TISSUE=Testis;
RE	Blum H., Banerachs S., Mewes H.-W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RF	-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherin may thus contribute to the sorting of heterogeneous cell types. Cadherin-24 mediate strong cell-cell adhesion.
RG	-1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
RH	-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
RI	-1- ALTERNATIVE PRODUCTS:
RJ	Name=1; Synonyms=Long form;
RK	Isoid-Q86UP0-1; Sequence=Displayed;
RL	Name=2; Synonyms=Short form;
RM	Isoid-Q86UP0-2; Sequence=VSP_008717;
RN	Name=3;
RO	Isoid-Q86UP0-3; Sequence=VSP_008718, VSP_008719;
RP	Note=No experimental confirmation available;
RQ	-1- SIMILARITY: Contains 5 cadherin domains.
RS	-----
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RV	-----
SW	EMBL; AY260900; AAP20590.1; -
SX	EMBL; AY260901; AAP20591.1; -
SY	EMBL; AY358199; AAQ88566.1; -
SZ	EMBL; AL137477; CAB70758.1; -
TA	PIR; T46418; T46418.
TB	HSSP; P09803; 11TW.
TC	DR
TD	Genev; HGNC:14265; CDH24.
TE	InterPro; IPR002126; Cadherin.
TF	InterPro; IPR002023; Cadherin_C term.
TG	DR Pfam; PF00028; Cadherin_5.
TH	DR Pfam; PF01049; Cadherin_C_1.
TI	PRINTS; PRO0205; CADHERIN.
TJ	DR PROSITE; PS00232; CADHERIN_1; 2.
TK	DR PROSITE; PS00268; CADHERIN_2; 5.
TL	KM Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein; Multigene family; Repeat; Signal; Transmembrane.
TM	FT SIGNAL
TN	FT PROPEP
TO	FT CHAIN
TP	FT DOMAIN
TR	FT TRANSMEM
TS	FT DOMAIN
TT	FT DOMAIN
TU	FT DOMAIN
TV	FT DOMAIN
TW	FT DOMAIN
TX	FT DOMAIN
TY	FT CARBOHYD
TZ	FT CARBOHYD
UA	FT CARBOHYD
UB	FT CARBOHYD
UC	FT CARBOHYD
UD	FT CARBOHYD
UE	FT CARBOHYD
UF	FT CARBOHYD
UG	FT CARBOHYD
UH	FT CARBOHYD
UI	FT CARBOHYD
UJ	FT CARBOHYD
UK	FT CARBOHYD
UL	FT CARBOHYD
UM	FT CARBOHYD
UN	FT CARBOHYD
UR	FT CARBOHYD
US	FT CARBOHYD
UT	FT CARBOHYD
UU	FT CARBOHYD
UV	FT CARBOHYD
UW	FT CARBOHYD
UX	FT CARBOHYD
UY	FT CARBOHYD
UZ	FT CARBOHYD
V	VARSLIC
V1	VARSLIC
V2	VARSLIC
V3	VARSLIC
V4	VARSLIC
V5	VARSLIC
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V96	VARSLIC
V97	VARSLIC
V98	VARSLIC
V99	VARSLIC
V100	VARSL


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OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=zygote;
RA MEDLINE=98202517; PubMed=9533396;
RA Hagedall B., Borchers A., Medlich D.;
RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the wg/mnt
RT signal";
RL Mech. Dev. 72:101-113(1998).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AF002983; AAC28073.1; -.
DR HSSP: P09803; 117W.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; C. 1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS00268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
FT SIGNAL 1 53 Potential.
FT CHAIN 54 794 cadherin.
SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEFA719DB CRC64;

Query Match 74.9%; Score 194; DB 2; Length 794;
Best Local Similarity 81.2%; Pred.No. 3,1e-15;
Matches 39; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

CY 1 PSEFIRGQDINDNPFPLGPRATYBEMSNVGTSTVOTAHADADP 48
DB 142 PSEFIRGQDINDNPFPLGPRATYBEMSNVGTSTVOTAHADADP 189

RESULT 7
CADA_HUMAN STANDARD; PRT; 796 AA.
AC P55287; Q15065; Q15066; Q9U093; Q9U094;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN Name=CDH11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA MEDLINE=95073006; PubMed=7982033;
RA Tanihara H., Sano K., Heimerl R.W., St John T., Suzuki S.;
RT "Cloning of five human cadherins clarifies characteristic features of
RT cadherin extracellular domain and provides further evidence for two
RT structurally different types of cadherin";
RL Cell Adhes. Commun. 2:15-26(1994).
CC [2]
CC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Osteosarcoma;
RX MEDLINE=94216322; PubMed=9163513;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
RA Amann E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts.";
RL J. Biol. Chem. 269:12092-12098(1994).

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RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal Brain;
RX MEDLINE=91283540; PubMed=20596658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
RT nervous tissue.";
RL Cell Regul. 2:261-270(1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Kools P.F., Hogendoorn P.C.W., Boye J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
RT molecules are detectable in both human cancer and normal cells.";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P55287-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P55287-2; Sequence=VSP_000640; VSP_000641;
CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
CC other tissues. Expressed in neuroblasts.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-stb.ch).
CC -----
DR EMBL: L34056; AAA35622.1; -.
DR EMBL: D12154; BAA04798.1; -.
DR EMBL: D12155; BAA04799.1; -.
DR EMBL: AF060370; AAD27755.1; -.
DR EMBL: AF060369; AAD27755.1; JOINED.
DR EMBL: AF060370; AAD27756.1; -.
DR EMBL: AF060369; AAD27756.1; JOINED.
DR PIR: A38992; A38992.
DR HSSP: P09803; 117W.
DR GeneW: HGNC:1750; CDH11.
DR MIM: 600023; -.
DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0007156; P:homophilic cell adhesion; NAS.
DR GO: GO:0001503; P:ossification; NAS.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; C. 1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS00268; CADHERIN_2; 5.
KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 53 Potential.
FT CHAIN 54 796 Cadherin-11.
FT DOMAIN 54 617 Extracellular (Potential).
FT TRANSMEM 618 640 Potential.
FT DOMAIN 641 796 Cytoplasmic (Potential).
FT DOMAIN 54 159 Cadherin 1.
FT DOMAIN 160 268 Cadherin 2.
FT DOMAIN 269 383 Cadherin 3.
FT DOMAIN 384 486 Cadherin 4.
FT DOMAIN 487 612 Cadherin 5.
FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).

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FT VARSPIC 632 693 VIVLVFVTLNRQKKEPLIVEEDVENITTYDDEGGGED
 FT TEADFIATLONPDINGFIR -> GCPSPMEPSPEDWR
 FT LLYVFMQLMFSYKVRFRCLGLGVFKLPFLVVAATESPT
 FT TLTSL (in isoform 2).
 FT /FTID=VSP_000640.
 FT Missing (in isoform 2).
 FT /FTID=VSP_000641.
 FT RL -> SV (in Ref. 2).
 FT CONFLICT 271 272 M -> I (in Ref. 2).
 FT CONFLICT 275 275 E -> K (in Ref. 2).
 FT CONFLICT 340 340 S -> A (in Ref. 2).
 FT CONFLICT 373 373 Q -> K (in Ref. 2).
 FT CONFLICT 471 471
 SQ SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB2E CRC64;

Query Match 73.0%; Score 189; DB 1; Length 796;
 Best Local Similarity 79.2%; Pred. No. 1.3e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFTIKGQDINDNPPIFLGPHATVPMSNVGTSVIQVTAHDADDP 48
 Db 142 PSEFTIKGQDINDNPPIFLGPHATVPMSNVGTSVIQVTAHDADDP 189

RESULT 8
 ID Q96CZ9 PRELIMINARY; PRT; 796 AA.
 AC Q96CZ9;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marneus K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RU Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC EMBL: BC013609; AAH13609.1; -.
 CC HSSP: P09803; 117W.
 CC GO: GO:0016020; C:membrane; IEA.
 CC GO: GO:0005509; P:calcium ion binding; IEA.

DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR InterPro: IPR001901; SECE.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR PROSITE: PS01067; SECE_SECEIG; UNKNOWN_1.
 DR Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;

Query Match 73.0%; Score 189; DB 2; Length 796;
 Best Local Similarity 79.2%; Pred. No. 1.3e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFTIKGQDINDNPPIFLGPHATVPMSNVGTSVIQVTAHDADDP 48
 Db 142 PSEFTIKGQDINDNPPIFLGPHATVPMSNVGTSVIQVTAHDADDP 189

RESULT 9
 ID CADB_CHICK STANDARD; PRT; 792 AA.
 AC Q933I9;
 DT 16-OCT-2001 (rel. 40, Created)
 DT 16-OCT-2001 (rel. 40, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA Wei U., Dong X.R., Topczus S., Zimmer W.E., Broders F., Thierry J.P.,
 RA Kotliarsky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: AF055342; AAC33675.1; -.
 DR HSSP: P09803; 117W.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.

FT PROPEP 23 53 Potential.
FT CHAIN 54 792 Cadherin-11.
FT DOMAIN 54 613 Extracellular (Potential).
FT TRAMEM 614 634 Potential.
FT DOMAIN 635 792 Cytoplasmic (Potential).
FT DOMAIN 54 159 Cadherin 1.
FT DOMAIN 160 268 Cadherin 2.
FT DOMAIN 269 383 Cadherin 3.
FT DOMAIN 384 486 Cadherin 4.
FT DOMAIN 487 608 Cadherin 5.
FT CAROXYD 455 455 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 536 536 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 594 594 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 792 AA; 87572 MW; 3E348C6868731AB CRC64;
Query Match 72.6%; Score 188; DB 1; Length 792;
Best Local Similarity 79.2%; Pred. No. 1.7e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Cy 1 PSEFIRKQDINDNPNPLGPHYATVPKSNVGTSTVIOYTAHADDP 48
Db 142 PSEFIRKQDINDNPNPLGPHYATVPKSNVGTSTVIOYTAHADDP 189
RESULT 10
CAD_MOUSE STANDARD; PRT; 796 AA.
AC P55288.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
GN Name=Cdh11; Synonyms=Cad-11;
OS Mus musculus (Mouse).
OC Bonyrhopalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95269886; PubMed=7750649;
RA Hofmann I.H., Balling R.;
RT "Cloning and expression analysis of a novel mesodermally expressed
RT cadherin.";
RL Dev. Biol. 169:337-346(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95269887; PubMed=7750650;
RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
RA Miyazaki T., Takeichi M.;
RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
RT in the head, somite, and limb bud of early mouse embryos.";
RL Dev. Biol. 169:347-358(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Calvaria;
RA MEDLINE=94216322; PubMed=6165113;
RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
RA Amanu E.;
RT "Molecular cloning and characterization of OB-cadherin, a new member
RT of cadherin family expressed in osteoblasts.";
RL J. Biol. Chem. 269:12092-12098(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Olfactory epithelium;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton K., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohizuki S., Carninci P., Prange C.,
RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP DEVELOPMENTAL STAGE.
RC STRAIN=C57BL/6; TISSUE=Testis;
RX MEDLINE=97033837; PubMed=8879495;
RA Munro S.B., Blaschuk O.W.;
RT "A comprehensive survey of the cadherins expressed in the testes of
RT fetal, immature, and adult mice utilizing the polymerase chain
RT reaction.";
RL Biol. Reprod. 55:822-827(1996).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
CC lines, precursor cell lines of osteoblasts, and primary
CC osteoblastic cells from calvaria, as well as in lung, testis, and
CC brain tissues at low levels.
CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
CC gonad and decreases 8-fold in newborn.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL, X77557; CAA54674.1; -;
DR EMBL, D31963; BA06730.1; -;
DR EMBL, D21253; BA004797.1; -;
DR EMBL, BC046314; AA046314.1; -;
DR PIR, A53584; A53584.
DR PIR, I48277; I48277.
DR PIR, I49556; I49556.
DR HSSP, P09803; I17W.
DR MGD, MGI:99217; Cdh11.
DR GO, GO:0005737; Cytoplasm; IDA.
DR GO, GO:0005886; Cytoplasmic membrane; IDA.
DR InterPro, IPR002126; Cadherin.
DR InterPro, IPR000233; Cadherin_C-term.
DR Pfam, PF00028; Cadherin_C-term.
DR Pfam, PF01049; Cadherin_C_1.
DR PRINTS, PRO0205; CADHERIN.
DR PROSITE, PS00232; CADHERIN_1; 3.
DR PROSITE, PS0268; CADHERIN_2; 5.
DR KX, K01268; CADHERIN_2; 5.
KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
KW SIGNAL 1 24
FT PROPEP 25 53 Potential.
FT CHAIN 54 796 Cadherin-11.
FT DOMAIN 54 617 Extracellular (Potential).
FT TRAMEM 618 640 Potential.
FT DOMAIN 641 796 Cytoplasmic (Potential).
FT DOMAIN 54 159 Cadherin 1.
FT DOMAIN 160 268 Cadherin 2.
FT DOMAIN 269 383 Cadherin 3.
FT DOMAIN 384 486 Cadherin 4.
FT DOMAIN 487 612 Cadherin 5.

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FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
FT CONFLICT 462 462 E -> D (in Ref. 1).
FT CONFLICT 589 589 T -> L (in Ref. 2).
FT CONFLICT 655 655 D -> N (in Ref. 2).
FT CONFLICT 751 751 V -> M (in Ref. 1).
FT CONFLICT 777 777 P -> Q (in Ref. 2).
FT CONFLICT 782 782 L -> P (in Ref. 2).
SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641D529 CRC64;

Query Match 72.2%; Score 187; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 2,3e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Cy 1 PSEFIRKQDINDNPPFLPGPYHATVPEMSNGVSVIQTADADDP 48
Db 142 PSEFIRKQDINDNPPFLPGPYHATVPEMSNGVSVIQTADADDP 189

RESULT 11
ID 08C706 PRELIMINARY; PRT; 796 AA.
AC 08C706:
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE enriched library, clone:C530015F15 product:cadherin 11, full insert
DE sequence.
GN Name=Cdh11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RT The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20493974; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=2030913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Harada A.,
RA Nishino T., Yoshitake T., Yoshitake T.

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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-11771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=2338257; PubMed=12477932;
RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK049652; EAC33860.1; -.
DR HSSP: P09803; ITW.
DR MGD: MGI:99217; Cdh11.
DR GO: GO:0005737; Cytoplasm; IDA.
DR GO: GO:0005886; Cytoplasmic membrane; IDA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
DR Calcium, Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 796 AA; 88126 MW; 71963374B2E1B29 CRC64;

Query Match 72.2%; Score 187; DB 2; Length 796;
Best Local Similarity 79.2%; Pred. No. 2,3e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Cy 1 PSEFIRKQDINDNPPFLPGPYHATVPEMSNGVSVIQTADADDP 48
Db 142 PSEFIRKQDINDNPPFLPGPYHATVPEMSNGVSVIQTADADDP 189

RESULT 12
ID 06PAN4 PRELIMINARY; PRT; 508 AA.
AC 06PAN4:
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleusner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.L., Wang J., Hsieh F.,
RA Ditschenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Udén T.B., Yoshitake T., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.E., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL: BC062000; AAH60200.1; -
 DR InterPro: IPR002126; Cadherin.
 DR Pfam: PF00028; Cadherin; 4.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SMO0112; CA; 4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS0268; CADHERIN_2; 4.
 DR Calcium-binding.
 KM SEQUENCE 508 AA; 5638 MW; 9053F774BCF52255 CRC64;
 SQ

Query Match 71.8%; Score 186; DB 2; Length 508;
 Best Local Similarity 79.2%; Pred. No. 1.9e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFTIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHADDP 48
 DB 150 PSEFTIKQDINDNAPFLNGPHATVPEMSILGTSVNTVATADDP 197

RESULT 13
 AAH60200 PRELIMINARY; PRT; 508 AA.

ID AAH60200
 AC AAH60200
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 NX
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL: BC062000; AAH60200.1; -
 DR InterPro: IPR002126; Cadherin.
 DR Pfam: PF00028; Cadherin; 4.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SMO0112; CA; 4.
 DR PROSITE: PS00232; CADHERIN_1; 2.
 DR PROSITE: PS0268; CADHERIN_2; 4.
 DR Calcium-binding.
 KM SEQUENCE 508 AA; 5638 MW; 9053F774BCF52255 CRC64;
 SQ

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC062000; AAH60200.1; -
 SQ SEQUENCE 508 AA; 5638 MW; 9053F774BCF52255 CRC64;
 SQ

Query Match 71.8%; Score 186; DB 2; Length 508;
 Best Local Similarity 79.2%; Pred. No. 1.9e-14;
 Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFTIKQDINDNPPFPLGPHATVPEMSNVGTSVQVTAHADDP 48
 DB 150 PSEFTIKQDINDNAPFLNGPHATVPEMSILGTSVNTVATADDP 197

RESULT 14
 O8C375 PRELIMINARY; PRT; 716 AA.

ID O8C375
 AC O8C375
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone: D930046N17 product: cadherin 8, full insert
 DE sequence.
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 NX
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Kitanai T., Tashiro H., Itoh M.,
 RA Saito N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayata N., Hiramoto K., Hirooka T., Hirozane T.,
RA Horii F., Imceni K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishii K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(CC By similarity).
CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK086711; BAC39724.1; -.
DR HSSP: P15116; INCU.
DR MGP: MGI:107434; Cdh8.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005099; F:calcium ion binding; IEA.
DR GO: GO:007156; F:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; 1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA: 5
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR KEGG: K04401; Cell adhesion; Transmembrane.
KW Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 716 AA; 79149 MW; 58BD598F638624A CISC64;
Query Match 71.8%; Score 186; DB 2; Length 716;
Best Local Similarity 79.2%; Pred. No. 2.8e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 1 PSEFIIKQDINDNPPIPLGPGYATVPEMSNVGTSTQVTAHDDP 48
DB 150 PSEFIIKQDINDNPPIPLGPGYATVPEMSNVGTSTQVTAHDDP 197
RESULT 15
Q8C449 PRELIMINARY; PRT; 716 AA.
AC Q8C449;
AC 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
DE library, clone:G53002D14 Product:cadherin 8, full insert sequence
DE (Cdh8 protein).
DE Name=Cdh8;
GN Mus musculus (Mouse).
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI-TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Mech. Enzymol. 303:13-44(1999).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[5]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[6]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[7]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.P., Zeeberg B., Bueltner K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
RA Brownstein M.J., Ueidi T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalka U., Smalls D.E., Scherch A., Schein J.E.,
RA Torres J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC -!- FUNCTION: (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: AK083092; BAC38758.1; -.
DR EMBL: BC057581; AAH57581.1; -.
DR HSSP: P15116; INCT
DR MGD: MGI:107434; Cdh8.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin_C; 1.
DR PRINTS: PR00205; CADHERIN.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 71.8%; Score 186; DB 2; Length 716;
Best local similarity 79.2%; Pred. No. 2.8e-14;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFLIKQDINDNPPIPLGPHATVPKSNVGTSVIQVTAHDADDP 48
Db 150 PSEFLIKQDINDNPPIPLGPHATVPKSNVGTSVIQVTAHDADDP 197

Search completed: December 8, 2004, 10:24:38
Job time : 20.2397 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.863 Seconds

(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-8

Perfect score: 259
Sequence: 1 PSEFIIKGGQINDNPPIFPL.....EMSNVGTSTVIQTAHADADP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	259	100.0	48	7	ADD29449 Human cad
2	259	100.0	620	7	ADD29448 Human cad
3	259	100.0	636	7	ADD29445 Human cad
4	250	96.5	493	5	AD116946 Human NOV
5	250	96.5	607	5	ABB53295 Human pol
6	250	96.5	781	5	ABB53296 Human pol
7	250	96.5	781	5	AAW48736 Human cad
8	250	96.5	781	5	ABG34078 Human pro
9	250	96.5	781	5	AD116604 Human NOV
10	250	96.5	781	5	AD116606 Human NOV
11	250	96.5	781	6	ABR40114 Human cel
12	250	96.5	781	6	ADA01366 Human PRO
13	250	96.5	781	6	ADA43795 Human sec
14	250	96.5	781	6	ADA43563 Human sec
15	250	96.5	781	6	ADA01238 Human PRO
16	250	96.5	781	7	ADA01122 Human sec
17	250	96.5	781	7	ADA43679 Human sec
18	250	96.5	781	7	ADA06941 Human PRO
19	250	96.5	781	7	ADA08429 Novel hum
20	250	96.5	781	7	ADB99722 Human PRO
21	250	96.5	781	7	ADB87005 Human PRO
22	250	96.5	781	7	ADB66160 Human sec
23	250	96.5	781	7	ADB99838 Human PRO
24	250	96.5	781	7	ADB99493 Novel hum
25	250	96.5	781	7	ADB66044 Human sec

26	250	96.5	781	7	ADC23442 Human tra
27	250	96.5	781	7	ADC26135 Human PRO
28	250	96.5	781	7	ADB04962 Human PRO
29	250	96.5	781	7	ADP11268 Human PRO
30	250	96.5	781	7	ADB88199 Human PRO
31	250	96.5	781	7	ADD95494 Human sec
32	250	96.5	781	7	ADB06424 Human PRO
33	250	96.5	781	7	ADB38199 Human PRO
34	250	96.5	781	7	ADB88315 Human PRO
35	250	96.5	781	7	ADD90896 Human sec
36	250	96.5	781	7	ADP99451 Human sec
37	250	96.5	781	7	ADG06544 Human PRO
38	250	96.5	781	7	ADG05495 Human PRO
39	250	96.5	781	7	ADG82496 Human PRO
40	250	96.5	781	8	ADE51749 Human sec
41	250	96.5	781	8	ADE51865 Human sec
42	250	96.5	781	8	ADE37723 Human sec
43	250	96.5	781	8	ADE37607 Human sec
44	250	96.5	781	8	ADP95378 Human sec
45	250	96.5	781	8	ADP38078 Human PRO

ALIGNMENTS

```
RESULT 1
ADD29449
ID ADD29449 standard; protein; 48 AA.
XX
AC ADD29449;
XX
DT 15-JUN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq I18.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytotactin; osteopetrotic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US200314491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (GODB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LITC/) LIT C.
PA (DEWA/) DEWMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
Liu C, Dymnac RT;
XX
DR WPI; 2003-829799/77.
XX
DE Novel isolated human secreted cadherin-like polypeptide useful for
treating diseases such as cancers, osteoporosis, Paget's disease,
osteomalacia, hyperostosis, osteopetrosis.
XX
CS Claim 11; SEQ ID NO 8; 63bp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
protein and the DNA sequence which encodes it. Cadherins are a family of
```

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, osteopetrosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 48 AA;

Query Match Best Local Similarity 100.0%; Score 259; DB 7; Length 48; Best Local Similarity 100.0%; Pred. No. 1.6e-28; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPFIFPLGPHATVPEMNGSVIQVTAHADDP 48
Db 1 PSEFIKQDINDNPFIFPLGPHATVPEMNGSVIQVTAHADDP 48

RESULT 2

ADD29448 standard; protein; 620 AA.

ADD29448;

15-JAN-2004 (first entry)

Human cadherin-like mature protein.

cadherin-like protein; transmembrane protein; cadherin domain; homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer; osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis; metastatic tumour; human.

Homo sapiens.

US2003144491-A1.

31-JUL-2003.

16-FEB-2001; 2001US-00788051.

03-FEB-2000; 2000US-0046914.

27-APR-2000; 2000US-00560875.

(GODB/) GODBOLE S D.

(KUC/) KUO C.

(ARTE/) ARTERBURN M C.

(YEUN/) YEUNG G.

(PALE/) PALENCIA S.

(TANG/) TANG Y T.

(LIUC/) LIU C.

(DRMA/) DRMANAC R T.

Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT, Liu C, Drmanac RT;

WPI; 2003-829799/77.

Novel isolated human secreted cadherin-like polypeptide useful for treating diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 7; 63bp; English.

cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, osteopetrosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the mature human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 620 AA;

Query Match Best Local Similarity 100.0%; Score 259; DB 7; Length 620; Best Local Similarity 100.0%; Pred. No. 4e-27; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPFIFPLGPHATVPEMNGSVIQVTAHADDP 48
Db 117 PSEFIKQDINDNPFIFPLGPHATVPEMNGSVIQVTAHADDP 164

RESULT 3

ADD29445 standard; protein; 636 AA.

ADD29445;

15-JAN-2004 (first entry)

Human cadherin-like protein amino acid sequence.

cadherin-like protein; transmembrane protein; cadherin domain; homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer; osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis; metastatic tumour; human.

Homo sapiens.

US2003144491-A1.

31-JUL-2003.

16-FEB-2001; 2001US-00788051.

03-FEB-2000; 2000US-0046914.

27-APR-2000; 2000US-00560875.

(GODB/) GODBOLE S D.

(KUC/) KUO C.

(ARTE/) ARTERBURN M C.

(YEUN/) YEUNG G.

(PALE/) PALENCIA S.

(TANG/) TANG Y T.

(LIUC/) LIU C.

(DRMA/) DRMANAC R T.

Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT, Liu C, Drmanac RT;

WPI; 2003-829799/77.

N-PEDB; ADD29461, ADD29446.

Novel isolated human secreted cadherin-like polypeptide useful for treating diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 4; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.
XX
SQ Sequence 636 AA:
Query Match 100.0%; Score 259; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 4, 2e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 PSEFIKQDINDNPFIFPGPHATVPENSNVGTSVIQVTAHDADDP 48
133 PSEFIKQDINDNPFIFPGPHATVPENSNVGTSVIQVTAHDADDP 180
RESULT 4
AD116946
ID AD116946 standard; protein, 493 AA.
XX
AC AD116946;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein homologue Segid 482.
XX
KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX
OS Homo sapiens.
XX
PN WO200268649-A2.
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002WO-US0002785.
XX
PF 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 02-MAR-2001; 2001US-0271858P.
PR 02-MAR-2001; 2001US-0272046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.

PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278782P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285135P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0286327P.
PR 03-MAY-2001; 2001US-0286504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0316415P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 18-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernyev VT, Spyrek KA, Zerhusen BD, Patrujan M, Shinkets RA;
PI Li L, Gangolli EA, Padigan M, Anderson DM, Rastelli L, Miller CB;
PI Gerlach VL, Taupier RJ, Gusev VI, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsdbrook JP, Legley DM, Rieger DK, Burgess CE;
XX
XX WFI; 2002-706998/76.
XX
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Disclosure; SEQ ID NO 482; 1498pp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC hemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antistimulant, nephroprotective, antibacterial, virucide, antiparasitic,
CC neuroprotective, nootropic, anticholinergic, anticholinergic, anticholinergic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.

XX SQ Sequence 493 AA;

Query Match 96.5%; Score 250; DB 5; Length 493;
 Best Local Similarity 97.9%; Pred. No. 5.5e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGYHATVPEMSNGSVIQVTAHADDP 48
 133 PSEFIKQDINDNPPFLPGYHATVPEMSNGSVIQVTAHADDP 180

Db 133 PSEFIKQDINDNPPFLPGYHATVPEMSNGSVIQVTAHADDP 180

RESULT 5
 ABB53295
 ID ABB53295 standard; protein, 607 AA.
 XX ABB53295;
 AC ABB53295;
 XX 12-FEB-2002 (first entry)
 DT 12-FEB-2002 (first entry)
 DE Human polypeptide #35.
 XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquilizer; antiarrhythmic; cardiant; antidiabetic;
 KM antiinflammatory; antilipemic; hepatotropic; vitruide; antidiabetic;
 KM nephrotropic; anorectic; cytotatic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200181363-A1.
 PN WO200181363-A1.
 XX 01-NOV-2001.
 PD 01-NOV-2001.
 XX 26-APR-2001; 2001WO-US013360.
 PF 26-APR-2001; 2001WO-US013360.
 XX 27-APR-2000; 2000US-0199963P.
 PR 11-MAY-2000; 2000US-0203336P.
 ER 25-MAY-2000; 2000US-0207087P.
 XX 26-MAY-2000; 2000US-0207546P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 PI Lal Y, Xie Q;
 DR WPI; 2002-041392/05.
 DR N-PSDB; ABA90360.
 XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated with the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX Claim 1; Page 106-108; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression, cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction,
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome, liver
 CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and

CC glomerulonephritis; skeletal muscle diseases including Ehlers-Danlos
 CC disease, hypoglycemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphoglandular diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type I and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX SQ Sequence 607 AA;

Query Match 96.5%; Score 250; DB 5; Length 607;
 Best Local Similarity 97.9%; Pred. No. 7.2e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPFLPGYHATVPEMSNGSVIQVTAHADDP 48
 133 PSEFIKQDINDNPPFLPGYHATVPEMSNGSVIQVTAHADDP 180

Db 133 PSEFIKQDINDNPPFLPGYHATVPEMSNGSVIQVTAHADDP 180

RESULT 6
 ABB53296
 ID ABB53296 standard; protein, 761 AA.
 XX ABB53296;
 AC ABB53296;
 XX 12-FEB-2002 (first entry)
 DT 12-FEB-2002 (first entry)
 DE Human polypeptide #36.
 XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquilizer; antiarrhythmic; cardiant; antidiabetic;
 KM antiinflammatory; antilipemic; hepatotropic; vitruide; antidiabetic;
 KM nephrotropic; anorectic; cytotatic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200181363-A1.
 PN WO200181363-A1.
 XX 01-NOV-2001.
 PD 01-NOV-2001.
 XX 26-APR-2001; 2001WO-US013360.
 PF 26-APR-2001; 2001WO-US013360.
 XX 27-APR-2000; 2000US-0199963P.
 PR 11-MAY-2000; 2000US-0203336P.
 ER 25-MAY-2000; 2000US-0207087P.
 XX 26-MAY-2000; 2000US-0207546P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 PI Lal Y, Xie Q;
 DR WPI; 2002-041392/05.
 DR N-PSDB; ABA90361.
 XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated with the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX Claim 1; Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including

CC Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including bulbar myo-
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphoedema; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
CC
CC
SQ Sequence 781 AA;

Query Match 96.5%; Score 250; DB 5; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFIFLPGYHATVPEMSNVGTSVIOVTAHDADDP 48
DB 133 PSEFIKQDINDNPFIFLPGYHATVPEMSNVGTSVIOVTAHDADDP 180

RESULT 7
AAM48736
ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
KW antidiabetic; neuroprotective; antiarthritic; antirheumatic;
KW dermatological; immunosuppressive; antiinflammatory; antipsoriatic;
KW antiaschemic; antiallergic; antileptotic; haemostatic; antipruritic;
KW antithyroid; hypotensive; antiarteriosclerotic; cardiant; antiarrhythmic;
KW anorectic; immunomodulatory; vasotropic; vituocic; cyostatic; liver;
KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
KW viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
KW gene therapy.

XX Homo sapiens.

OS WO200130145-A2.

PN 29-NOV-2001.

PD 18-MAY-2001; 2001WO-US016013.

PF 19-MAY-2000; 2000US-0205674P.

PR (MILL-) MILLENNIUM PHARM INC.

PA Curtis RAU;

XX WPI; 2002-083082/11.

DR N-PSDB; ABA96406, ABA96407.

PT New human cadherin family protein and polynucleotides, useful for

PT diagnosing and treating disorders e.g. obstructive jaundice, multiple

PT sclerosis, encephalomyelitis and atherosclerosis and to identify

PS modulators of therapeutic use.

XX The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
CC neuroprotective, antiarthritic, antirheumatic, dermatological,
CC immunosuppressive, antiinflammatory, antipsoriatic, antiaschemic,
CC antiallergic, antileptotic, haemostatic, antipruritic, antithyroid,
CC hypotensive, antiarteriosclerotic, cardiant, antiarrhythmic, anorectic,
CC immunomodulatory, vasotropic, vituocic, cyostatic, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecule are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune disease including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy; cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy
CC
CC
SQ Sequence 781 AA;

Query Match 96.5%; Score 250; DB 5; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFIFLPGYHATVPEMSNVGTSVIOVTAHDADDP 48
DB 133 PSEFIKQDINDNPFIFLPGYHATVPEMSNVGTSVIOVTAHDADDP 180

ABG34078

DE Human Pro peptide #49.

DT 15-JUL-2002 (first entry)

XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;

XX tumour; cancer.

XX Homo sapiens.

OS WO200224688-A2.

PN 28-MAR-2002.

PD 29-AUG-2001; 2001WO-US027099.

PF 01-SEP-2000; 2000US-0229896P.

PR 05-SEP-2000; 2000US-0230621P.

PR 22-SEP-2000; 2000US-0235147P.

PR 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.

PR 16-JAN-2001; 2001US-0261910P.

PR 16-JAN-2001; 2001US-0261939P.

PR 16-JAN-2001; 2001US-0262150P.

PR 25-JAN-2001; 2001US-0264395P.

PR 02-FEB-2001; 2001US-0264421P.

PR 09-FEB-2001; 2001US-0267623P.

PR 28-FEB-2001; 2001WO-US006520.

PR 09-MAR-2001; 2001US-0274399P.

PR 03-APR-2001; 2001US-0280382P.

PR 04-APR-2001; 2001US-0282129P.

PR 04-APR-2001; 2001US-0282199P.

PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 DR WPI; 2002-362426/39.
 DR N-PSDB; ABK70009.
 XX
 XX New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 XX
 PS Claim 11; Fig 98; 218pp; English.
 CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. Polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention
 XX
 SQ Sequence 781 AA:
 Query Match 96.5%; Score 250; DB 5; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSEFIKQDINDNPPIFFPLGPHATVPENSVGTSTVIGTADADDP 48
 DB 133 PSEFIKQDINDNPPIFFPLGPHATVPENSVGTSTVIGTADADDP 180
 RESULT 9
 AD116604
 ID AD116604 standard; protein, 781 AA.
 XX
 AC AD116604;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human NOXV protein to treat human pathological conditions Segid140.
 XX
 XX human; NOXV; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytosolic; cardiac; anti-infective; immunosuppressive; antiallergic;
 KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
 KW anasthenic; nephrotropic; antiarrhythmic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW

KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
 KW single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO200268649-A2.
 XX
 XX 06-SEP-2002.
 PD
 XX
 XX 31-JAN-2002; 2002WO-US002785.
 XX
 XX 31-JAN-2001; 2001US-0265395P.
 PR 31-JAN-2001; 2001US-0265412P.
 PR 31-JAN-2001; 2001US-0265514P.
 PR 31-JAN-2001; 2001US-0265517P.
 PR 02-FEB-2001; 2001US-0266406P.
 PR 05-FEB-2001; 2001US-0266767P.
 PR 07-FEB-2001; 2001US-0266975P.
 PR 08-FEB-2001; 2001US-0267459P.
 PR 09-FEB-2001; 2001US-0267823P.
 PR 15-FEB-2001; 2001US-0268974P.
 PR 26-FEB-2001; 2001US-0271664P.
 PR 27-FEB-2001; 2001US-0271833P.
 PR 27-FEB-2001; 2001US-0271855P.
 PR 02-MAR-2001; 2001US-0272788P.
 PR 02-MAR-2001; 2001US-0273046P.
 PR 14-MAR-2001; 2001US-0275925P.
 PR 14-MAR-2001; 2001US-0275947P.
 PR 14-MAR-2001; 2001US-0275950P.
 PR 14-MAR-2001; 2001US-0275989P.
 PR 15-MAR-2001; 2001US-0276448P.
 PR 15-MAR-2001; 2001US-0276450P.
 PR 16-MAR-2001; 2001US-0276397P.
 PR 16-MAR-2001; 2001US-0276768P.
 PR 20-MAR-2001; 2001US-0278652P.
 PR 26-MAR-2001; 2001US-0278775P.
 PR 26-MAR-2001; 2001US-0278778P.
 PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 11-APR-2001; 2001US-0283092P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-032379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 XX
 PA (CURAGEN CORP.
 PI Tchernav VT, Spytek KA, Zernusen BD, Patturajan M, Shinkets RA;
 PI Li L, Gangolli EA, Padigaru M, Anderson DW, Raselli L, Miller CE;
 PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CB, Burgess CZ;
 PI Rutak K, Grosse WM, Alsebrook JP, Lepley DM, Rieger DK,

DR WPI; 2002-706998/76.
DR N-PSDB; AD116603.
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

PS Claim 1; SEQ ID NO 140; 1498bp; English.

CC This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC haemostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
CC antiasthmatic, neurotrophic, antidiabetic, antiarteriosclerotic, anorectic,
CC antiautismic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, nocotropic, antibacterial, vitricide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.

CC Sequence 781 AA;

Query Match 96.5%; Score 250; DB 5; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPFIPFLGPHATVEMSNVGTSTVIQVTAHDDP 48
Db 133 PSEFIKQDINDNPFIPFLGPHATVEMSNVGTSTVIQVTAHDDP 180

RESULT 10
AD11606
ID AD11606 standard; protein; 781 AA.

AC AD11606;

DT 15-APR-2004 (first entry)

DE Human NOVX protein to treat human pathological conditions SeqId142.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW cytostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KW antiasthmatic; nephrotropic; antiarthritic; hepatotropic;
KW neuroprotective; nocotropic; antibacterial; vitricide; antiparasitic;
KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.

OS Homo sapiens.

XX WO200268649-A2.
PN

XX 06-SEP-2002.
FD 31-JAN-2002; 2002WO-US002785.
XX 31-JAN-2001; 2001US-0265395P.
PF 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 08-FEB-2001; 2001US-0267057P.
PR 09-FEB-2001; 2001US-0267459P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296364P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

XX Tchernev VT, Spyrek KA, Zernhusen BD, Patnirajan M, Shinkets RA;
PI Li L, Ganggoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
PI Gerlach VL, Taupier RU, Gusev VI, Colman SD, Wolene AR, Pena CA;
PI Furrak K, Grosse WM, Alsdorck JF, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706998/76.
DR N-PSDB; AD116605.

PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

```
PT pharmacogenomics.
XX
XX Claim 1; SEQ ID NO 142; 1498bp; English.
XX
XX
XX This invention relates to a novel nucleic acid, and encoded polypeptides
XX thereof, which have properties related to the stimulation of biochemical
XX or physiological responses in a cell, tissue, organ or organism.
XX Specifically, it refers to the use of biologically active fragments for
XX diagnostic and prognostic assays and furthermore in the treatment of
XX diverse pathological conditions. The present invention describes novel
XX human and murine NOVX proteins, as well as methods to modulate their
XX expression using antisense oligos, ribozymes and peptide nucleic acids.
XX The NOVX polypeptides, polynucleotides and antibodies are useful in
XX treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in
XX treating or preventing diseases such as inflammation, autoimmune
XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome
XX (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
XX and epilepsy. Accordingly, these molecules have many activities including
XX cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
XX haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
XX antiasthmatic, nephroprotective, hepatotropic, neurotrophic,
XX neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
XX relaxant and anticonvulsant. In addition, they are useful in screening
XX assays to identify small molecules that modulate or inhibit, for example,
XX neurogenesis, wound healing and angiogenesis. The nucleic acids are also
XX used as in chromosome mapping, tissue typing, preventive medicine and
XX pharmacogenomics. This polypeptide is a human NOVX protein of the
XX invention.
XX
XX Sequence 781 AA;
SQ
Query Match 96.5%; Score 250; DB 5; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSEFTIKGQDINDNPPIFPLGPHATVPEMSNVTSTVQYTAHADDP 48
Db 133 PSEFTIKQDINDNPPIFPLGPHATVPEMSNVTSTVQYTAHADDP 180

RESULT 11
ABR40114
ID ABR40114 standard; protein; 781 AA.
XX
XX ABR40114;
AC
XX
XX 04-JUL-2003 (first entry)
DT
XX
XX Human cell adhesion and extracellular matrix protein, CADECM-11.
DE
XX
XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
XX anticonvulsant; neurotrophic; neuroprotective; immunosuppressive;
XX dermatological; anti-inflammatory; cyostatic; antiarteriosclerotic;
XX gene therapy; cell adhesion; extracellular matrix; CADCM;
XX immune system disorder; AIDS; allergy; neurological disorder; stroke;
XX Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
XX cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
XX genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
XX atherosclerosis.
XX
XX Homo sapiens.
OS
XX
XX W02003027230-A2.
PN
XX
XX 03-APR-2003.
PD
XX
XX 02-AUG-2002; 2002MO-US024649.
PF
XX
XX 03-AUG-2001; 2001US-030964P.
PR
XX 03-AUG-2001; 2001US-031011P.
PR 17-AUG-2001; 2001US-0313031P.
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PR 31-AUG-2001; 2001US-0316771P.
PR 07-SEP-2001; 2001US-0317866P.
PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
XX (INCYTE GENOMICS INC.
PA
XX
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H,
PI Forythe JU, Elliott VS, Griffin JA, Gorvad AE, Azimzal Y,
PI Kallick DA, Xu Y, Honchell CD, Baughn ME, Gietzen KJ, Lee S;
PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Rammkumar J;
XX
XX WPI. 2003-354645/33.
DR
XX N-PSDB; ACC00402.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
XX Claim 1; Page 192-194; 234pp; English.
PS
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX proliferative disorders (e.g. cancer or atherosclerosis)
XX
XX Sequence 781 AA;
SQ
Query Match 96.5%; Score 250; DB 6; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PSEFTIKGQDINDNPPIFPLGPHATVPEMSNVTSTVQYTAHADDP 48
Db 133 PSEFTIKQDINDNPPIFPLGPHATVPEMSNVTSTVQYTAHADDP 180

RESULT 12
ADA01366
ID ADA01366 standard; protein; 781 AA.
XX
XX ADA01366;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human PRO polypeptide #49.
DE
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
XX Homo sapiens.
OS
XX
XX US2003068779-A1.
PN
XX
XX 10-APR-2003.
PD
XX
XX 16-SEP-2002; 2002US-00245107.
PF
XX
XX 09-MAY-2001; 2001US-0290589P.
PR
```

PR 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENENTECH INC.)
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21381 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumor necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumor in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumors). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumors, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 XX
 SQ Sequence 781 AA;
 XX
 Query Match 96.5%; Score 250; DB 6; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSEFIKQDINDNPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 48
 DB 133 PSEFIKQDINDNPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 180
 XX
 RESULT 13
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumor; lung tumor; colon tumor;
 KW breast tumor; prostate tumor; rectal tumor; kidney tumor;
 XX liver tumor; cytosolic; vaccine.
 XX
 OS Homo sapiens.
 XX
 AC US2003064474-A1.
 XX
 PN 03-APR-2003.

XX
 XX 16-SEP-2002; 2002US-00245859.
 XX
 XX 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENENTECH INC.)
 XX
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX WPI; 2003-605867/57.
 DR N-PSDB; ADA43794.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21381, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 11; Fig 98; 308pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21381 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6011, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumor in a mammal, including tumors of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SQ Sequence 781 AA;
 XX
 Query Match 96.5%; Score 250; DB 6; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PSEFIKQDINDNPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 48
 DB 133 PSEFIKQDINDNPIPLGPHATVPEMSNVGTSVIQVTAHDADDP 180
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 ADA43563
 ID ADA43563 standard; protein; 781 AA.
 XX
 AC ADA43563;
 XX
 DT 20-NOV-2003 (first entry)
 XX

DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003073196-A1.
 XX
 XX 17-APR-2003.
 PD
 XX 18-SEP-2002; 2002US-00246210.
 PF
 XX 04-APR-2001; 2001US-0282199P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX
 DR MPI; 2003-743814/70.
 DR N-PSDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1317, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 CC
 XX Sequence 781 AA;
 SQ

Query Match 96.5%; Score 250; DB 6; Length 781;
 Best Local Similarity 97.9%; Pred. No. 9.9e-26;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPENSGTSTVQTVAHADDP 48
 DB 133 PSEFIKQDINDNPPIPLGPHATVPENSGTSTVQTVAHADDP 180
 RESULT 15
 ADA01238
 ID ADA01238 standard; protein; 781 AA.
 XX
 AC ADA01238;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
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 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 KW microvascular endothelial cell; endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 PN US2003068782-A1.
 XX
 XX 10-APR-2003.
 PD
 XX 16-SEP-2002; 2002US-00245851.
 PF
 XX 27-APR-1999; 99US-0131271P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028551.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 XX
 DR MPI; 2003-625487/59.
 DR N-PSDB; ADA01237.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 11; Fig 98; 308pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 XX Sequence 781 AA;
 SQ

Wed Dec 8 11:46:34 2004

us-09-788-051-8.rag

Page 11

Query Match 96.5%; Score 250; DB 6; Length 781;
Best Local Similarity 97.9%; Pred. No. 9.9e-26;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PSEFIKQDINDNPPIFGPYHATVPEMSNVGTSVIQVTAHDADDP 48
Db 133 PSEFIKQDINDNPPIFGPYHATVPEMSNVGTSVIQVTAHDADDP 180

Search completed: December 8, 2004, 10:13:05
Job time : 20.863 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 : Search time 49.0484 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-8

Perfect score: 259
Sequence: 1 PSEFIKQDINDNPPIFLP.....EMSNVGTSTVIVTAHADDP 48

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep:*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	259	100.0	48	10	US-09-788-051-8
2	259	100.0	620	10	US-09-788-051-7
3	259	100.0	636	10	US-09-788-051-4
4	250	96.5	493	15	US-10-072-012-482
5	250	96.5	607	15	US-10-258-951-74
6	250	96.5	781	9	US-09-860-868-2
7	250	96.5	781	14	US-10-245-752-98
8	250	96.5	781	14	US-10-245-859-98
9	250	96.5	781	14	US-10-245-103-98
10	250	96.5	781	14	US-10-245-107-98
11	250	96.5	781	14	US-10-245-113-98
12	250	96.5	781	14	US-10-245-771-98
13	250	96.5	781	14	US-10-245-851-98

14	250	96.5	781	14	US-10-245-883-98	Sequence 98, Appl
15	250	96.5	781	14	US-10-237-535-98	Sequence 98, Appl
16	250	96.5	781	14	US-10-238-183-98	Sequence 98, Appl
17	250	96.5	781	14	US-10-238-283-98	Sequence 98, Appl
18	250	96.5	781	14	US-10-238-370-98	Sequence 98, Appl
19	250	96.5	781	14	US-10-245-055-98	Sequence 98, Appl
20	250	96.5	781	14	US-10-245-147-98	Sequence 98, Appl
21	250	96.5	781	14	US-10-245-730-98	Sequence 98, Appl
22	250	96.5	781	14	US-10-246-210-98	Sequence 98, Appl
23	250	96.5	781	14	US-10-239-156-98	Sequence 98, Appl
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25	250	96.5	781	14	US-10-243-409-98	Sequence 98, Appl
26	250	96.5	781	14	US-10-245-621-98	Sequence 98, Appl
27	250	96.5	781	14	US-10-245-880-98	Sequence 98, Appl
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31	250	96.5	781	14	US-10-245-427-98	Sequence 98, Appl
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35	250	96.5	781	14	US-10-245-320-98	Sequence 98, Appl
36	250	96.5	781	14	US-10-162-435-13	Sequence 13, Appl
37	250	96.5	781	14	US-10-242-743-98	Sequence 98, Appl
38	250	96.5	781	14	US-10-242-845-98	Sequence 98, Appl
39	250	96.5	781	14	US-10-237-636-98	Sequence 98, Appl
40	250	96.5	781	14	US-10-238-325-98	Sequence 98, Appl
41	250	96.5	781	14	US-10-238-346-98	Sequence 98, Appl
42	250	96.5	781	14	US-10-238-411-98	Sequence 98, Appl
43	250	96.5	781	14	US-10-245-124-98	Sequence 98, Appl
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ALIGNMENTS

RESULT 1
US-09-788-051-8
Sequence 8, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dymac, Radocic T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
US-09-788-051-8
ORGANISM: Homo sapiens
TYPE: PRT
LENGTH: 48
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Best Local Similarity 100.0%; Pred. No. 6.4e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

US-09-788-051-7

Sequence 7, Application US/09788051

Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D

APPLICANT: Kuo, Chiaoyun

APPLICANT: Arterburn, Matthew C

APPLICANT: Yeung, George

APPLICANT: Palencia, Servando

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND

FILE REFERENCE: POLYNUCLEOTIDES

FILE REFERENCE: HYS-39

CURRENT APPLICATION NUMBER: US/09/788,051

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 7

LENGTH: 620

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-051-7

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Best Local Similarity 100.0%; Pred. No. 1.4e-25;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 117 PSEFIKGQDINDNPPIFPLGPHATVPENSVGTSTVQTADADDP 164

RESULT 3

US-09-788-051-4

Sequence 4, Application US/09788051

Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D

APPLICANT: Kuo, Chiaoyun

APPLICANT: Arterburn, Matthew C

APPLICANT: Yeung, George

APPLICANT: Palencia, Servando

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN

FILE REFERENCE: POLYNUCLEOTIDES

FILE REFERENCE: HYS-39

CURRENT APPLICATION NUMBER: US/09/788,051

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 4

LENGTH: 636

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-051-4

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US-10-072-012-482

Sequence 482, Application US/10072012

Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar

APPLICANT: Spyrek, Kimberly

APPLICANT: Zernusen, Bryan

APPLICANT: Patuturajan, Meera

APPLICANT: Shinkets, Richard

APPLICANT: Li, Li

APPLICANT: Gangolli, Esha

APPLICANT: Padigaru, Muralidhara

APPLICANT: Anderson, David W.

APPLICANT: Rastelli, Luca

APPLICANT: Miller, Charles E.

APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Colman, Steven D.

APPLICANT: Molenc, Adam R.

APPLICANT: Pena, Carol E. A

APPLICANT: Futrak, Katarzyna

APPLICANT: Groesse, William M.

APPLICANT: Alsobrook II, John P.

APPLICANT: Lepley, Denise M.

APPLICANT: Rieger, Daniel K.

APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-258

CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR FILING DATE: 2001-02-08

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NUMBER OF SEQ ID NOS: 1391

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 482

LENGTH: 493

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-482

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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98
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; Publication No. US20030068780A1
; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,143
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
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Best Local Similarity 97.9%; Pred. No. 2.9e-24;
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US-10-245-771-98
; Sequence 98, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-98
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Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 133 PSEFIKQDINDNPFIPLGPHATVPEMSVGTSVIQVTAHDADDP 180
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RESULT 13
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
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/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-851-98

Query Match      96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 PSEFIKQDINDNPIPLPGYHATVPENSVGTSVIQTADADDP 48
Db      133 PSEFIKQDINDNPIPLPGYHATVPENSVGTSVIQTADADDP 180

RESULT 14
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
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/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
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/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-883-98

Query Match      96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 PSEFIKQDINDNPIPLPGYHATVPENSVGTSVIQTADADDP 48
Db      133 PSEFIKQDINDNPIPLPGYHATVPENSVGTSVIQTADADDP 180

RESULT 15
US-10-237-535-98
/ Sequence 98, Application US/10237535
/ Publication No. US20030073188A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3630R1C3
/ CURRENT APPLICATION NUMBER: US/10/237,535
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
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Wed Dec 8 11:46:35 2004

us-09-788-051-8.rapb

Page 7

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? PRIOR APPLICATION NUMBER: 60/087607
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PRIOR FILING DATE: 2001-08-13
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PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/081056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 96.5%; Score 250; DB 14; Length 781;
Best Local Similarity 97.9%; Pred. No. 2.9e-24;
Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPENSNVGTSTVIQVTAHDADDP 48
133 PSEFIKQDINDNPPIPLGPHATVPENSNVGTSTVIQVTAHDADDP 180

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Job time : 49.0484 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 : Search time 5.72373 seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-8
Perfect score: 259
Sequence: 1 PSEFIIKGDINDNPPIPL.....EMSNVGSVIVTAHDADDP 48

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Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	189	73.0	693	2	US-08-738-349-6 Sequence 6, Appl
2	189	73.0	693	4	US-09-919-497-55 Sequence 55, Appl
3	189	73.0	796	1	US-08-188-228-58 Sequence 58, Appl
4	189	73.0	796	1	US-08-333-643-52 Sequence 52, Appl
5	189	73.0	796	1	US-08-333-638-58 Sequence 58, Appl
6	189	73.0	796	2	US-08-738-349-4 Sequence 4, Appl
7	189	73.0	796	4	US-09-654-348-2 Sequence 2, Appl
8	188.5	72.8	615	2	US-08-738-349-12 Sequence 12, Appl
9	187	72.2	9	9	US-08-188-228-44 Sequence 44, Appl
10	186	71.8	532	1	US-08-333-638-44 Sequence 44, Appl
11	186	71.8	532	1	US-08-188-228-54 Sequence 54, Appl
12	186	71.8	793	1	US-08-332-643-48 Sequence 48, Appl
13	186	71.8	793	1	US-08-332-643-48 Sequence 54, Appl
14	186	71.8	793	1	US-08-332-638-54 Sequence 42, Appl
15	186	71.8	799	1	US-08-188-228-42 Sequence 42, Appl
16	186	71.8	799	1	US-08-332-638-42 Sequence 46, Appl
17	164	63.3	653	1	US-08-188-228-46 Sequence 46, Appl
18	164	63.3	653	1	US-08-333-638-46 Sequence 46, Appl
19	162	62.5	794	1	US-08-188-228-60 Sequence 54, Appl
20	162	62.5	794	1	US-08-332-643-54 Sequence 54, Appl
21	162	62.5	794	1	US-08-332-638-60 Sequence 60, Appl
22	144	55.6	780	1	US-08-188-228-50 Sequence 50, Appl
23	144	55.6	780	1	US-08-332-643-44 Sequence 44, Appl
24	144	55.6	780	1	US-08-332-638-50 Sequence 50, Appl
25	117	45.2	109	3	US-09-187-859-5 Sequence 5, Appl
26	117	45.2	109	4	US-09-639-542B-5 Sequence 5, Appl
27	117	45.2	109	4	US-09-535-852-5 Sequence 5, Appl

28	115	44.4	109	3	US-09-187-859-17 Sequence 17, Appl
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33	114	44.0	109	4	US-09-535-852-11 Sequence 11, Appl
34	111	42.9	713	1	US-08-188-228-62 Sequence 62, Appl
35	111	42.9	713	1	US-08-332-643-56 Sequence 56, Appl
36	111	42.9	713	1	US-08-332-638-62 Sequence 62, Appl
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41	106	40.9	712	2	US-08-474-067-2 Sequence 2, Appl
42	106	40.9	717	2	US-08-474-067A-2 Sequence 4, Appl
43	106	40.9	717	2	US-08-474-068A-4 Sequence 4, Appl
44	106	40.9	717	2	US-08-472-481-4 Sequence 4, Appl
45	106	40.9	906	4	US-09-417-029-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 73.0%; Score 189; DB 2; Length 693;
Best Local Similarity 79.2%; Pred. No. 2.5e-18;
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Qy 1 PSEFIIGQDINDNPPIPLGPHATVPENSVGTSTVQTADADDP 48
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RESULT 2
US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Muller, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 73.0%; Score 189; DB 4; Length 693;
Best Local Similarity 79.2%; Pred. No. 2.5e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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RESULT 3
US-08-188-228-58
Sequence 58, Application US/08188228
Patent No. 559725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6400 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 73.0%; Score 189; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIIGQDINDNPPIPLGPHATVPENSVGTSTVQTADADDP 48
Db 142 PSEFIIVKQDINDNPPEFLHETHTANVPERSNVGTSTVQTASDADDP 189

RESULT 4
US-08-332-643-52
Sequence 52, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query Match 73.0%; Score 189; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIIGQDINDNPPIPLGPHATVPENSVGTSTVQTADADDP 48
Db 142 PSEFIIVKQDINDNPPEFLHETHTANVPERSNVGTSTVQTASDADDP 189

RESULT 5

US-08-332-638-58
Sequence 58, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 73.0%; Score 189; DB 1; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPMSNVGTSVIQVTAHDADDP 48
DB 142 PSEFIKQDINDNPPIPLGPHATVPMSNVGTSVIQVTAHDADDP 189

RESULT 6

US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869618
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match 73.0%; Score 189; DB 2; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPMSNVGTSVIQVTAHDADDP 48
DB 142 PSEFIKQDINDNPPIPLGPHATVPMSNVGTSVIQVTAHDADDP 189

RESULT 7
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier

TITLE OF INVENTION: Methods and Compositions for Treatment
of Inflammatory Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/ERP/NAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 73.0%; Score 189; DB 4; Length 796;
Best Local Similarity 79.2%; Pred. No. 3e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVPMSNVGTSVIQVTAHDADDP 48

Db 142 PSEFIVKQDINDNPPEFLHETVHANVPERSNVGTSVIQVTASDADDP 189

RESULT 8

US-08-738-349-12

Sequence 12, Application US/08738349

Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takekoshi, Sunao

APPLICANT: Kawaji, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Amano, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE:

APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481.1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 615 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-738-349-12

Query Match 72.8%; Score 188.5; DB 2; Length 615;

Best Local Similarity 81.2%; Pred. No. 2.6e-18;

Matches 39; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Qy 1 PSEFIKGGDINNPPFIPGPHATVPENSNVGTSVIQVTADDDP 48

Db 136 PSEFIVKQDINDNPPEFLHETVHANVPERSNVGTSVIQVTASDADDP 182

RESULT 9

US-08-738-349-2

Sequence 2, Application US/08738349

Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takekoshi, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Amano, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE:

APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481.1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-738-349-2

Query Match 72.2%; Score 187; DB 2; Length 796;

Best Local Similarity 79.2%; Pred. No. 5.9e-18;

Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKGGDINNPPFIPGPHATVPENSNVGTSVIQVTADDDP 48

Db 142 PSEFIVKQDINDNPPEFLHETVHANVPERSNVGTSVIQVTASDADDP 189

RESULT 10

US-08-188-228-44

Sequence 44, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 71.8%; Score 186; DB 1; Length 532;
Best Local Similarity 79.2%; Pred. No. 4,8e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPPFPLGPHYATVPEMSNVGTSGVQTADADDP 48
Db 150 PSEFIKQDINDNAPFLNGPYHATVPEMSILGTSVNTATADDP 197

RESULT 11
US-08-332-638-44
Sequence 44, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 564625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 71.8%; Score 186; DB 1; Length 532;
Best Local Similarity 79.2%; Pred. No. 4,8e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPPFPLGPHYATVPEMSNVGTSGVQTADADDP 48
Db 150 PSEFIKQDINDNAPFLNGPYHATVPEMSILGTSVNTATADDP 197

RESULT 12
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 71.8%; Score 186; DB 1; Length 793;
Best Local Similarity 79.2%; Pred. No. 8,1e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSEFIKQDINDNPPFPLGPHYATVPEMSNVGTSGVQTADADDP 48
Db 143 PSEFIKQDINDNAPFLNGPYHATVPEMSILGTSVNTATADDP 190

RESULT 13
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 71.8%; Score 186; DB 1; Length 793;
Best Local Similarity 79.2%; Pred. No. 8.1e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVEMSNVGTSVYQVTAHADDP 48
DB 143 PSEFIKQDINDNAPFLNGPHATVEMSIIGTSVNTATADDDP 190

RESULT 14
US-08-332-638-54
Sequence 54, Application US/08332638
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 71.8%; Score 186; DB 1; Length 793;
Best Local Similarity 79.2%; Pred. No. 8.1e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSEFIKQDINDNPPIPLGPHATVEMSNVGTSVYQVTAHADDP 48
DB 143 PSEFIKQDINDNAPFLNGPHATVEMSIIGTSVNTATADDDP 190

RESULT 15
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5587725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:

Wed Dec 8 11:46:35 2004

us-09-788-051-8.rai

Page 7

LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 71.8%; Score 186; DB 1; Length 799;
Best Local Similarity 79.2%; Pred. No. 8.2e-18;
Matches 38; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 1 PSEFIKGDINDNPPIFPLGYPYHATVPEMSNVGTSYIQYTAHDADDP 48
Db 150 PSEFIKVDINDNAPRFLNGPYHATVPEMSILGTSTNTVTATDADDP 197

Search completed: December 8, 2004, 10:01:12
Job time : 5.72373 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 : Search time 3.88194 seconds
[without alignments]
1189.717 Million cell updates/sec

Title: US-09-788-051-9
Perfect score: 247
Sequence: 1 STVTVTLSVDVNDNPKPKFQ.....ETAGPGLVGRRLRAQDDPLG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_79:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	180	72.9	796	2	cadherin-11 - mouse
2	180	72.9	796	2	cadherin-11 - mouse
3	180	72.9	796	2	cadherin-11 - mouse
4	178	72.1	796	2	cadherin-11 - mouse
5	169	68.4	789	2	cadherin-11 - mouse
6	169	68.4	789	2	cadherin-11 - mouse
7	163	66.0	793	2	cadherin-6 - human
8	150	60.7	790	2	cadherin-6 - human
9	150	60.7	790	2	cadherin-6 - human
10	147	59.5	794	2	cadherin-14 - huma
11	140	56.7	790	2	cadherin-12 - huma
12	139	56.3	785	2	cadherin-7 - chick
13	120	48.6	709	2	cadherin-7 - chick
14	120	48.6	709	2	cadherin-7 - chick
15	114	45.2	5147	1	cadherin-11 - mouse
16	111.5	45.1	3343	1	cadherin-11 - mouse
17	110	44.5	784	1	cadherin-11 - mouse
18	110	44.5	784	1	cadherin-11 - mouse
19	110	44.5	784	1	cadherin-11 - mouse
20	106.5	43.1	2809	2	cadherin-11 - mouse
21	106.5	43.1	2809	2	cadherin-11 - mouse
22	105	42.5	2610	2	cadherin-11 - mouse
23	104	42.1	1200	2	cadherin-11 - mouse
24	103	41.7	3034	1	cadherin-11 - mouse
25	100	40.5	732	1	cadherin-11 - mouse
26	100	40.5	732	1	cadherin-11 - mouse
27	96	38.9	826	1	cadherin-11 - mouse
28	96	38.9	826	1	cadherin-11 - mouse
29	96	38.9	826	1	cadherin-11 - mouse

30	96	38.9	896	2	A55363	desmocollin, type
31	95	38.5	373	2	T34563	hypothetical prote
32	95	38.5	505	2	S43064	cadherin - African
33	95	38.5	1544	2	T29482	hypothetical prote
34	94.5	38.3	1311	2	T33757	hypothetical prote
35	94	38.1	701	2	T17243	hypothetical prote
36	92	37.2	141	2	PC4298	cadherin FIB2 - hu
37	92	37.2	809	1	TUBODD	desmocollin 2b pre
38	92	37.2	822	1	TUBSCP	P-cadherin precurs
39	92	37.2	863	1	TUBODC	desmocollin 2a pre
40	92	37.2	884	2	S34438	uvomorulin - mouse
41	92	37.2	4307	2	T20721	hypothetical prote
42	91	36.8	3097	2	T00021	DN-cadherin - fru1
43	90.5	36.6	137	2	PC4297	cadherin FIB1 - hu
44	90.5	36.6	829	2	T45336	Ksp-cadherin - rab
45	90	36.4	895	1	IUXLCP	EP-cadherin precur

ALIGNMENTS

RESULT 1
148277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148277
R/Hoffmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: 148277; PMID:95269866; PMID:7750649
A/Accession: 148277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:g642796; PDB:CA54674.1; PDB:g666
C/Genetics:
A/Gene: cad-11
C/Superfamily: cadherin; cadherin repeat homology
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 72.9%; Score 180; DB 2; Length 796;
Best Local Similarity 68.8%; Pred. No. 2.7e-15;
Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 STVTVTLSVDVNDNPKPKFQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
Db 251 TTKVTTTLTDVNDNPKPKFQSLYQFSVETAGPGLVGRRLRAQDDPLG 298

RESULT 2

149556
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 149556
R/Kamura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, Dev. Biol. 169, 347-358, 1995
A/Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the hea
A/Reference number: 149556; PMID:95269867; PMID:7750650
A/Accession: 149556
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; GB:D31963; NID:g974190; PDB:BA06730.1; PDB:g97419
C/Superfamily: cadherin; cadherin repeat homology
F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 72.9%; Score 180; DB 2; Length 796;
Best Local Similarity 68.8%; Pred. No. 2.7e-15;
Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 STVTVTLSVDVNDNPKPKFQSLYQFSVETAGPGLVGRRLRAQDDPLG 48

A; Cross-references: GDB:5822911

Keywords: calcium binding; cell adhesion; duplication
F,163-269/Domain: cadherin repeat homology <CDH>

Query Match	65.0%;	Score 163;	DB 2;	Length 793;
Best Local Similarity	64.6%;	Pred. No. 4.6e-13;		
Matches 31,	Conservative	7,	Mismatches 10,	Indels 0,
				Gaps 0,

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QY      1 STVTVTLSDVDNDNPKPFQSLXQFSVEIAGPGTIVGRRAQDPDLG 48
        :|::|||:|||::|||::|||::|||::|||::|||::|||::|||
DB      252 TTTLLTVLITDVNDNPPKFAQSILYHFSVPEDVVLGTALGRVKANDQDIG 299
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RESULT 8
I50178

C:Species: Gallus gallus (chicken)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: 1501/8
R;Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995

A;Title: Neutral crest cell adhesion controlled by
A;Reference number: I50178; MUID:95309115; PMID:7540531
A;Accession: I50178

A:Status: preliminary; translated from GB/EMBL/DBS
A:Molecule type: mRNA
A:Residues: 1-790 <NAK>

A:Cross-references: UNIPROT:Q90762; GB:D42149; NID:g867998; PID:BA007120.1; PID:g867998
F:162-268/Domain: cadherin repeat homology <CDH>
C:Superfamily: cadherin; cadherin repeat homology

Query Match	60.7%	Score 150;	DB 2;	Length 790;
Best Local Similarity	55.3%	Pred. No. 2.3e-11;		
Matches 26; Conservative	10;	Mismatches 11;	Indels 0;	Gaps 0

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Qy      1 STTVITLSDVNDNPPKFPGLYQFSVETAGGTLVGRRLRAQDDL 47
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db     251 TTTVNITLTDVNDNPPRFPGSTYQFRAPESTPDPSPIGRIKANDAV 29
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RESULT
G02678

Cadherin-14 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text change 09-Jul-2004

C/Accession: G02678
R/Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S
submitted to the EMBL Data Library, May 1996

A/Reference number: H01584
A/Accession: G02678
A/Status: preliminary; translated from GB/EMBL/D

A.Molecule type: mRNA
A.Residues: 1-790 <SHI>
A.Cross-references: UNIPROT:O13634; EMBL:U59335; NID:5f1389852; PIDD:AAE02933.1; PID:G138

Query Match 60.7%; Score 150; DB 2; Length 790;

MACCHIE
OY

Db 251 STVNITLTDVNDNPPRFQKH YQLYPESAQVGSAVGKIKANDADTG 29

RESULT 10	R.Nakagawa, S.; Takeichi, M. Development 121, 1321-1332, 1995
TS0372	A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe

cadherin 12 - human	A:Reference number: I50178; MUID:95309115; PMID:7540531
N:Alternate names: Br-cadherin	A:Accession: I50180
C:Species: Homo sapiens (man)	A>Status: Preliminary; translated from GB/EMBL/DBJ

C;Date: 31-May-1996 #sequence 31-May-1996 #text_change 09-Jul-2000

[illegible]

RESULT 10
159372
Rinnakagawa, S.; Iakelcuk, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell adhesion controlled by sequential and subpopulation-specific
D'Effects: 159372, 159373, 159374, 159375, 159376, 159377, 159378, 159379, 159380, 159381, 159382, 159383, 159384, 159385, 159386, 159387, 159388, 159389, 159390, 159391, 159392, 159393, 159394, 159395, 159396, 159397, 159398, 159399, 159400, 159401, 159402, 159403, 159404, 159405, 159406, 159407, 159408, 159409, 159410, 159411, 159412, 159413, 159414, 159415, 159416, 159417, 159418, 159419, 159420, 159421, 159422, 159423, 159424, 159425, 159426, 159427, 159428, 159429, 159430, 159431, 159432, 159433, 159434, 159435, 159436, 159437, 159438, 159439, 159440, 159441, 159442, 159443, 159444, 159445, 159446, 159447, 159448, 159449, 159450, 159451, 159452, 159453, 159454, 159455, 159456, 159457, 159458, 159459, 159460, 159461, 159462, 159463, 159464, 159465, 159466, 159467, 159468, 159469, 159470, 159471, 159472, 159473, 159474, 159475, 159476, 159477, 159478, 159479, 159480, 159481, 159482, 159483, 159484, 159485, 159486, 159487, 159488, 159489, 159490, 159491, 159492, 159493, 159494, 159495, 159496, 159497, 159498, 159499, 159500, 159501, 159502, 159503, 159504, 159505, 159506, 159507, 159508, 159509, 159510, 159511, 159512, 159513, 159514, 159515, 159516, 159517, 159518, 159519, 159520, 159521, 159522, 159523, 159524, 159525, 159526, 159527, 159528, 159529, 159530, 159531, 159532, 159533, 159534, 159535, 159536, 159537, 159538, 159539, 159540, 159541, 159542, 159543, 159544, 159545, 159546, 159547, 159548, 159549, 159550, 159551, 159552, 159553, 159554, 159555, 159556, 159557, 159558, 159559, 159560, 159561, 159562, 159563, 159564, 159565, 159566, 159567, 159568, 159569, 159570, 159571, 159572, 159573, 159574, 159575, 159576, 159577, 159578, 159579, 159580, 159581, 159582, 159583, 159584, 159585, 159586, 159587, 159588, 159589, 159590, 159591, 159592, 159593, 159594, 159595, 159596, 159597, 159598, 159599, 159600, 159601, 159602, 159603, 159604, 159605, 159606, 159607, 159608, 159609, 159610, 159611, 159612, 159613, 159614, 159615, 159616, 159617, 159618, 159619, 159620, 159621, 159622, 159623, 159624, 159625, 159626, 159627, 159628, 159629, 159630, 159631, 159632, 159633, 159634, 159635, 159636, 159637, 159638, 159639, 159640, 159641, 159642, 159643, 159644, 159645, 159646, 159647, 159648, 159649, 159650, 159651, 159652, 159653, 159654, 159655, 159656, 159657, 159658, 159659, 159660, 159661, 159662, 159663, 159664, 159665, 159666, 159667, 159668, 159669, 159670, 159671, 159672, 159673, 159674, 159675, 159676, 159677, 159678, 159679, 159680, 159681, 159682, 159683, 159684, 159685, 159686, 159687, 159688, 159689, 159690, 159691, 159692, 159693, 159694, 159695, 159696, 159697, 159698, 159699, 159700, 159701, 159702, 159703, 159704, 159705, 159706, 159707, 159708, 159709, 159710, 159711, 159712, 159713, 159714, 159715, 159716, 159717, 159718, 159719, 159720, 159721, 159722, 159723, 159724, 159725, 159726, 159727, 159728, 159729, 159730, 159731, 159732, 159733, 159734, 159735, 159736, 159737, 159738, 159739, 159740, 159741, 159742, 159743, 159744, 159745, 159746, 159747, 159748, 159749, 159750, 159751, 159752, 159753, 159754, 159755, 159756, 159757, 159758, 159759, 159760, 159761, 159762, 159763, 159764, 159765, 159766, 159767, 159768, 159769, 159770, 159771, 159772, 159773, 159774, 159775, 159776, 159777, 159778, 159779, 159780, 159781, 159782, 159783, 159784, 159785, 159786, 159787, 159788, 159789, 159790, 159791, 159792, 159793, 159794, 159795, 159796, 159797, 159798, 159799, 159800, 159801, 159802, 159803, 159804, 159805, 159806, 159807, 159808, 159809, 159810, 159811, 159812, 159813, 159814, 159815, 159816, 159817, 159818, 159819, 159820, 159821, 159822, 159823, 159824, 159825, 159826, 159827, 159828, 159829, 159830, 159831, 159832, 159833, 159834, 159835, 159836, 159837, 159838, 159839, 159840, 159841, 159842, 159843, 159844, 159845, 159846, 159847, 159848, 159849, 159850, 159851, 159852, 159853, 159854, 159855, 159856, 159857, 159858, 159859, 159860, 159861, 159862, 159863, 159864, 159865, 159866, 159867, 159868, 159869, 159870, 159871, 159872, 159873,

cadherin 12 - human
 N:Alternate names: Br-cadherin
 C:Species: Homo sapiens (man)
 A:Accession: 150180
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Reference number: 150180; M014350243; EMBL:550043

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C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
A;Molecule type: mRNA
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Wed Dec 8 11:46:38 2004

us-09-788-051-9.rpr

Page 5

Db 256 VNVTLIDVNDNPPFIHSDYVNSLNETALPGTPVVTVMASDNDLG 300

Search completed: December 8, 2004, 10:27:06
Job time : 4.88194 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.2397 Seconds
(without alignments)

1435.471 Million cell updates/sec

Title: US-09-788-051-9
Perfect score: 247
Sequence: 1 STVTVTLSVDNDNPKFQ.....ETAGPTLVGRRLRADPDPLG 48

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprotc.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	100.0	370	Q86T00	Q86T00 homo sapien
2	247	100.0	493	Q86L07	Q86L07 homo sapien
3	247	100.0	819	CAD0_HUMAN	Q86L07 homo sapien
4	244	98.8	781	Q86F06	Q86F06 mus musculu
5	244	98.8	781	AAH57373	AAH57373 mus muscu
6	180	72.9	792	CAD6_CHICK	Q93139 Gallus gall
7	180	72.9	796	CAD6_MOUSE	P55288 mus musculu
8	180	72.9	796	Q8C706	Q8C706 mus musculu
9	178	72.1	796	CAD6_HUMAN	P55287 homo sapien
10	174	70.4	796	Q86C29	Q86C29 homo sapien
11	173	70.0	794	Q93264	Q93264 xenopus lae
12	172	69.6	813	CAD6_MOUSE	Q93265 mus musculu
13	172	69.6	813	CAD6_RAT	Q63135 rattus norv
14	172	69.6	828	CAD6_HUMAN	Q94199 homo sapien
15	169	68.4	789	CAD6_RAT	P55280 rattus norv
16	169	68.4	790	CAD6_HUMAN	P55285 homo sapien
17	169	68.4	790	CAD6_MOUSE	P97326 mus musculu
18	163	66.0	508	Q86F04	Q86F04 mus musculu
19	163	66.0	508	AAH60200	AAH60200 mus muscu
20	163	66.0	716	Q8C375	Q8C375 mus musculu
21	163	66.0	716	Q8C449	Q8C449 mus musculu
22	163	66.0	716	AAH57581	AAH57581 mus muscu
23	163	66.0	754	Q8BRK4	Q8BRK4 mus musculu
24	163	66.0	799	CAD8_HUMAN	P55286 homo sapien
25	163	66.0	799	CAD8_MOUSE	P97291 mus musculu
26	163	66.0	799	CAD8_RAT	O54800 rattus norv
27	158	64.0	789	CAD9_HUMAN	Q941b4 homo sapien
28	150	60.7	337	Q8B1B5	Q8B1b5 mus musculu
29	150	60.7	790	CAD6_CHICK	Q90762 Gallus gall
30	150	60.7	790	CAD7_HUMAN	Q11634 homo sapien
31	147	59.5	794	CAD0_HUMAN	P55289 homo sapien

32	147	59.5	794	Q86UND2	Q86UND2 homo sapien
33	147	59.5	798	Q7ZYV7	Q7ZYV7 Gallus gall
34	147	59.5	798	Q8CGH3	Q8CGH3 Gallus gall
35	146	59.1	801	CADK_HUMAN	Q941b6 homo sapien
36	146	59.1	801	Q920M3	Q920M3 mus musculu
37	142	57.5	790	Q8V522	Q8V522 homo sapien
38	141	57.1	340	Q8BLT4	Q8BLT4 mus musculu
39	141	57.1	630	Q81Y78	Q81Y78 homo sapien
40	141	57.1	785	CAD7_HUMAN	Q941b5 homo sapien
41	141	57.1	785	Q8BM92	Q8BM92 mus musculu
42	140	56.7	790	Q91838	Q91838 xenopus lae
43	139	56.3	551	Q8AWM2	Q8AWM2 Gallus gall
44	139	56.3	785	CAD7_CHICK	Q90763 Gallus gall
45	138	55.9	963	CHC1_HUMAN	Q91158 homo sapien

ALIGNMENTS

RESULT 1					ALIGNMENTS				
ID	Q86T00	PRELIMINARY;	PRT;	370 AA.					
AC	Q86T00;								
DT	01-JUN-2003 (TREMBLrel. 24, Created)								Q86UND2
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								Q7ZYV7
DE	Full-length cDNA clone CSDBK003Y017 of HeLa cells of Homo sapiens (human) (Fragment).								Q8CGH3
DE	Homo sapiens (Human).								Q941b6
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								Q920M3
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.								Q8V522
OX	NCBI_TaxID=9606;								Q8BLT4
RN	[1]								Q81Y78
RP	SEQUENCE FROM N.A.								Q941b5
RC	TISSUE=HeLa cells;								Q8BM92
RA	Genoscope;								Q91838
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.								Q8AWM2
CC	-1- SIMILARITY: Contains 4 cadherin domains.								CAD7_CHICK
DR	EMBL: BX248303; CAD62630.1; -								Q91158
DR	GO: GO:0016020; C:membrane; IEA.								
DR	GO: GO:0005509; F:calcium ion binding; IEA.								
DR	GO: GO:0007156; P:homophilic cell adhesion; IEA.								
DR	InterPro: IPR002126; Cadherin; 3.								
DR	Pfam: PF00028; Cadherin; 3.								
DR	PRINTS: PR00205; CADHERIN.								
DR	SMART: SM00112; CA; 2.								
DR	PROSITE: PS00232; CADHERIN_1; 1.								
DR	PROSITE: PS0268; CADHERIN_2; 4.								
KW	Calcium; Calcium-binding.								
FT	NON_TER 1								
FT	NON_TER 370								
SQ	SEQUENCE 370 AA; 39479 MW; 3996DAF8A4500E0 CRC64;								
Query Match									
Best Local Similarity 100.0%; Score 247; DB 2; Length 370;									
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	STVTVTLSVDNDNPKFQSVETAGPTLVGRRLRADPDPLG 48							
DB	3	STVTVTLSVDNDNPKFQSVETAGPTLVGRRLRADPDPLG 50							
RESULT 2									
ID	Q86L07	PRELIMINARY;	PRT;	493 AA.					
AC	Q86L07;								
DT	01-DEC-2001 (TREMBLrel. 19, Created)								
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)								

RA	Godowski P., Gray A.;
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."
RL	Genome Res. 13:2265-2270(2003).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 3) .
RC	TISSUE=Testis;
RA	Bilm H., Bauraschs S., Mewes H.-W., Gassenhuber J., Wiemann S. ;
RL	Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
CC	-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. Cadherin-24 mediate strong cell-cell adhesion.
CC	-1- SUBUNIT: Associates with alpha-, beta- and delta-catennins.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC	-1- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=3;
CC	Name=1; Synonyms=Long form;
CC	NameId=Q86UP0-1; Sequence=Displayed;
CC	Name=2; Synonyms=Short form
CC	IsoId=Q86UP0-2; Sequence=VSP_008717;
CC	Name=3;
CC	IsoId=Q86UP0-3; Sequence=VSP_008718; VSP_008719;
CC	Note=No experimental confirmation available;
CC	-1- SIMILARITY: Contains 5 cadherin domains.
CC	-----
CC	This SWISS-PROT entry is copyright It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outpost - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/or send an email to jlicense@isb-sib.ch).
CC	-----
DR	EMBL; AY260900; AAP20590.1; --
DR	EMBL; AY260901; AAP20591.1; --
DR	EMBL; AY358199; AAQ88566.1; --
DR	EMBL; AL137477; CAB70758.1; --
DR	PIR; T46418; T46418.
DR	HSSP; PO9803; 117M.
DR	GeneX; HGNC:14265; CDR24.
DR	InterPro; IPROU0126; Cadherin.
DR	InterPro; IPRO00233; Cadherin_C_term.
DR	Pfam; PF00028; Cadherin_5.
DR	Pfam; PF01049; Cadherin_C_1.
DR	PRINTS; PR00205; CADHERIN.
DR	PROSITE; PS00232; CADHERIN_1; 2.
DR	PROSITE; PS02658; CADHERIN_2; 5.
KW	Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW	Multigene family; Repeat; Signal; Transmembrane.
KW	SIGNAL
FT	PROPEP 21 19 Potential.
FT	CHAIN 45 819 Extracellular (Potential).
FT	DOMAIN 45 641 Potential.
FT	TRANSMEM 642 662 Cytoplasmic (Potential).
FT	DOMAIN 663 819 Potential.
FT	DOMAIN 46 150 Cadherin 1.
FT	DOMAIN 151 259 Cadherin 2.
FT	DOMAIN 260 374 Cadherin 3.
FT	DOMAIN 375 517 Cadherin 4.
FT	DOMAIN 517 630 Cadherin 5.
FT	CARBHYD 446 .. (Potential).
FT	CARBHYD 348 .. (Potential).
FT	CARBHYD 563 .. (Potential).
FT	VARSPLIC 455 492 Missing (in isoform 2).
FT	/ftid=VSP_008717.
FT	VARSPLIC 1 427 Missing (in isoform 3).
FT	/ftid=VSP_008718.
FT	ESTTTTAAPLDREAFAMENUTYATLATELGWSKSGBERGWPLL
FT	VAEWSPAAPPQRSVGSAVGAIPO -> MNIVCTWCSTHS
FT	ATLFSTCLTHAVMFCMLVASCGIHAAHPMRVRNCVCVC

FT VMAPCFGVLPB (4n isoform 3).
 FT /FTId=VSP_008719.
 SQ SEQUENCE 819 AA; 87751 MW; 9083034f18x7e84 CRC64;

Query Match 100.0%; Score 247; DB 1; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.9e-22;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVTVTLSDVNDNPKPKFPOSLYQFSVETAGPGLVGRKADPPDLG 48
 DB 242 STVTVTLSDVNDNPKPKFPOSLYQFSVETAGPGLVGRKADPPDLG 289

RESULT 4

Q6PFX6 PRELIMINARY; PRT; 781 AA.
 AC Q6PFX6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=ch24;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxId=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC057373; AAH57373.1; -;
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR Pfam: PF00028; Cadherin_S.
 DR Pfam: PF01049; Cadherin_C; 1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 4.
 DR PROSITE: PS00332; CADHERIN_1; 2.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Query Match 98.8%; Score 244; DB 2; Length 781;
 Best Local Similarity 97.9%; Pred. No. 4.2e-22;

Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVTVTLSDVNDNPKPKFPOSLYQFSVETAGPGLVGRKADPPDLG 48
 DB 242 STVTVTLSDVNDNPKPKFPOSLYQFSVETAGPGLVGRKADPPDLG 289

RESULT 5

AAH57373 PRELIMINARY; PRT; 781 AA.
 ID AAH57373;
 AC AAH57373;
 DT 02-MAR-2004 (TREMBLrel. 27, Created)
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN CDH24.
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxId=10090;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC057373; AAH57373.1; -;
 SQ SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Query Match 98.8%; Score 244; DB 2; Length 781;
 Best Local Similarity 97.9%; Pred. No. 4.2e-22;
 Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

CADH-CHICK STANDARD; PRT; 792 AA.
 ID CADH-CHICK
 AC 093319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.
 OX NCBI_TaxId=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn;
 RA Wei J., Dong X.R., Topoluzis S., Zimmer W.E., Broders F., Thierry J.P.,
 RA Kotliansky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media.";
 RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>;
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AF055342; AAC33675.1; -;
 DR HSSP; P09803; 117W.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam; PF01049; Cadherin_5.
 DR Pfam; PF01049; Cadherin_5.
 DR PRINTS; PR0205; CADHERIN.
 DR SMART; SM00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSEM 614 634 Cytoplasmic (Potential).
 FT DOMAIN 635 792 Potential.
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 384 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3498C686731AB CRC64;
 Query Match 72.9%; Score 180; DB 1; Length 792;
 Best Local Similarity 68.8%; Pred. No. 6e-14;
 Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 STVTYVLSVDNVPKPKFQSLQFQSVETAGGCTLVKRRADPDGL 48
 DB 251 TTKVITLTVNDNPKPKFQSVQVQMSYSAVAEGEEVGRKADPDIG 298
 RESULT 7
 CADA_MOUSE STANDARD; PRT; 796 AA.
 AC P55286;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=ch11; Synonym=Cad-11;
 OS Mus musculus (Mouse)
 CC Buiatryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95269886; PubMed=7750649;
 RA Hoffman I.H., Balling R.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RT cadherin.";
 RL Dev. Biol. 169:337-346(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95269887; PubMed=7750650;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 RT in the head, somite, and limb bud of early mouse embryos.";
 RL Dev. Biol. 169:347-358(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takehita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amanu B.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts.";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Murnane K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein W.J., USCIN T.B., Toshimura S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 RT fetal, immature, and adult mice utilizing the polymerase chain
 RT reaction.";
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announce/>
 CC or send an email to license@ebi.ac.uk).

CC EMBL; X77557; CAAS4674.1; -
 DR EMBL; D31863; BA06730.1; -
 DR EMBL; D21533; BA04797.1; -
 DR EMBL; BC046314; AA046314.1; -
 DR PIR; A53584; A53584.
 DR PIR; I48277; I48277.
 DR PIR; I49556; I49556.
 DR HSSP; P09803; I17W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 potential.
 FT PROPEP 25 53 potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 160 268 Cadherin 1.
 FT DOMAIN 269 383 Cadherin 2.
 FT DOMAIN 384 486 Cadherin 3.
 FT DOMAIN 487 612 Cadherin 4.
 FT DOMAIN 612 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> W (in Ref. 1).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 FT CONFLICT 796 AA; 88112 MW; 0D58AD24641DD529 CRC64;
 SQ SEQUENCE

Query Match 72.9%; Score 180; DB 1; Length 796;
 Best Local Similarity 68.8%; Pred. No. 6.1e-14;
 Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 STTVVLTSDVNDNPPKPSLYCPSTVETAGPTLVRLRPODPDLG 48
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 DB 251 TTKVITITLVDVNDNPPKPSLYCPSTVETAGPTLVRLRPODPDLG 258

RESULT 8

OC8C706 PRELIMINARY; PRT; 796 AA.

AC 08C706;
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone: C530015F15 product: cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCB1_TaxID=10090;
 RX [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).

[2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=21085660; PubMed=11217651;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).

[3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).

[4]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20493374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).

[5]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).

[6]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hagiwara T., Hara A., Hashizume M.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Kato H., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasaiwa K.,
 RA Kishihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.

[7]

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK046552; BK33860.1; -
 DR HSSP; P09803; I17W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.

DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 88126 MW; 7196337482E1BE29 CRC64;

Query Match 72.1%; Score 180; DB 2; Length 796;
 Best Local Similarity 68.8%; Pred. No. 6, 1e-13;
 Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

CY 1 STTTVTLSVDNDNPPKPPQSLYQFSVETAGPGLTVGLRAQDDPDIG 48
 Db 251 TTKVTITLTDVNDNPPKPPQSLYQFSVETAGPGLTVGLRAQDDPDIG 298

RESULT 9

CADB_HUMAN STANDARD; PRT; 796 AA.
 AC P55287; Q15065; Q15066; Q9U093; Q9U094;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT structurally different types of cadherin.",
 RL Cell Adhes. Commun. 2:1526(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts.",
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [3]
 RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue.",
 RL Cell Regul. 2:261-270(1991).
 RN [4]
 RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 RA Kools P.F.J., Hogendoorn P.C.W., Boyce J.V.M.G., Van Roy F.;
 RT "Alternative cadherin-11 transcripts encoding truncated adhesion
 RT molecules are detectable in both human cancer and normal cells.",
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P55287-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P55287-2; Sequence=VSP 000640, VSP 000641;
 CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 CC other tissues. Expressed in neuroblasts.

CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).

DR EMBL; I34056; AAA35622.1; -
 DR EMBL; D1254; BAA04798.1; -
 DR EMBL; D1255; BAA04799.1; -
 DR EMBL; AF060370; AAD27755.1; -
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR EMBL; AF060370; AAD27755.1; -
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR PIR; A38992; A38992.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:1750; CDH11.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0007156; P:hemophilic cell adhesion; NAS.
 DR GO; GO:0001503; P:osification; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 632 693 VIVVFLVLRCKEPLVPEEDVRENTITVDGGEED
 FT TLEPDIATLQNDGNGIPR -> GQPSLMEPSPEDMR
 FT LTVGFLQMLFSYKYNRRPCLLGVFLKPLVYVATESPT
 FT TLTSL (in isoform 2).
 FT FTID=VSP_000640.
 FT Missing (in isoform 2).
 FT VARSPLIC 694 796 /FTID=VSP_000641.
 FT CONFLICT 271 272 RL -> SV (in Ref. 2).
 FT CONFLICT 275 275 M -> I (in Ref. 2).
 FT CONFLICT 340 340 E -> K (in Ref. 2).
 FT CONFLICT 373 373 S -> A (in Ref. 2).
 FT CONFLICT 471 471 Q -> K (in Ref. 2).
 SQ SEQUENCE 796 AA; 88049 MW; 206704478ADB32E CRC64;

Query Match 72.1%; Score 178; DB 1; Length 796;
 Best Local Similarity 68.8%; Pred. No. 1, 1e-13;
 Matches 33; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

CY 1 STTTVTLSVDNDNPPKPPQSLYQFSVETAGPGLTVGLRAQDDPDIG 48
 Db 251 TTKVTITLTDVNDNPPKPPQSLYQFSVETAGPGLTVGLRAQDDPDIG 298

RESULT 10
 Q96CZ9 PRELIMINARY; PRT; 796 AA.
 ID Q96CZ9

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AC Q95C29; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cadherin 11, type 2, isoform 1 preproprotein.
GN Name=CDH11
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Narasina K., Farmer A.A., Rubin G.W., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carroll P., Prange C.,
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RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hallyk S.W.,
RA Villalon D.K., Wozny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Vadan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravitski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
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RX MEDLINE=22388257; PubMed=12477932;
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RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RA Jones S.J., Marr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
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RA Jones S.J., Marr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
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RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko
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AC 093264; 1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Cadherin precursor.
GN Name:Xcad-11;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Zygote;
RX MEDLINE=98202517; PubMed=9533956;
RA Hadeball B., Borchers A., Wedlich D.;
RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
RT signal."
RL Mech. Dev. 72:101-113(1998).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL; AF002983; AAC28073.1; -.
DR HSSP; P03803; 117W.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF000028; Cadherin_5.
DR Pfam; PF010049; Cadherin_C_1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
FT SIGNAL 1 53 potential.
FT CHAIN 54 794 cadherin.
SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEA719DB CRC64;

Query Match 70.0%; Score 173; DB 2; Length 794;
Best local similarity 66.7%; Pred. No. 4,7e-13;
Matches 32; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Cy 1 STTTATLSDVNDNPKPKFOSLYGFSVETAGPGLTVGRARAOPDDIG 48
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 251 TTKVITLTDVNDNPKPKFOSAYPMVSSEAAVGEVEGRIRAKPDIDG 256

RESULT 12
CADM_MOUSE STANDARD; PRT; 813 AA.
AC Q9WTF5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-22 precursor (PB-cadherin).
GN Name=Cdh22;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND DEVELOPMENTAL STAGE.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=99326347; PubMed=10398531;
RA Kitajima K., Koshimizu U., Nakamura T.;
RT "Expression of a novel type of classic cadherin, PB-cadherin in
RT developing brain and limb buds."
RL Dev. Dyn. 215:206-214(1999).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic

```

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CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. pb-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain. Abundant in
CC olfactory bulb, cerebellum, and cerebellum, less in pons, medulla,
CC and spinal cord. Low expression in heart. No expression in lung,
CC liver, spleen, kidney, testis, stomach, intestine, colon, and
CC placenta.
CC -1- DEVELOPMENTAL STAGE: Expressed at 9.5 dpc onwards. At 10.5 dpc, in
CC brain (telencephalic vesicles and isthmus), spinal cord and limb
CC buds (in the zone of polarizing activity). At 14.5 dpc, in
CC olfactory bulb and cerebellum.
CC -1- INDUCTION: Down-regulated by thyroid hormone.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AB019618; BAA34426.1; -.
CC DR HSSP; P09803; 117W.
CC DR MGD; MGI:1341843; Cdh22.
CC DR InterPro; IPR002126; Cadherin.
CC DR InterPro; IPR002033; Cadherin_C_term.
CC DR Pfam; PF00028; Cadherin_5.
CC DR Pfam; PF01049; Cadherin_C_1.
CC DR PRINTS; PR00205; CADHERIN.
CC DR SMART; SM00112; CA; 5.
CC DR PROSITE; PS00232; CADHERIN_1; 2.
CC DR PROSITE; PS0268; CADHERIN_2; 5.
CC DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
CC Transmembrane.
CC KW SIGNAL 1 33 Potential.
CC FT CHAIN 34 813 Cadherin-22.
CC FT DOMAIN 33 621 Extracellular (Potential).
CC FT TRANSMEM 622 642 Potential.
CC FT DOMAIN 643 813 Cytoplasmic (Potential).
CC FT DOMAIN 61 165 Cadherin_1.
CC FT DOMAIN 166 274 Cadherin_2.
CC FT DOMAIN 275 391 Cadherin_3.
CC FT DOMAIN 392 495 Cadherin_4.
CC FT DOMAIN 496 613 Cadherin_5.
CC FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 609 609 N-linked (GlcNAc...) (Potential).
CC SQ SEQUENCE 813 AA; 88021 MW; 5510F9848D976567 CRC64;

Query Match 69.6%; Score 172; DB 1; Length 813;
Best Local Similarity 62.5%; Pred. No. 6,5e-13;
Matches 30; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 STTYVTLSVDVNDNPKPKFQPSLIQFSVETAGSGTLVGRADDPDLG 48
DB 257 STTYVTLSVDVNDNPKPKFQPSLIQFSVETAGSGTLVGRADDPDLG 304

RESULT 13
CADM_RAT STANDARD; PRT; 813 AA.
AC Q63315; Q63315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 41, Last annotation update)
DE Cadherin-22 precursor (PB-cadherin).
GN Name=Cdh22;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxID=10116;
CC [1]
CC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
CC STRAIN=Wiistar; Tissue=Brain, and Pituitary;
CC MEDLINE=96212232; PubMed=8626716;
CC RA Sugimoto K., Honda S., Yamamoto T., Ueki T., Monden M., Kaji A.,
CC RA Matsumoto K., Nakamura T.;
CC RT "Molecular cloning and characterization of a newly identified member
CC of the cadherin family, PB-cadherin.";
CC J. Biol. Chem. 271:11548-11556(1996).
CC -1- FUNCTION: Cadherins are calcium dependent cell-adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. pb-cadherins may have a role
CC in the morphological organization of pituitary gland and brain
CC tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1; IsoId=Q63315-1; Sequence=Displayed;
CC Name=2; IsoId=Q63315-2; Sequence=VSP_000643, VSP_000644;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Strongly expressed in the pituitary gland and
CC the brain (in the inner granular and glomerular layers of the
CC olfactory bulb, anterior olfactory nucleus, primary olfactory
CC cortex, Parkinje cell layer of cerebellum, and pineal gland). Low
CC expression in lung and heart. No expression in submandibular
CC gland, thymus, liver, spleen, adrenal, and kidney.
CC -1- DEVELOPMENTAL STAGE: Expressed strongly in fetal brain.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; D83348; BAA11894.1; -.
CC DR EMBL; D83349; BAA11895.1; -.
CC DR HSSP; P09803; 117W.
CC DR GSD; 2321; Cdh22.
CC DR InterPro; IPR002126; Cadherin.
CC DR InterPro; IPR002033; Cadherin_C_term.
CC DR Pfam; PF00028; Cadherin_5.
CC DR Pfam; PF01049; Cadherin_C_1.
CC DR PRINTS; PR00205; CADHERIN.
CC DR SMART; SM00112; CA; 5.
CC DR PROSITE; PS00232; CADHERIN_1; 2.
CC DR PROSITE; PS0268; CADHERIN_2; 5.
CC DR Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
CC Repeat; Signal; Transmembrane.
CC KW SIGNAL 1 33 Potential.
CC FT CHAIN 34 813 Cadherin-22.
CC FT DOMAIN 33 621 Extracellular (Potential).
CC FT TRANSMEM 622 642 Potential.
CC FT DOMAIN 643 813 Cytoplasmic (Potential).
CC FT DOMAIN 61 165 Cadherin_1.
CC FT DOMAIN 166 274 Cadherin_2.
CC FT DOMAIN 275 391 Cadherin_3.
CC FT DOMAIN 392 495 Cadherin_4.
CC FT DOMAIN 496 613 Cadherin_5.
CC FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 609 609 N-linked (GlcNAc...) (Potential).
CC FT VARSPLIC 668 694 NDEGCGDPRAYDMSLRLTYDPEGL -> TLGSGHRTGS
CC FT VARSPLIC 695 813 Missing (in isoform 2).
CC FT VARSPLIC 695 813 Missing (in isoform 2).

```


FT		/Fftid=VSP_000644.
SQ	SEQUENCE	813 AA; 87978 MW; 30BEA60B5D2d467B CRC64;
Query Match		69.6%; Score 172; DB 1; Length 813;
Best Local Similarity		62.5%; Pred. No. 6.5e-13;
Matches	30; Conservative	11; Mismatches 7; Indels 0; Gaps 0;
Oy	1 STTVTLTLDVNNDNPKPFOSLYGFSVFETAGPTGLYRLRAQPDLIG 48 : : : : : : : : : :	
Dg	257 STVTIVLVTDVDNDRPRFPKMYGSISDESAPIGRAVERVAEDSDVG 304 	

CC	RESULT 14
CC	CADM_HUMAN
ID	_CADM_HUMAN STANDARD; PRT; 828 AA.
AC	Ceu939;_O433205;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Cadherin-22 precursor.
DN	Name=CDH22; Synonyms=C2orf225;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=2638749; PubMed=11780052; DOI=10.1038/444855a;
RA	DeJoncks P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA	Jones M., Stavrides G., Almeida J.P., Babage A.K., Baggaley C.L.,
RA	Balley J., Balow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.W., Brown A.J.,
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA	Collison A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden U.L., Howden P.J.,
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.X., Lawlor S.,
RA	Lavaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA	Marsh V.L., Martin S.L., McConachie I.J., McLay K., Murray A.A.,
RA	Malne S.A., Mastey D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA	Olivek K., Parker D., Patel R., Pearce T.A.V., Peck A.I.,
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showcseen R., Sims S.,
RA	Skane C.D., Smith M.L., Soderlund C., Stewart C.A., Suleston J.B.,
RA	Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA	Tracey A., Tromans A.C., Vandin M., Wall M., Wallis J.W.,
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA	Wilning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA	Rogers J.;
RT	"The DNA sequence and comparative analysis of human chromosome 20.";
RL	Nature 414:655-871(2001).
RN	[2]
RFP	SEQUENCE OF 449-828 FROM N.A.
RRC	TISU5=Brain;
RL	Yu W., Sarginson J., Gibbs R.A.;
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC	They preferentially interact with themselves in a homophilic
CC	manner in connecting cells; cadherins may thus contribute to the
CC	sorting of heterogeneous cell types; PB-cadherins may have a role
CC	in the morphological organization of pituitary gland and brain
CC	tissues (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-I- SIMILARITY: Contains 5 cadherin domains.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL contribution -
CC	I-
CC	use by non-profit institutions as long as its content is in no way

	CC	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).
	CC	-----
	CC	-EMBL; AL031687; CABSI587.2; -.
	DR	EMBL; AF035300; AA888193.1; -.
	DR	HSSP; P15116; INCU.
	DR	Genew; HGNC:13251; CDR22.
	DR	InterPro; IPR002126; Cadherin.
	DR	InterPro; IPR000233; cadherin_C_term.
	DR	Pfam; PF00028; Cadherin_5.
	DR	Pfam; Pf01049; Cadherin_C_1.
	DR	PRINTS; PRO0205; CADHERIN.
	DR	SMART; SMO0112; CA; 5.
	DR	PROSITE; PS00232; CADHERIN_1; 2.
	DR	PROSITE; PSS0268; CADHERIN_2; 5.
	KM	Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
	KM	Transmembrane.
	FT	SIGNAL
	FT	CHAIN
	FT	DOMAIN
	FT	TRANSMEM
	FT	DOMAIN
	FT	DOMAIN
	FT	DOMAIN
	FT	DOMAIN
	FT	DOMAIN
	FT	DOMAIN
	FT	CARBOHYD
	FT	CARBOHYD
	FT	CARBOHYD
	SEQ	SEQUENCE
		Query Match
		Best Local Similarity
		Matches
Oy	1	STWTATLSDVNDNPKEFPOSILYGSVETGPGTLVRLRADPDLG 48
Dd	260	STTAVTVVDVNDFRPFOKTFPSIDESAPIGTAVGVRVAEDSVG 307
		: : : :
		69.6%; Score 172; DB 1; Length 828;
		62.5%; Pred.No.6.e-13;
		Conservative 11; Mismatches 7; Indels 0; Gaps 0
		RESULT 15
		CAD6_RAT
		ID _CAD6_RAT STANDARD; PRT; 789 AA.
		P5280;
DT	01-OCT-1996	(Rel. 34, Created)
DT	01-OCT-1996	(Rel. 34, Last sequence update)
DT	05-JUL-2004	(Rel. 44, Last annotation update)
DE	Cadherin-6 precursor (Kidney-cadherin) (K-cadherin).	
GN	Name=Cdh6; Synonyms=Kcad;	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxId=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ACI; TISSUE=Kidney;	
RX	MEDLINE=94243827; PubMed=8187093;	
RA	Xiang Y.Y., Tanaka M., Suzuki M., Igaraashi H., Kiyokawa E., Naito Y.,	
RA	Ohtawara Y., Shen Q., Sugimura H., Kino I.;	
RT	"Isolation of complementary DNA encoding K-cadherin, a novel rat	
RT	cadherin preferentially expressed in fetal kidney and kidney	
RT	carcinoma.";	
RL	Cancer Res. 54:3034-3041(1994).	
CC	-!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.	
CC	They preferentially interact with themselves in a homophilic	
CC	manner in connecting cells; cadherins may thus contribute to the	
CC	sorting of heterogeneous cell types.	
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-!- TISSUE SPECIFICITY: Highly expressed in kidney and brain.	
CC	-!- SIMILARITY: Contains 5 cadherin domains.	
	CC	-----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation,
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; D25290; BAA04975.1; -.
DR PIR; I52701; I52701.
DR HSSP; P09803; 117W.
DR RGD; 2322; Cdh6.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR00233; Cadherin_C_term.
DR Pfam; PF00028; Cadherin_5.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
KW
FT SIGNAL 1 18 Potential.
FT PROPEP 19 53 Potential.
FT CHAIN 54 789 Cadherin-6.
FT DOMAIN 54 615 Extracellular (Potential).
FT TRANSMEM 616 636 Potential.
FT DOMAIN 637 789 Cytoplasmic (Potential).
FT DOMAIN 54 159 Cadherin 1.
FT DOMAIN 160 268 Cadherin 2.
FT DOMAIN 269 383 Cadherin 3.
FT DOMAIN 384 486 Cadherin 4.
FT DOMAIN 487 608 Cadherin 5.
FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 399 399 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 437 437 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 789 AA; 88340 MW; BE7474F0B07FE403 CRC64;

Query Match 68.4%; Score 169; DB 1; Length 789;
Best Local Similarity 60.4%; Pred. No. 1.5e-12;
Matches 29; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 STVTVLSDVNDNPKPKFQSLYQFSVETAGPGTLVGRRLAODPDIG 48
Db 251 TTVNITLTDVNDNPKPKFQSLYQFSVETAGPGTLVGRRLAODPDIG 298

Search completed: December 8, 2004, 10:24:38
Job time: 19.2397 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.863 Seconds

(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-9
Perfect score: 247
Sequence: 1 STVTVTLSVDVNDNPKFPQ.....ETAGPGLVGLRLAQPDLG 48

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: Geneseqp1980s.*
2: Geneseqp1950s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	100.0	48	7	ADD29450 Human cad
2	247	100.0	493	5	AD116946 Human NOV
3	247	100.0	607	5	ABBS3295 Human pol
4	247	100.0	620	7	ADD29448 Human cad
5	247	100.0	636	7	ADD29445 Human pol
6	247	100.0	781	5	ABBS3296 Human pol
7	247	100.0	781	5	AAW48736 Human cad
8	247	100.0	781	5	ABG34078 Human NOV
9	247	100.0	781	5	AD116604 Human NOV
10	247	100.0	781	5	AD116606 Human NOV
11	247	100.0	781	6	ABR40114 Human cel
12	247	100.0	781	6	ADA01366 Human PRO
13	247	100.0	781	6	ADA43795 Human PRO
14	247	100.0	781	6	ADA43563 Human sec
15	247	100.0	781	6	ADA01238 Human PRO
16	247	100.0	781	6	ADA01122 Human sec
17	247	100.0	781	7	ADA43579 Human sec
18	247	100.0	781	7	ADA06941 Human PRO
19	247	100.0	781	7	ADA08429 Novel hum
20	247	100.0	781	7	ADBS9722 Human PRO
21	247	100.0	781	7	ADBS7005 Human PRO
22	247	100.0	781	7	ADBS6160 Human sec
23	247	100.0	781	7	ADBS9938 Human PRO
24	247	100.0	781	7	ADBS9493 Novel hum
25	247	100.0	781	7	ADB66044 Human sec

26	247	100.0	781	7	ADC23442 Human tra
27	247	100.0	781	7	ADC26135 Human PRO
28	247	100.0	781	7	ADE04962 Human PRO
29	247	100.0	781	7	ADE11268 Human PRO
30	247	100.0	781	7	ADD88199 Human PRO
31	247	100.0	781	7	ADD95494 Human sec
32	247	100.0	781	7	ADE06424 Human PRO
33	247	100.0	781	7	ADE38199 Human PRO
34	247	100.0	781	7	ADE88315 Human PRO
35	247	100.0	781	7	ADD90896 Human sec
36	247	100.0	781	7	ADFS9451 Human sec
37	247	100.0	781	7	ADG06544 Human PRO
38	247	100.0	781	7	ADG05495 Human PRO
39	247	100.0	781	7	ADG82496 Human PRO
40	247	100.0	781	8	ADE51749 Human sec
41	247	100.0	781	8	ADE51865 Human sec
42	247	100.0	781	8	ADE37723 Human sec
43	247	100.0	781	8	ADG37607 Human sec
44	247	100.0	781	8	ADG35378 Human sec
45	247	100.0	781	8	ADE38078 Human PRO

ALIGNMENTS

RESULT 1
ADD29450
ID ADD29450 standard; protein; 48 AA.
XX
AC ADD29450:
XX
DT 15-JUN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seg 109.
XX
XX cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytostatic; osteopetrosis; cancer;
KW osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (GODB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI Liu C, Drmanac RT;
PI
DR WPI; 2003-829759/77.
XX
PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteopetrosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX
PS Claim 11; SEQ ID NO 9; 63bp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
protein and the DNA sequence which encodes it. Cadherins are a family of

Sequence 493 AA7

Query Match 100.0%; Score 247; DB 5; Length 493;
Best Local Similarity 100.0%; Pred. No. 3, 3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 48
DB 242 STTAVTLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 289

RESULT 3
ABBS3295
ID ABBS3295 standard; protein; 607 AA.

AC ABB53295;

XX 12-FEB-2002 (first entry)

DE Human polypeptide #35.

XX Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
KM neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
KM antiinflammatory; antilipemic; hepatotropic; vituicide; antidiabetic;
KM nephrotoxic; anorectic; cytostatic; vaccine; neurological disease;
KM cardiovascular disease; respiratory disease; liver disease;
KM renal disease; skeletal muscle disease; gastrointestinal disease;
KM placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

PD 26-APR-2001; 2001WO-US013360.

PF 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203338P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM P.L.C.

XX Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnack KS;

PI Lal Y, Xie Q;

XX WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

XX Claim 1; Page 106-108; 116pp; English.

CC The invention relates to an isolated polypeptide comprising a 277, 480,
CC 583, 581, 628, 424, 639, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
CC 844, 782, 262, 354, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
CC given in the specification. The polypeptides, modulators of the
CC polypeptides and antibodies against the polypeptides are useful for
CC treating diseases such as neurological and psychiatric diseases including
CC Alzheimer's, paraspinal palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Ehlers-Danlos
CC syndrome, hypodysplasia and obesity; gastrointestinal diseases including

CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including choriochorionoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type I and II diabetes and obesity. The
CC present sequence is a polypeptide of the invention

SQ Sequence 607 AA;
Query Match 100.0%; Score 247; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 4, 2e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 48
DB 242 STTAVTLSDVNDNPKFPQSLYQPSVETAGPGLVGRRAQDPDLG 289

RESULT 4
ADD29448
ID ADD29448 standard; protein; 620 AA.

AC ADD29448;

XX 15-JUN-2004 (first entry)

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;
KM homotypic cell-cell adhesion; cytoskeletal; osteopathic; cancer;
KM osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KM metastatic tumour; human.

XX Homo sapiens.

XX US2003144491-A1.

XX 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

XX (GDB/) GODSOLE S D.

PA (KLOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

XX WPI; 2003-829799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 7; 63pp; English.

CC This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutics useful for the treatment of diseases

CC such as cancers, osteoporosis, Paget's disease, osteomalacia,

CC hyperostosis and osteopetrosis. The protein and DNA sequence of the

CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the mature human secreted
CC cadherin-like protein which was used during the exemplification of the
CC invention.

XX SQ Sequence 620 AA;

Query Match 100.0%; Score 247; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTSLDVNDNPKFPKPSLYQFSVETAGPGLVGRRAQDPDGG 48
Db 226 STTAVTSLDVNDNPKFPKPSLYQFSVETAGPGLVGRRAQDPDGG 273

RESULT 5
ADD29445
ID ADD29445 standard; protein; 636 AA.

XX AC ADD29445;

XX DT 15-JAN-2004 (first entry)

XX DE Human cadherin-like protein amino acid sequence.

XX KW cadherin-like protein; transmembrane protein; cadherin domain;
XX KW homotypic cell-cell adhesion; cyostatic; osteopathic; cancer;
XX KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX KW metastatic tumour; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..16

XX FT Protein /label=Signal_peptide

XX FT /label=17..636

XX PN US2003144491-A1

XX PD 31-JUL-2003.

XX PF 16-FEB-2001; 2001US-00788051.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX PA (GODD/) GODDLE S D.

XX PA (KUC/) KUC C.

XX PA (ARTE/) ARTERBURN M C.

XX PA (YEUN/) YEUNG G.

XX PA (PALE/) PALENCIA S.

XX PA (TANG/) TANG Y T.

XX PA (LIUC/) LIU C.

XX PA (DRMA/) DRMANAC R T.

XX PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

XX PI Liu C, Drmanac RT;

XX DR WPI; 2003-829799/77.

XX DR N-PSDB; ADD29445, ADD29446.

XX PT Novel isolated human secreted cadherin-like polypeptide useful for

XX PT treating diseases such as cancers, osteoporosis, Paget's disease,

XX PT osteomalacia, hyperostosis, osteopetrosis.

XX PS Claim 11; SEQ ID NO 4; 636p; English.

XX CC This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

XX SQ Sequence 636 AA;

Query Match 100.0%; Score 247; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTAVTSLDVNDNPKFPKPSLYQFSVETAGPGLVGRRAQDPDGG 48
Db 242 STTAVTSLDVNDNPKFPKPSLYQFSVETAGPGLVGRRAQDPDGG 289

RESULT 6
ABBS3296
ID ABBS3296 standard; protein; 781 AA.

XX AC ABBS3296;

XX DT 12-FEB-2002 (first entry)

XX DE Human polypeptide #36.

XX KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
XX KW neuroleptic; tranquilizer; antiarrhythmic; cardiant; antidiabetic;
XX KW antinflammatory; antilipemic; hepatotropic; virucide; antidiabetic;
XX KW nephrotropic; anorectic; cyostatic; vaccine; neurological disease;
XX KW cardiovascular disease; respiratory disease; liver disease;
XX KW renal disease; skeletal muscle disease; gastrointestinal disease;
XX KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX OS Homo sapiens.

XX PN WO200181363-A1.

XX PD 01-NOV-2001.

XX PF 26-APR-2001; 2001WO-US013360.

XX PR 27-APR-2000; 2000US-0199963P.

XX PR 11-MAY-2000; 2000US-0203336P.

XX PR 25-MAY-2000; 2000US-0207087P.

XX PR 26-MAY-2000; 2000US-0207546P.

XX PA (SMK) SMITHLINE BECHAM CORP.

XX PA (SMK) SMITHLINE BECHAM PLC.

XX PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;

XX PI Lai Y, Xie Q;

XX DR WPI; 2002-041392/05.

XX DR N-PSDB; ABA90361.

XX PT Novel polypeptides and polynucleotides useful as a vaccine for preventing

XX PT diseases, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

XX PS Claim 1; Page 108-109; 116pp; English.

XX CC The invention relates to an isolated polypeptide comprising a 277, 480,

CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,

CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,

CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as

CC given in the specification. The polypeptides, modulators of the

CC polypeptides and antibodies against the polypeptides are useful for

CC treating diseases such as neurological and psychiatric diseases including

CC Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myocenta congenita and intestinal obstruction; lymph diseases including
CC lymphoedema; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketocidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention

SQ Sequence 781 AA;

Query Match 100.0%; Score 247; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDPDLG 48
DB 242 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDPDLG 289

RESULT 7
AAM48736
ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

KW Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
KW antididiabetic; neuroprotective; antiarthritic; antirheumatic;
KW dermatological; immunosuppressive; antiinflammatory; antipsoriatic;
KW antiasthmatic; antiallergic; antileptotic; haemostatic; antipruritic;
KW antihypertensive; antidiabetic; antidiabetic; cardiomyopathic;
KW anorectic; immunomodulatory; vasotropic; vitruous; cytoskeletal; liver;
KW thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
KW viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
KW osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
KW thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
KW gene therapy.

OS Homo sapiens.

PN WO200190145-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

DR WPI; 2002-083082/11.

DR N-PSDB; ABA96406, ABA96407.

PT New human cadherin family protein and polynucleotides, useful for
PT diagnosing and treating disorders e.g. obstructive jaundice, multiple
PT sclerosis, encephalomyelitis and atherosclerosis and to identify
PT modulators of therapeutic use.

PS Claim 9; Page 105; 119pp; English

XX The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopathic, hepatotropic, antibacterial, antiallergic,
CC neuroprotective, antiinflammatory, antipsoriatic, dermatological,
CC immunosuppressive, antiarthritic, antirheumatic, antipruritic,
CC antiallergic, antileptotic, haemostatic, antipruritic, antihypertensive,
CC antidiabetic, antidiabetic, cardiomyopathic, anorectic,
CC immunomodulatory, vasotropic, vitruous, cytoskeletal, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecules are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune diseases including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy; cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy

SQ Sequence 781 AA;

Query Match 100.0%; Score 247; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDPDLG 48
DB 242 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRAQDPDLG 289

RESULT 8
ABG34078
ID ABG34078 standard; protein; 781 AA.

AC ABG34078;

DT 15-JUL-2002 (first entry)

DE Human Pro peptide #49.

KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
KW tumour; cancer.

OS Homo sapiens.

PN WO200224888-A2.

PD 28-MAR-2002.

PF 29-AUG-2001; 2001WO-US027099.

PR 01-SEP-2000; 2000US-0229896P.

PR 05-SEP-2000; 2000US-0230621P.

PR 22-SEP-2000; 2000US-0235147P.

PR 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.

PR 16-JAN-2001; 2001US-0261810P.

PR 16-JAN-2001; 2001US-0261939P.

PR 25-JAN-2001; 2001US-0262150P.

PR 02-FEB-2001; 2001US-0264355P.

PR 02-FEB-2001; 2001US-0266421P.

PR 03-FEB-2001; 2001US-0267623P.

PR 28-FEB-2001; 2001WO-US006520.

PR 03-MAR-2001; 2001US-0274359P.

PR 03-APR-2001; 2001US-0280982P.

PR 04-APR-2001; 2001US-0282129P.

PR 04-APR-2001; 2001US-0282199P.

PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017890.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi UC;
PI Guirney AL, Smith V, Stephan J, Matarabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2002-362426/39.
DR N-PSDB; ABK70009.
XX
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX
XX
PS Claim 11; Fig 98; 218pp; English.
XX
XX This invention relates to the cDNA and protein sequences of novel
XX secreted and transmembrane polypeptides PRO polypeptides. The invention
XX also comprises a method for producing the proteins of the invention by
XX recombinant means and antibodies specific for the protein of the
XX invention. The antibody may be used for detecting the PRO proteins of the
XX invention and may be used to modify their activity. Polynucleotides may
XX be used as hybridisation probes for a cDNA library to isolate the full-
XX length PRO cDNA or to isolate other cDNAs, to construct hybridisation
XX probes for mapping the gene which encodes that PRO and for genetic
XX analysis of individuals with genetic disorders, in assays to identify
XX other proteins or molecules involved in binding reaction, to generate
XX transgenic animals or knock-out animals which in turn are useful in the
XX development and screening of therapeutically useful reagents, for
XX chromosome identification, and tissue typing. The PRO polypeptides are
XX useful in gene therapy, and as molecular weight markers for protein
XX electrophoresis purposes. The sequences may also be used to detect
XX overexpression on PRO polypeptides in cancerous tumours and for screening
XX for differentially expressed genes using microarray technology. The
XX present sequence represents a human PRO protein of the invention
SQ Sequence 781 AA;
Query Match 100.0%; Score 247; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5; 7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 STVTVTLSVDNDNPKFQSLYQFVETAGPFTLVGRRAQDPDUG 48
Db 242 STVTVTLSVDNDNPKFQSLYQFVETAGPFTLVGRRAQDPDUG 269
RESULT 9
AD116604
ID AD116604 standard; protein; 781 AA.
XX
XX
AC AD116604;
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Human NOVX protein to treat human pathological conditions SegID140.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
XX haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
XX antiashtmatic; nephrotoxic; antiarthritic; hepatotropic;
XX neuroprotective; nootropic; antibacterial; vitinocde; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW

KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
KW single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200268649-A2.
XX
XX
PD 06-SEP-2002.
XX
XX
PF 31-JAN-2002; 2002WO-US002785.
XX
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 09-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0276552P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278778P.
XX 29-MAR-2001; 2001US-0278882P.
XX 29-MAR-2001; 2001US-0278884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282992P.
XX 11-APR-2001; 2001US-0283039P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296564P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-031020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 21-AUG-2001; 2001US-0312908P.
XX 28-AUG-2001; 2001US-0313390P.
XX 31-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323379P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0333701P.
XX
XX (CUBA-) CUBAGEN CORP.
XX
XX Tchernev VT, Spytek KA, Zernhusen BD, Paturajan M, Shinkets RA;
XX Li L, Gangolli EA, Padiguru M, Anderson SM, Rastelli L, Miller CE;
XX Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
XX Furek K, Grosse WM, Alsebrook JP, Lepley DM, Rieger DK, Burgess CB;
XX

PT pharmacogenomics.
XX
PS Claim 1; SEQ ID NO 142; 1498bp; English.
XX
CC This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antiaslomatic, nephroprotective, antibacterial, hepatotropic,
CC neuroprotective, neurotropic, antiparasitic, vitruide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
CC
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 247; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 STTVTVTLSDVNDNPKPKFQSLVQFSVETAGPGLVGRRAADPDIG 48
ID ABR40114
XX ABR40114 standard; protein; 781 AA.
XX
AC ABR40114;
XX
DT 04-JUL-2003 (first entry)
XX
DE Human cell adhesion and extracellular matrix protein, CADECM-11.
XX
XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
XX anticonvulsant; neurotropic; neuroprotective; immunosuppressive;
XX dermatological; anti-inflammatory; cytostatic; antiatherosclerotic;
XX gene therapy; cell adhesion; extracellular matrix; CADECM;
XX immune system disorder; AIDS; allergy; neurological disorder; stroke;
XX Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
XX cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
XX genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
XX atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO2003027230-A2.
XX
PD 03-APR-2003.
XX
PF 02-AUG-2002; 2002MO-US024649.
XX
XX 03-AUG-2001; 2001US-030964P.
XX
PR 03-AUG-2001; 2001US-031011P.
XX
PR 17-AUG-2001; 2001US-0313091P.

PR 31-AUG-2001; 2001US-0316771P.
PR 07-SEP-2001; 2001US-031786P.
PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Burford N, Warren BA, Duggan BM, Mason PM, Richardson TM, Yue H;
PI Forsythe IV, Elliott VS, Griffin DA, Gorvad AE, Azimzai Y;
PI Kallick DA, Xu Y, Honchell CD, Baughn MR, Gietzen KU, Lee S;
PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
DR MPI; 2003-354645/33.
DR N-PsDB; ACC00402.
XX
XX
PT New human cell adhesion and extracellular matrix proteins (CADECM),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
PS Claim 1; Page 192-194; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX proliferative disorders (e.g. cancer or atherosclerosis)
SQ
Sequence 781 AA;
Query Match 100.0%; Score 247; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 STTVTVTLSDVNDNPKPKFQSLVQFSVETAGPGLVGRRAADPDIG 48
ID ABR40114
XX ABR40114 standard; protein; 781 AA.
XX
AC ABR40114;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #49.
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; antineumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003068779-A1.
XX
PD 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0290589P.

29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Eaton DV, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith Y, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S,
XX
XX WPI; 2003-625484/59.
DR N-PSDB; ADA01365.
XX
XX Novel isolated PRO113, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
XX Claim 11; Fig 98; 307pp; English.
PS
PS The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for inducing endothelial cell
XX tube formation and for treating sports-related joint problems, articular
XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
XX represents a human PRO polypeptide of the invention.
XX
XX Sequence 781 AA;
XX
XX Query Match 100.0%; Score 247; DB 6; Length 781;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-26;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX 1 STTAVTSLSDVNDNPPKFPQSLGYPSVYETAGPGLTVGLRAQDDPLG 48
XX |||||
XX 242 STTAVTSLSDVNDNPPKFPQSLGYPSVYETAGPGLTVGLRAQDDPLG 289
XX
XX RESULT 13
XX ADA43795
XX ID ADA43795 standard; protein; 781 AA.
XX
XX ADA43795;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO34009.
XX
XX Human, PRO, secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
XX
XX US2003064474-A1.
XX
XX 03-APR-2003.

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XX PF 16-SEP-2002; 2002US-00245859 .
XX XX
XX FR 29-AUG-2001; 2001WO-US027099 .
XX PR 18-JUL-2002; 2002US-00197942 .
XX XX
XX PA (GENTH ) GENENTECH INC.
XX PI Baker KP, Eaton DU, Filvaroff E, Goddard A, Grimaldi JC;
XX PT Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WI, Zhang Z;
XX PT Fong S;
XX DR N-PSDB; ADA43794 .
XX PS WPI; 2003-605867/57.
XX XX
XX CC The invention relates to an isolated secreted/transmembrane (PRO)
XX CC polypeptide, having at least 80% sequence identity to a sequence selected
XX CC from any one of the 57 amino acid sequences given in specification, or to
XX CC a sequence encoded by a nucleic acid molecule selected from any one of
XX CC the nucleic acids deposited under any of the ATCC accession numbers given
XX CC in specification, or a sequence having at least 80% identity to PRO
XX CC lacking its associated signal peptide, an extracellular domain of PRO
XX CC with or without its associated signal peptide. Also included are vectors,
XX CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
XX CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX CC an oligonucleotide probe derived from any one of the above nucleotide
XX CC sequences. PRO6018 polypeptide is useful for stimulating the
XX CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
XX CC and PRO21183 polypeptides are useful for stimulating the proliferation of
XX CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX CC polypeptides are useful for inhibiting the proliferation of human
XX CC microvascular endothelial cells. PRO polypeptides are useful for
XX CC detecting the presence of tumour in a mammal, including tumours of lung,
XX CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX CC PRO18189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
XX CC PRO34274 polypeptides are useful for inducing endothelial cell tube
XX CC formation. PRO or the antibody are useful in the preparation of a
XX CC medicament for treating a condition responsive to PRO polypeptide. The
XX CC oligonucleotide probes are useful for isolating genomic and cDNA
XX CC nucleotide sequences, for measuring or detecting the expression of an
XX CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX CC hybridisation probe, in chromosome and gene mapping, in the generation of
XX CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX CC present sequence represents a PRO protein.
XX XX
XX SQ Sequence 781 AA;
XX
XX Query Match 100.0%; Score 247; DB 6; Length 781;
XX Best Local Similarity 100.0%; Pred. No. 5,7e-26;
XX Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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XX Db 242 STTVTLSDVNDNPKPFQSLYSQSVETAGFTLVGLRLRAQDPDLG 289
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XX RESULT 14
XX ADA433563
XX ID ADA43563 standard; protein; 781 AA.
XX AC
XX ADAA33563;
XX XX
XX DT 20-NOV-2003 (first entry)
XX XX

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DE Human secreted/transmembrane polypeptide PRO34009.
 XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytosol; vaccine.
 XX Homo sapiens.
 OS
 XX US2003073196-A1.
 PN
 XX 17-APR-2003.
 PD
 XX 18-SEP-2002; 2002US-00246210.
 PF
 XX 04-APR-2001; 2001US-0282199P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENTH) GENENTECH INC.
 PA
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurey AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 PI WPI, 2003-743614/70.
 DR N-PDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO308, PRO600,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6008, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SO Sequence 781 AA.

Query Match 100.0%; Score 247; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5, 7e-26;
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 ID ADA01238 standard; protein; 781 AA.
 AC ADA01238;
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 DT 06-NOV-2003 (first entry)
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 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 KW microvascular endothelial cell; endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 PN US2003068782-A1.
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245851.
 XX
 PR 27-APR-1999; 99US-0131271P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028551.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurey AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S;
 PI WPI, 2003-625487/59.
 DR N-PDB; ADA01237.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 11; Fig 98; 308pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SO Sequence 781 AA;

Wed Dec 8 11:46:36 2004

us-09-788-051-9.rag

Page 11

Query Match 100.0%; Score 247; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.7e-26;
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242 STVTVTLSVDYNDNPPKFPQSLYQFSVETAGPSTLVGRRLRAQDPDLG 289
Search completed: December 8, 2004, 10:13:05
Job time : 19.863 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 (Search time 49.0484 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-9

Perfect score: 247

Sequence: 1 STVTYTLSDVNDNPKFPQ.....ETAGPGLVGRLEAQPDLG 48

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1585576 segs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	247	100.0	48	10	US-09-788-051-9
2	247	100.0	493	15	US-10-072-012-482
3	247	100.0	607	15	US-10-258-851-74
4	247	100.0	620	10	US-08-788-051-7
5	247	100.0	636	10	US-09-788-051-4
6	247	100.0	781	9	US-09-860-868-2
7	247	100.0	781	14	US-10-245-752-98
8	247	100.0	781	14	US-10-245-859-98
9	247	100.0	781	14	US-10-245-103-98
10	247	100.0	781	14	US-10-245-107-98
11	247	100.0	781	14	US-10-245-143-98
12	247	100.0	781	14	US-10-245-771-98
13	247	100.0	781	14	US-10-245-851-98

14	247	100.0	781	14	US-10-245-883-98	Sequence 98, Appl
15	247	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
16	247	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
17	247	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
18	247	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
19	247	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
20	247	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
21	247	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
22	247	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
23	247	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
24	247	100.0	781	14	US-10-239-156-98	Sequence 98, Appl
25	247	100.0	781	14	US-10-245-024-98	Sequence 98, Appl
26	247	100.0	781	14	US-10-245-409-98	Sequence 98, Appl
27	247	100.0	781	14	US-10-245-621-98	Sequence 98, Appl
28	247	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
29	247	100.0	781	14	US-10-245-033-98	Sequence 98, Appl
30	247	100.0	781	14	US-10-245-095-98	Sequence 98, Appl
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33	247	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
34	247	100.0	781	14	US-10-245-770-98	Sequence 98, Appl
35	247	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
36	247	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
37	247	100.0	781	14	US-10-245-320-98	Sequence 98, Appl
38	247	100.0	781	14	US-10-162-435-13	Sequence 13, Appl
39	247	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
40	247	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
41	247	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
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43	247	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
44	247	100.0	781	14	US-10-238-411-98	Sequence 98, Appl
45	247	100.0	781	14	US-10-245-124-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-9
Sequence 9, Application US/09788051
Publicat. No. US2003014491A1
GENERAL INFORMATION:
APPLICANT: Geobole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dimanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-9

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Best Local Similarity 100.0%; Pred. No. 6.8e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zeehuseen, Bryan
APPLICANT: Paturajan, Meera
APPLICANT: Shimkova, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esna
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grose, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 482
LENGTH: 493
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-482

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Best Local Similarity 100.0%; Pred. No. 1.2e-24;
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RESULT 3
US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kadnick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing

TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: G950025
CURRENT APPLICATION NUMBER: US/10/258,951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

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Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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242 STTAVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAADPDIG 289

RESULT 4
US-09-788-051-7
Sequence 7, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drenth, Radjoe T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 620
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 247; DB 10; Length 620;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
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 ; Sequence 4, Application US/09788051
 ; Publication No. US20030144491A1
 ; GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
 APPLICANT: Kuo, Chiaoyun
 APPLICANT: Atterburn, Matthew C
 APPLICANT: Yeung, George
 APPLICANT: Palencia, Servando
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Dimnac, Radoje T
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
 ; TITLE OF INVENTION: POLYNUCLEOTIDES
 ; FILE REFERENCE: HVS-39
 ; CURRENT APPLICATION NUMBER: US/09/788,051
 ; CURRENT FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: US 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: US 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 17
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 ; SEQ ID NO 4
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-788-051-4

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 US-09-860-868-2
 ; Sequence 2, Application US/09860868
 ; Patent No. US20020076757A1
 ; GENERAL INFORMATION:

APPLICANT: Curtis, Roy A. J.
 TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
 ; TITLE OF INVENTION: MEMBER AND USES THEREOF
 ; FILE REFERENCE: 10448-050001
 ; CURRENT FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: 60/205,674
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-09-860-868-2

Query Match 100.0%; Score 247; DB 9; Length 781;
 Best Local Similarity 100.0%; Pred. No. 2.1e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
 |||||
 DB 242 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRLRAQDDPLG 289

RESULT 7

US-10-245-752-98
 ; Sequence 98, Application US/10245752
 ; Publication No. US20030064473A1
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin
 APPLICANT: Baton, Dan
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Goddard, Audrey
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurley, Austin
 APPLICANT: Smith, Victoria
 APPLICANT: Stephan, Jean-Philippe
 APPLICANT: Watanabe, Colin
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 APPLICANT: Fong, Sherman
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630R1C66
 ; CURRENT APPLICATION NUMBER: US/10/245,752
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/197942
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See file wrapper or PAM.
 ; NUMBER OF SEQ ID NOS: 116
 ; SEQ ID NO 98
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-245-752-98

Query Match 100.0%; Score 247; DB 14; Length 781;
 Best Local Similarity 100.0%; Pred. No. 2.1e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRLRAQDDPLG 48
 |||||
 DB 242 STTVTVTLSDVNDNPKPFQSLYQFSVETAGPGLVGRRLRAQDDPLG 289

RESULT 8
 US-10-245-859-98

; Sequence 98, Application US/10245859
 ; Publication No. US20030064474A1
 ; GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Baton, Dan
 APPLICANT: Filvaroff, Ellen

```

/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, V. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matembe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245, 859
/ PRIOR FILING DATE: 2002-09-15
/ PRIOR APPLICATION NUMBER: 60/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-859-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  STTATVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 48
Db      242 STTATVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 289

RESULT 9
/ US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication No. US2003006879A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matembe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C12
/ CURRENT APPLICATION NUMBER: US/10/245, 103
/ PRIOR FILING DATE: 2002-09-17
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/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-245-103-98

Query Match      100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  STTATVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 48
Db      242 STTATVTLSDVNDNPKPKFQSLYQFSVETAGPGLVGRRAQDPDLG 289

RESULT 10
/ US-10-245-107-98
/ Sequence 98, Application US/10245107
/ Publication No. US2003006879A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matembe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C71
/ CURRENT APPLICATION NUMBER: US/10/245, 107
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
DB 242 STTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 11
US-10-245-143-98
Sequence 98, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
DB 242 STTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 12
US-10-245-771-98
Sequence 98, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-771-98

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 48
DB 242 STTVTLSDVNDNPPKPFQSLYQFSVETAGPGLVGRRAQDDPLG 289

RESULT 13
US-10-245-851-98
Sequence 98, Application US/10245851
Publication No. US20030068782A1
GENERAL INFORMATION:

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/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Wacande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P363OR1C93
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98

Query Match          100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STTAVTILSDVNDNPKFPOSILYQFSVETAGCGTLVGRRAODPDLG 48
DB      242 STTAVTILSDVNDNPKFPOSILYQFSVETAGCGTLVGRRAODPDLG 289

RESULT 14
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Wacande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
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/ FILE REFERENCE: P363OR1C70
/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98

Query Match          100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 STTAVTILSDVNDNPKFPOSILYQFSVETAGCGTLVGRRAODPDLG 48
DB      242 STTAVTILSDVNDNPKFPOSILYQFSVETAGCGTLVGRRAODPDLG 289

RESULT 15
US-10-237-535-98
/ Sequence 98, Application US/10237535
/ Publication No. US20030073188A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Eaton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Wacande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P363OR1C3
/ CURRENT APPLICATION NUMBER: US/10/237,535
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
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PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/123957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
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PRIOR FILING DATE: 1999-05-25
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PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
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PRIOR APPLICATION NUMBER: 60/145228
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
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PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
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PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/229896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
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PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/264395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/923404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 247; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 STVTVTLLSDVNDNPKPKPOSTLYQFSVETAGPCTIVGRRAQDDPDG 48
Db 242 STVTVTLLSDVNDNPKPKPOSTLYQFSVETAGPCTIVGRRAQDDPDG 289

Search completed: December 8, 2004, 11:34:28
Job time : 49.0484 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 5.72373 Seconds

(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-9

Perfect score: 247

Sequence: 1 STVTVTLSVDNDNPKFPQ.....ETAGPGLVGRLRAPDPDLG 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	72.9	693	2	US-08-738-349-6 Sequence 6, Appl
2	180	72.9	693	4	US-09-919-497-55 Sequence 55, Appl
3	180	72.9	796	2	US-08-738-349-2 Sequence 2, Appl
4	180	72.9	796	2	US-08-738-349-4 Sequence 4, Appl
5	178	72.1	796	1	US-08-188-228-58 Sequence 58, Appl
6	178	72.1	796	1	US-08-332-643-52 Sequence 52, Appl
7	178	72.1	796	1	US-08-332-638-58 Sequence 58, Appl
8	178	72.1	796	4	US-09-654-328-2 Sequence 2, Appl
9	169.5	68.6	615	2	US-08-738-349-12 Sequence 12, Appl
10	163	66.0	532	1	US-08-188-228-44 Sequence 44, Appl
11	163	66.0	532	1	US-08-332-638-44 Sequence 44, Appl
12	163	66.0	793	1	US-08-188-228-54 Sequence 54, Appl
13	163	66.0	793	1	US-08-332-643-48 Sequence 48, Appl
14	163	66.0	793	1	US-08-332-638-54 Sequence 54, Appl
15	163	66.0	799	1	US-08-188-228-42 Sequence 42, Appl
16	163	66.0	799	1	US-08-332-638-42 Sequence 42, Appl
17	144	58.3	794	1	US-08-188-228-60 Sequence 60, Appl
18	144	58.3	794	1	US-08-332-643-54 Sequence 54, Appl
19	144	58.3	794	1	US-08-332-638-60 Sequence 60, Appl
20	137	55.5	653	1	US-08-188-228-46 Sequence 46, Appl
21	137	55.5	653	1	US-08-332-638-46 Sequence 46, Appl
22	110	44.5	780	1	US-08-188-228-50 Sequence 50, Appl
23	110	44.5	780	1	US-08-332-643-44 Sequence 44, Appl
24	110	44.5	780	1	US-08-332-638-50 Sequence 50, Appl
25	109	44.1	348	4	US-09-270-767-46673 Sequence 46673, A
26	104	42.1	616	1	US-08-453-695A-115 Sequence 115, App
27	104	42.1	616	1	US-08-268-161A-115 Sequence 115, App

ALIGNMENTS

28	104	42.1	616	2	US-08-453-702A-115	Sequence 115, App
29	104	42.1	616	3	US-09-099-639-115	Sequence 115, App
30	104	42.1	616	5	PCT-US95-08071-115	Sequence 115, App
31	104	42.1	747	3	US-09-035-648-18	Sequence 18, Appl
32	104	42.1	747	3	US-09-001-951-18	Sequence 18, Appl
33	104	42.1	747	4	US-08-818-829-18	Sequence 18, Appl
34	100	40.5	797	1	US-08-453-695A-112	Sequence 112, App
35	100	40.5	797	1	US-08-268-161A-112	Sequence 112, App
36	100	40.5	797	2	US-08-453-702A-112	Sequence 112, App
37	100	40.5	797	3	US-09-099-639-112	Sequence 112, App
38	100	40.5	797	5	PCT-US95-08071-112	Sequence 112, App
39	100	40.5	1184	4	US-10-140-002-394	Sequence 394, App
40	99	40.1	884	2	US-08-474-067-8	Sequence 8, Appl
41	99	40.1	884	2	US-08-474-068A-8	Sequence 8, Appl
42	99	40.1	884	2	US-08-472-481-7	Sequence 7, Appl
43	98	39.7	148	1	US-07-998-003A-36	Sequence 36, Appl
44	98	39.7	148	1	US-08-453-274B-36	Sequence 36, Appl
45	98	39.7	148	1	US-08-453-695A-36	Sequence 36, Appl

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Kawasaki, Makoto
APPLICANT: Okazaki, Shinji
APPLICANT: Tsujimura, Aetsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 72.9%; Score 180; DB 2; Length 796;
Best Local Similarity 68.8%; Pred. No. 4, 1e-17;
Matches 33; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 STTWTTLSDVNDNPKPFPQSVYQISVSEAAVGESEVGRKAKDPDYG 48
DB 251 TTKVITLIDVNDNPKPFPQSVYQISVSEAAVGESEVGRKAKDPDYG 298

RESULT 5

US-08-188-228-58
Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725end, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 72.1%; Score 178; DB 1; Length 796;
Best Local Similarity 68.8%; Pred. No. 8e-17;
Matches 33; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 STTWTTLSDVNDNPKPFPQSVYQISVSEAAVGESEVGRKAKDPDYG 48
DB 251 TTKVITLIDVNDNPKPFPQSVYQISVSEAAVGESEVGRKAKDPDYG 298

RESULT 6
US-08-332-643-52
Sequence 52, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Bicknell, Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query Match 72.1%; Score 178; DB 1; Length 796;
Best Local Similarity 68.8%; Pred. No. 8e-17;
Matches 33; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 STTWTTLSDVNDNPKPFPQSVYQISVSEAAVGESEVGRKAKDPDYG 48
DB 251 TTKVITLIDVNDNPKPFPQSVYQISVSEAAVGESEVGRKAKDPDYG 298

RESULT 7
US-08-332-638-58
Sequence 58, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match 72.1%; Score 178; DB 1; Length 796;
Best Local Similarity 68.8%; Pred. No. 9e-17; Mismatches 8; Indels 0; Gaps 0;
Matches 33; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 STVTVTLSVDNDNPKPKFQSLYQFSVETAGPGLVGRRAADPDIG 48
Db 251 TTKVTITLTDVNDNPKPKFQSLYQMSVSAVPGEEVGRVAKDPDIG 298

RESULT 8
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
TITLE OF INVENTION: Of Inflammatory Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match 72.1%; Score 178; DB 4; Length 796;
Best Local Similarity 68.8%; Pred. No. 8e-17; Mismatches 8; Indels 0; Gaps 0;
Matches 33; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 STVTVTLSVDNDNPKPKFQSLYQFSVETAGPGLVGRRAADPDIG 48
Db 251 TTKVTITLTDVNDNPKPKFQSLYQMSVSAVPGEEVGRVAKDPDIG 298

RESULT 9
US-08-738-349-12
Sequence 12, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-738-349-12

Query Match 68.6%; Score 169.5; DB 2; Length 615;
Best Local Similarity 68.8%; Pred. No. 9.5e-16; Mismatches 6; Indels 1; Gaps 1;
Matches 33; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

Qy 1 STVTVTLSVDNDNPKPKFQSLYQFSVETAGPGLVGRRAADPDIG 48
Db 244 TTKVTITLTDVNDNPKPKFQSVYQSVSEAVPGEEVGRVAKDPDIG 290

RESULT 10
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559772sand, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 66.0%; Score 163; DB 1; Length 532;
Best Local Similarity 64.6%; Pred. No. 6,8e-15;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPPKPFQSLYQFSVYETAGPGLVGRRAQDPDLG 48
DB 259 TTTLVTVTLSDVNDNPPKPFQSLYHFSVPEVDVLTGTAIGRVKANDODIG 306

RESULT 11
US-08-332-638-44
Sequence 44, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 66.0%; Score 163; DB 1; Length 532;
Best Local Similarity 64.6%; Pred. No. 6,8e-15;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPPKPFQSLYQFSVYETAGPGLVGRRAQDPDLG 48
DB 259 TTTLVTVTLSDVNDNPPKPFQSLYHFSVPEVDVLTGTAIGRVKANDODIG 306

RESULT 12
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559772sand, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 66.0%; Score 163; DB 1; Length 793;
Best Local Similarity 64.6%; Pred. No. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 STTVTVTLSDVNDNPPKPFQSLYQFSVYETAGPGLVGRRAQDPDLG 48
DB 252 TTTLVTVTLSDVNDNPPKPFQSLYHFSVPEVDVLTGTAIGRVKANDODIG 299

RESULT 13
US-08-332-643-48
Sequence 48, Application US/08332634
Patent No. 5639634

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 66.0%; Score 163; DB 1; Length 793;
Best Local Similarity 64.6%; Pred. No. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db 1 STTVTLSDVNDNPKPKFPOSLYOFSVETAGPCTLVGRRAODPDUG 48
252 TTTLVTLLTVNDNPKPKFQSLYHFVPEVDVLTALGRVANDQDIG 299

RESULT 14
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 66.0%; Score 163; DB 1; Length 793;
Best Local Similarity 64.6%; Pred. No. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Db 1 STTVTLSDVNDNPKPKFPOSLYOFSVETAGPCTLVGRRAODPDUG 48
252 TTTLVTLLTVNDNPKPKFQSLYHFVPEVDVLTALGRVANDQDIG 299

RESULT 15
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:

LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 66.0%; Score 163; DB 1; Length 799;
Best Local Similarity 64.6%; Pred. NO. 1.1e-14;
Matches 31; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 STTVVTLSDVNDNPPKFPQSLYQFSVETAGPGTLVGRRLRAQDDPLG 48
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 259 TTTLTVTLTDVNDNPPKFAQSLYHFSVPEDVVLGTALGRVXANDQDIG 306

Search completed: December 8, 2004, 10:01:13
Job time : 6.72373 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 2.66883 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-10
Perfect score: 180
Sequence: 1 LLRTSRGMWNQPFVIEEYAGPEPVILGKLHSD 33

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	152	84.4	796 2	A38992
2	152	84.4	796 2	cadherin-11 - precu
3	152	84.4	796 2	cadherin-11 - mous
4	152	84.4	796 2	cadherin-11 - mous
5	142	78.9	785 2	A53584
6	140	77.8	790 2	OB-cadherin precu
7	139	77.2	793 2	cadherin-7 - chick
8	133	73.9	794 2	F-cadherin - chick
9	127	70.6	790 2	cadherin 8 - human
10	122	67.8	789 2	cadherin-12 - huma
11	122	67.8	790 2	cadherin-14 - huma
12	121	67.2	790 2	K-cadherin - rat
13	121	67.2	790 2	cadherin-6B - chic
14	121	67.2	790 2	cadherin-6 - human
15	121	67.2	790 2	cadherin 5 precurs
16	121	67.2	790 2	P-cadherin precurs
17	121	67.2	790 2	CLIAA protein - ra
18	121	67.2	790 2	latrophilin-1, bra
19	121	67.2	790 2	latrophilin-1, bra
20	121	67.2	790 2	latrophilin-1, bra
21	121	67.2	790 2	latrophilin-1, bra
22	121	67.2	790 2	latrophilin-1, bra
23	121	67.2	790 2	latrophilin-1, bra
24	121	67.2	790 2	latrophilin-1, bra
25	121	67.2	790 2	latrophilin-1, bra
26	121	67.2	790 2	latrophilin-1, bra
27	121	67.2	790 2	latrophilin-1, bra
28	121	67.2	790 2	latrophilin-1, bra
29	121	67.2	790 2	latrophilin-1, bra

30	50	27.8	887 1	IUCHCL
31	49.5	27.5	445 2	P90562
32	49.5	27.5	598 2	I51368
33	49.5	27.5	1006 2	S76892
34	49.5	27.5	244 2	AC3341
35	49.5	27.2	305 2	T44845
36	49.5	27.2	315 2	A88043
37	49.5	27.2	513 2	A63701
38	49.5	27.2	687 2	A46636
39	49.5	27.2	1107 1	S52517
40	49.5	27.2	1109 2	S53601
41	49.5	27.2	1254 1	A32686
42	48.5	26.9	394 2	C83840
43	48.5	26.7	570 2	D65364
44	48.5	26.7	637 2	A82301
45	48.5	26.7	655 2	G89189

ALIGNMENTS

RESULT 1
A38992
cadherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; PMID:91283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
C/Accession: UNIPROT:P55287; GB:U34056; NID:9506403; PIDN:AAA5622.1; PID:950640
C/Genetics:
A/Gene: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
A/Map position: 16q22.1-16q22.1
C/Suprafamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/56-159/Domain: cadherin repeat homology <CR1>
F/162-268/Domain: cadherin repeat homology <CR2>
F/271-383/Domain: cadherin repeat homology <CR3>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 8.9e-14;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 LLRTSRGMWNQPFVIEEYAGPEPVILGKLHSD 33
48 LQSKRGWNNQPFVIEEYAGPEPVILGKLHSD 80

RESULT 2
148277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 148277
R/Hoffmann, I.; Bailling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: 148277; PMID:95269886; PMID:7750649
A/Accession: 148277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
C/Accession: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:9666
C/Genetics:

A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 48 LQSRKRGVWVWVNFVIEEYTGPDPLVGLRLHSD 80

RESULT 3

149556
cadherin-11 - mouse

C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: U19556
R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.

Dev. Biol. 169, 347-358, 1995
A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head

A:Reference number: 149556; MUID:95269887; PMID:7750650
A:Accession: U19556

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-796 <RBS>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:G974190; PIDN:BA06730.1; PID:G974191

C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 48 LQSRKRGVWVWVNFVIEEYTGPDPLVGLRLHSD 80

RESULT 4

A53584
OB-cadherin precursor - mouse

C:Species: Mus musculus (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Mann, E.

J. Biol. Chem. 269, 12092-12098, 1994
A:Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin

A:Reference number: A53584; MUID:94216322; PMID:8163513
A:Accession: A53584

A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:G994774; PIDN:BA04797.1; PID:G994775

C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein

F:156-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>

F:386-488/Domain: cadherin repeat homology <CR4>

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 48 LQSRKRGVWVWVNFVIEEYTGPDPLVGLRLHSD 80

RESULT 5
150180
cadherin-7 - chicken

C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: U50180

R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1337, 1995

A:Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec

A:Reference number: U50178; MUID:95309115; PMID:7540531
A:Accession: U50180

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-785 <NAX>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:G868000; PIDN:BA07721.1; PID:G868000

C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match
Best Local Similarity 78.9%; Score 142; DB 2; Length 785;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RTRRSWVWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 44 RTKRSWVWVWVNFVIEEYMGSDPLVYGKLSHD 74

RESULT 6
151638
F-cadherin - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: U51638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.

Mol. Cell. Neurosci. 6, 199-212, 1995
A:Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole

A:Reference number: U51638; MUID:96035533; PMID:7456627
A:Accession: U51638

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-790 <ESP>
A:Cross-references: UNIPROT:Q91638; EMBL:X85330; NID:G854634; PIDN:CA059679.1; PID:G8546

C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match
Best Local Similarity 77.8%; Score 140; DB 2; Length 790;
Matches 23; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RTRRSWVWVWVNFVIEEYAGPEPVLIGKLSHD 33
Db 49 RIKRSWVWVWVNFVIEEYTGTEPLVYGKLSHD 79

RESULT 7
D38992
cadherin 8 - human

C:Species: Homo sapiens (man)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A:Reference number: S24305; MUID:91283540; PMID:12059658
A:Accession: D38992

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-793 <STZ>
A:Cross-references: GB:L34060; NID:G506411; PIDN:AAA35628.1; PID:G506412

C:Genetics: GDB:CDH8
A:Gene: GDB:CDH8

A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 77.2%; Score 139; DB 2; Length 793;
 Best Local Similarity 63.6%; Pred. No. 6,7e-12;
 Matches 21; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 LTRRSWVWVNFVIEEYAGPEPVILGKLHSD 33
 DB 49 LRSKRGVWVNFVLEESGPEFVLGRHLD 81

RESULT 8

159372
 cadherin 12 - human
 N:Alternate names: E-cadherin
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C/Accession: I59372
 R:SeqId: S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.M.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
 A>Title: Expressed cadherin pseudogenes are localized to the critical region of the spin
 A/Reference number: I59372; MUID:9524541; PMID:7731968
 A/Accession: I59372
 A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME
 A/Molecule type: mRNA
 A/Residues: 1-794 <RBS>
 A/Cross-references: UNIPROT:P55289; GB:L33477; NID:G793942; PIDN:ABA46539.1; PID:G793943
 C/Genetics:
 A/Gene: GDB:CDH12
 A/Cross-references: GDB:596324
 A/Map position: 5p13-5p14
 A/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
 F:57-160/Domain: cadherin repeat homology <CR1>
 F:163-269/Domain: cadherin repeat homology <CR2>
 F:327-384/Domain: cadherin repeat homology <CR3>
 F:387-489/Domain: cadherin repeat homology <CR4>
 F:491-601/Domain: cadherin repeat homology <CR5>
 F:610-637/Domain: transmembrane #status predicted <TM>
 F:638-794/Domain: intracellular #status predicted <INT>

Query Match 73.9%; Score 133; DB 2; Length 794;
 Best Local Similarity 71.0%; Pred. No. 5e-11;
 Matches 22; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 RTRRSWVWVNFVIEEYAGPEPVILGKLHSD 33
 DB 51 RYKRGVWVNFVLEESGPEFVLGRHLD 81

RESULT 9

G02678
 cadherin-14 - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C/Accession: G02678
 R:Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.
 submitted to the EMBL Data Library, May 1995
 A/Reference number: H01584
 A/Accession: G02678
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <SH1>
 A/Cross-references: UNIPROT:Q1334; EMBL:U59325; NID:G1389852; PIDN:AA02933.1; PID:G138
 C/Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 70.6%; Score 127; DB 2; Length 790;
 Best Local Similarity 64.5%; Pred. No. 3.6e-10;
 Matches 20; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 RTRRSWVWVNFVIEEYAGPEPVILGKLHSD 33
 DB 50 RPKRGVWVNFVLEESGPEFVLGRHLD 80

RESULT 10
 152701
 K-cadherin - rat

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I52701
 R:Yang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara,
 Cancer Res. 54, 3034-3041, 1994
 A>Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
 A/Reference number: I52701; MUID:94243827; PMID:8187093
 A/Accession: I52701
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-789 <RBS>
 A/Cross-references: UNIPROT:P55280; GB:ID25290; NID:9435460; PIDN:BA04975.1; PID:9435460
 C/Genetics:
 A/Gene: KCAD
 A/Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 67.8%; Score 122; DB 2; Length 789;
 Best Local Similarity 60.6%; Pred. No. 1.9e-09;
 Matches 20; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 LTRRSWVWVNFVIEEYAGPEPVILGKLHSD 33
 DB 48 LRSKRGVWVNFVLEESGPEFVLGRHLD 80

RESULT 11

150178
 cadherin-6B - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: I50178
 R:Nakagawa, S.; Takeichi, M.
 Development 121, 1321-1332, 1995
 A>Title: Neutral crest cell-cell adhesion controlled by sequential and subpopulation-spe
 A/Reference number: I50178; MUID:95309115; PMID:7540531
 A/Accession: I50178
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <NAK>
 A/Cross-references: UNIPROT:Q90762; GB:ID42149; NID:9867998; PIDN:BA07720.1; PID:986799
 C/Superfamily: cadherin; cadherin repeat homology
 F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 67.8%; Score 122; DB 2; Length 790;
 Best Local Similarity 60.6%; Pred. No. 1.9e-09;
 Matches 20; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 LTRRSWVWVNFVIEEYAGPEPVILGKLHSD 33
 DB 48 LRSKRGVWVNFVLEESGPEFVLGRHLD 80

RESULT 12

137016
 cadherin-6 - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I37016
 R:Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitejima, M.; Hirohashi, S.
 Cancer Res. 55, 2206-2211, 1995
 A>Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the
 A/Reference number: I37016; MUID:95262134; PMID:7743525
 A/Accession: I37016
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <RBS>
 A/Cross-references: UNIPROT:P55285; GB:D31784; NID:9574184; PIDN:BA06562.1; PID:957418

C/Genetics:

A:Gene: GDB:CDH6
A:Cross-references: GDB:5822908
C:Superfamily: cadherin, cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 67.2%; Score 121; DB 2; Length 790;
Best Local Similarity 60.6%; Pred. No. 2.7e-09;
Matches 20; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LRTSRWVWNOFPVIEYAGPEPVLIGKLSHD 33
Db 48 LRRSRWVWNOFPVIEYAGPEPVLIGKLSHD 80

RESULT 13
IGHUC5
cadherin 5 precursor - human
N:Alternate names: 7B4 antigen, cadherin, endothelial-specific, VE-cadherin
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: S49893; S24305; A43418
R:Brevario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A:Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov
A:Reference number: S49893
A:Accession: S49893
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-784

A:Cross-references: UNIPROT:P3151; EMBL:X79981; NID:G599833; PIDN:CA56306.1; PID:G5998
R:Snukl, S.; Sano, K.; Tanihara, H.
Call Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: S24305
A:Molecule type: mRNA
A:Residues: 5-516, 'I', 518-784 <SU>
A:Cross-references: EMBL:X59796; NID:G639976; PIDN:CA442468.1; PID:G29593
R:Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Houen, G.; Ruco,
J. Cell Biol. 118, 1511-1522, 1992
A:Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
A:Reference number: A43418; MUID:92394977; PMID:1522121
A:Accession: A43418
A:Molecule type: protein
A:Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-
A:Experimental source: cultured endothelial cells
A:Note: sequence extracted from NCBI database (NCBI:P:113040, NCBI:P:113045, NCBI:P:113047,
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought b
C:Genetics:
A:Gene: GDB:CDH5
A:Cross-references: GDB:134230; OMIM:601120
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin, cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-47/Domain: propeptide #status predicted <PRO>
F:48-784/Domain: extracellular #status predicted <EXT>
F:50-151/Domain: cadherin repeat homology <CR1>
F:154-258/Domain: cadherin repeat homology <CR2>
F:261-312/Domain: cadherin repeat homology <CR3>
F:375-479/Domain: cadherin repeat homology <CR4>
F:481-587/Domain: cadherin repeat homology <CR5>
F:594-650/Domain: transmembrane #status predicted <TM>
F:621-784/Domain: intracellular #status predicted <INT>
F:736-753/Region: serine-rich
F:61,112,157,362,442,523,533/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 36.7%; Score 66; DB 1; Length 784;
Best Local Similarity 40.0%; Pred. No. 0.24;
Matches 12; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

Qy 3 RTRSRWVWNOFPVIEYAGPEPVLIGKLSHD 32

Db 44 ROKRDMWNOFPVIEYAGPEPVLIGKLSHD 73

RESULT 14
ITMSCP
P-cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: S03163; S34458
R:Nose, A.; Nagatuchi, A.; Takeichi, M.
EMBO J. 6, 3655-3661, 1987
A:Title: Isolation of placental cadherin cDNA: identification of a novel gene family of
A:Reference number: S03163; MUID:8811554; PMID:3428270
A:Accession: S03163
A:Molecule type: mRNA
A:Residues: 1-822 <NOS>
A:Cross-references: UNIPROT:P10287; EMBL:X06340
R:Faraldo, M.L.M.; Cano, A.
J. Mol. Biol. 231, 935-941, 1993
A:Title: The 5' flanking sequences of the mouse P-cadherin gene. Homologies to 5' sequen
A:Reference number: S34458; MUID:99294853; PMID:8515462
A:Accession: S34458
A:Molecule type: DNA
A:Residues: 1-55 <PAR>
A:Cross-references: EMBL:X68057
C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
C:Genetics:
A:Introns: 16/3
C:Superfamily: cadherin, cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; placenta; transmem
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-99/Domain: propeptide #status predicted <PRO>
F:100-822/Product: P-cadherin #status predicted <MT>
F:102-207/Domain: extracellular #status predicted <EXT>
F:210-320/Domain: cadherin repeat homology <CR1>
F:323-432/Domain: cadherin repeat homology <CR2>
F:433-540/Domain: cadherin repeat homology <CR3>
F:541-643/Domain: cadherin repeat homology <CR4>
F:646-670/Domain: transmembrane #status predicted <TM>
F:671-822/Domain: intracellular #status predicted <INT>
F:778-793/Region: serine-rich
F:192,558/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.1%; Score 56; DB 1; Length 822;
Best Local Similarity 39.4%; Pred. No. 7.1;
Matches 13; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 LRTSRWVWNOFPVIEYAGPEPVLIGKLSHD 33
Db 94 LRRRGEVWMPPIFVPEWKGKPPFQRLNQLKSN 126

RESULT 15
TI138
CLIAA protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17138
R:Krasnoperov, V.G.; Bitner, M.A.; Davis, R.; Huang, Y.; Salnikow, K.V.; Chepurny, O.C.
Neuron 18, 925-937, 1997
A:Title: Alpha-latrotoxin stimulates exocytosis by the interaction with a neuronal G-pro
A:Reference number: Z18710; MUID:97352465; PMID:9208860
A:Accession: T17138
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-1466 <KRA>
A:Cross-references: UNIPROT:O88917; EMBL:AF081144; NID:G3695114; PID:G3695115; PIDN:AAACG
C:Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 29.2%; Score 52.5; DB 2; Length 1466;
Best Local Similarity 36.0%; Pred. No. 44;

Wed Dec 8 11:46:19 2004

us-09-788-051-10.rpr

Page 5

	Matches	9;	Conservative	6;	Mismatches	7;	Indels	3;	Gaps	1;
QY	3	RTSRWVWNGFFVIE---	ETVAGPEP	24						
		: : : : : :	: :							
Db	372	RDNQLYWNNYFVRYSLF	FGPPDP	396						

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Search completed: December  8, 2004, 10:27:07
Job time : 3.66883 secs
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FT VMPYCGVGLS (in isoform 3).
 FT /FTId=VSP_008719.
 SQ SEQUENCE 819 AA; 87751 MW; 9083034F18BA7BE4A CRC64;
 Query Match 100.0%; Score 180; DB 1; Length 819;
 Best Local Similarity 100.0%; Pred. No. 1.5e-16;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 33
 |||||
 DB 39 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 4
 Q6PFX6 PRELIMINARY; PRT; 781 AA.
 AC Q6PFX6
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Roshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC -1- (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC EMBL; BC057373; AAH57373.1; -
 CC InterPro: IPR002126; Cadherin.
 CC InterPro: IPR002233; Cadherin.
 CC Pfam: PF000028; Cadherin; 5
 CC Pfam: PF01049; Cadherin; 1
 CC PRINTS: PRO0205; CADHERIN.
 CC SMART; SM00112; CA; 4.
 CC PROSITE; PS00232; CADHERIN_1; 2.
 CC PROSITE; PS0268; CADHERIN_2; 5.
 CC Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 KW Sequence 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 33
 |||||
 DB 39 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 5
 AAH57373 PRELIMINARY; PRT; 781 AA.
 ID AAH57373
 AC AAH57373
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Roshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057373; AAH57373.1; -
 SQ SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;

Query Match 98.3%; Score 177; DB 2; Length 781;
 Best Local Similarity 97.0%; Pred. No. 3.8e-16;
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 33
 |||||
 DB 39 LKTRRSWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 6
 CADD_HUMAN STANDARD; PRT; 796 AA.
 ID CADD_HUMAN
 AC P55287; Q15065; Q15066; Q9UG93; Q9UG94;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxId=9606;
 [1]
 SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE=Brain;
 MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Heimerl R.L., St John T., Suzuki S.,
 "Cloning of five human cadherin cDNAs: characterization of
 cadherin extracellular domain and provides further evidence for two
 structurally different types of cadherin.";
 Cell Adhes. Commun. 2:15-26(1994).
 [2]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 TISSUE=Osteosarcoma;
 MEDLINE=94216322; PubMed=8163513;
 Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 "Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts.";
 J. Biol. Chem. 269:12092-12098(1994).
 [3]
 SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
 TISSUE=Cerebral brain;
 MEDLINE=91283540; PubMed=2059658;
 Suzuki S., Sano K., Tanhara H.,
 "Diversity of the cadherin family: evidence for eight new cadherins in
 nervous tissue.";
 Cell Regul. 2:261-270(1991).
 [4]
 SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 Koolis P.F., Hogendoorn P.C.W., Boyee J.V.M.G., Van Roy F.,
 "Alternative cadherin-11 transcripts encoding truncated adhesion
 molecules are detectable in both human cancer and normal cells.";
 Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 They preferentially interact with themselves in a homophilic
 manner in connecting cells; cadherins may thus contribute to the
 sorting of heterogeneous cell types.
 -1- SUBCELLULAR LOCATION: Type I membrane protein.
 -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=1;
 IsoId=P55287-1; Sequence=Displayed;
 Name=2;
 IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
 -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 other tissues. Expressed in neuroblasts.
 -1- SIMILARITY: Contains 5 cadherin domains.

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 or send an email to license@lsb-sib.ch).

 EMBL, L34056; AAA35622.1; -;
 EMBL, D21254; BA04798.1; -;
 EMBL, D21255; BA04799.1; -;
 EMBL, AF060370; AAD27755.1; -;
 EMBL, AF060369; AAD27755.1; JOINED.
 EMBL, AF060370; AAD27756.1; -;
 EMBL, AF060369; AAD27756.1; JOINED.
 PIR, A38992; A38992.
 HSSP, P09603; 11TW.
 DR Genew; HGNC:1750; CDPH1.
 DR MIM; 600023; -;
 DR GO; GO:0016021; C:Integral to membrane; NAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
 DR GO; GO:0001503; P:ossification; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.

DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KM Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53
 FT CHAIN 54 796
 FT DOMAIN 54 617
 FT TRANSMEM 618 640
 FT DOMAIN 641 796
 FT DOMAIN 641 796
 FT DOMAIN 641 796
 FT DOMAIN 160 268
 FT DOMAIN 269 383
 FT DOMAIN 384 486
 FT DOMAIN 487 612
 FT CARBOHYD 455 455
 FT CARBOHYD 540 540
 FT VARSPLIC 632 693
 FT
 FT VARSPLIC 694 796
 FT
 FT CONFLICT 271 272
 FT CONFLICT 275 275
 FT CONFLICT 340 340
 FT CONFLICT 373 373
 FT CONFLICT 471 471
 SQ SEQUENCE 796 AA; 88049 MW; 2C67044C78ADBB2E CXC64;
 Query Match 84.4%; Score 152; DB 1; Length 796;
 Best Local Similarity 75.8%; Pred. No. 1,3e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LRTSRWVWVQFVIEEYAGEPYLICKLSD 33
 DB 48 LQSRKGVWVQFVIEEYGTGDPVLVGRLLSD 80
 RESULT 7
 CADB_MOUSE
 ID CADB_MOUSE STANDARD; PRT; 796 AA.
 AC P55288;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=Cdh11; Synonyms=Cad-11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RP MEDLINE=95269867; PubMed=7750649;
 RA Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 Miyazaki T., Takeichi M.,
 "Cadherin-11 expressed in association with mesenchymal morphogenesis
 in the head, somite, and limb bud of early mouse embryos.";
 Dev. Biol. 169:347-358(1995).
 RL (3)
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 Amann E.,
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts.";
 RL J. Biol. Chem. 269.12092-12098 (1994).
 [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Olfactory epithelium;
 RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903 (2002).
 [5]
 RN DEVELOPMENTAL STAGE.
 RP STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.,
 RT "A comprehensive survey of the cadherins expressed in the testes of
 fetal, immature, and adult mice utilizing the polymerase chain
 reaction.";
 RL Biol. Reprod. 55.822-827 (1996).
 [6]
 RN FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC [7]
 RN SUBCELLULAR LOCATION: Type I membrane protein.
 CC [8]
 RN TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC [9]
 RN DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC [10]
 RN SIMILARITY: Contains 5 cadherin domains.
 CC [11]
 RN This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC [12]
 RN EMBL; X77557; CAA54674.1; -
 DR EMBL; D31963; BAA06730.1; -
 DR EMBL; D1253; BAA04797.1; -
 DR EMBL; BC046314; AAH46314.1; -
 DR PIR; A53584; A53584;
 DR PIR; I48277; I48277;
 DR PIR; I49556; I49556;
 DR HSSP; P09803; I17W.
 DR MGD; MGI:99217; Cdh11.
 DR GO; GO:0005737; Cytoplasm; IDA.
 DR GO; GO:0005886; Cytoplasmic membrane; IDA.
 DR InterPro; IPR002126; Cadherin.

DR InterPro; IPR002123; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 DR KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat, Signal,
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 462 462 E -> D (in Ref. 1).
 FT CONFLICT 589 589 T -> L (in Ref. 2).
 FT CONFLICT 655 655 D -> N (in Ref. 2).
 FT CONFLICT 751 751 V -> M (in Ref. 1).
 FT CONFLICT 777 777 P -> Q (in Ref. 2).
 FT CONFLICT 782 782 L -> P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D24641D529 CRC64;
 Query Match 84.4%; Score 152; DB 1; Length 796;
 Best Local Similarity 75.8%; Pred. No. 1.3e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LIRTRSWYVNOFVIEBYAGPEVILIGLHSD 33
 Db 48 LQSKRGWVNOFVIEBYAGPEVILIGLHSD 80
 RESULT 8
 ID Q96C29 PRELIMINARY; PRT; 796 AA.
 AC Q96C29;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=Cdh11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strussberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(CC By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: BC013609; AAH13609.1; -.
DR HSSP: P09803; 117W.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin.
DR InterPro: IPR001901; SACE.
DR Pfam: PF00028; Cadherin_C_1.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
DR PROSITE: PS01067; SACE; SEC61G; UNKNOWN 1.
DR Calcium: Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;
SQ

Query Match 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1,3e-12;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLRTSRGWNQPFVIEYAGPEPVLLIGKXHS 33
Db 48 LQSRKRGWNQPFVIEYTGPDVLVGRHSD 80

RESULT 9
ID 08C706 PRELIMINARY; PRT; 796 AA.
CD 08C706
AC 08C706
DT 01-MAR-2003 (TRENBLREL 23, Created)
DT 01-MAR-2003 (TRENBLREL 23, Last sequence update)
DT 01-MAR-2004 (TRENBLREL 26, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE enriched library, clone: C530015F15 product: cadherin 11, full insert
DE sequence.
GN Name=ch11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=99279253; PubMed=10349636;
RA Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=20499374; PubMed=11042159;
RA Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.,
RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA MEDLINE=20530913; PubMed=11076861;
RA Shibata K.; Itoh M.; Alzawa K.; Nagaoka S.; Sasaki N.; Carninci P.,
RA Kono H.; Akiyama J.; Nishi K.; Katsunai T.; Tashiro H.; Itoh M.,
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishino T.; Harada A.,
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.,
RA Fujisawa S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watanabe M.,
RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsura S.; Kawai U.,
RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kita A.; Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi J.; Alzawa K.; Akimura T.; Arikawa T.; Bono H.; Carninci P.,
RA Fukuda S.; Furuno M.; Hanagaki T.; Hara A.; Hashizume W.,
RA Hayashida K.; Hayatsu N.; Hiramoto K.; Hirooka T.; Hirozawa T.,
RA Horii F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.,
RA Katoh H.; Kawai Y.; Kojima Y.; Kondo S.; Kono H.; Konda M.; Koya S.,
RA Kurihara C.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.,
RA Nishi K.; Nomura K.; Numazaki R.; Ono M.; Ohnato N.; Okazaki Y.,
RA Saito R.; Saitoh H.; Sakai C.; Sakazume N.; Sano H.,
RA Sasaki D.; Shibata K.; Shinagawa A.; Shiraki T.; Sogabe Y.; Tagami M.,
RA Tagawa A.; Takahashi F.; Takaku-Akahira S.; Takeda Y.; Tanaka T.,
RA Tomaru A.; Toya T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(CC By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK049652; BAC33860.1; -.
DR HSSP: P09803; 117W.
DR MGD: MGI:99217; Cdh11.
DR GO: GO:0005737; C:cytoplasm; IEA.
DR GO: GO:0005886; C:plasma membrane; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_C_1.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 796 AA; 88126 MW; 71963374B2E1BE29 CRC64;

Query Match 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1,3e-12;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LLRTSRGWNQPFVIEYAGPEPVLLIGKXHS 33
Db 48 LQSRKRGWNQPFVIEYTGPDVLVGRHSD 80

RESULT 10
CADD_CHICK STANDARD; PRT; 792 AA.
ID CADD_CHICK
AC 093319;

```

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thierry J.P.,
 RA Koteliansky V., Majesky M.W.;
 RT "Molecular cloning of chick cadherin 11 and its expression during
 RT smooth muscle differentiation and formation of the tunica media."
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@ebi.ac.uk).
 CC
 CC EMBL; AF055342; AAC33675.1; -
 DR HSSP; P09803; 117W.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; PS50268; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Cadherin-11.
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSMEM 614 634 Potential.
 FT DOMAIN 635 792 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3486C666731AB CRC64;

Query Match 83.9%; Score 151; DB 1; Length 792;
 Best Local Similarity 75.8%; Pred. No. 1.8e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWYNQPFVIEEYAGPEPVLIGLHSD 33
 DB 48 LHRSKRGWYNQPFVIEEYAGPEPVLIGLHSD 80
 ID 093264 PRELIMINARY; PRT; 794 AA.

AC 093264;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cadherin precursor.
 GN Name=Xcad-11;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eggs;
 RA Hagedall B., Borchers A., Medlich D.;
 RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
 RT signal."
 RL Mech. Dev. 72:101-113 (1998).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC EMBL; AF002983; AAC28073.1; -
 DR HSSP; P09803; 117W.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0005509; F-calcium ion binding; IEA.
 DR GO; GO:0007156; P-homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 Potential.
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CFEA719DB CRC64;

Query Match 83.9%; Score 151; DB 2; Length 794;
 Best Local Similarity 75.8%; Pred. No. 1.8e-12;
 Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWYNQPFVIEEYAGPEPVLIGLHSD 33
 DB 48 LHRSKRGWYNQPFVIEEYAGPEPVLIGLHSD 80
 ID 093264 PRELIMINARY; PRT; 801 AA.

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CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in placenta, adult brain, and fetal
CC brain.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF217289; AAC3739.1; -
CC HSSP: P09803; 117X.
CC Genew: H8NC:1760; CDH20.
CC MIN: 605807; -
CC GO: GO:0016021; C:integral to membrane; NAS.
CC GO: GO:0007156; P:homophilic cell adhesion; NAS.
CC InterPro: IPR002126; Cadherin.
CC InterPro: IPR000233; Cadherin_C-term.
CC Pfam: PF00028; Cadherin_5.
CC Pfam: PF01049; Cadherin_C_1.
CC PRINTS: PR00205; CADHERIN.
CC SMART: SM00112; CA; 5.
CC PROSITE: PS00232; CADHERIN_1; 3.
CC PROSITE: PS0268; CADHERIN_2; 5.
CC KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
CC Transmembrane.
CC FT SIGNAL: 1 ? Potential.
CC FT PROPEP: 1 59 Potential.
CC FT CHAIN: 60 801 Cadherin-20.
CC FT DOMAIN: 1 619 Extracellular (Potential).
CC FT TRANSMM: 620 640 Potential.
CC FT DOMAIN: 641 801 Cytoplasmic (Potential).
CC FT DOMAIN: 61 165 Cadherin 1.
CC FT DOMAIN: 166 274 Cadherin 2.
CC FT DOMAIN: 275 389 Cadherin 3.
CC FT DOMAIN: 390 494 Cadherin 4.
CC FT DOMAIN: 494 610 Cadherin 5.
CC FT CARBOHYD: 261 261 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD: 420 420 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD: 461 461 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD: 542 542 N-linked (GlcNAc...) (Potential).
CC SEQUENCE: 801 AA; 89104 MW; F8SD3C53B161866 CRC64;

Query Match 79.4%; Score 143; DB 1; Length 801;
Best Local Similarity 74.2%; Pred. No. 2.5e-11;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

CY 3 RTSRSWNNOFVIEEYAGPEPVIGLTHSD 33
Db 56 RTKRSWVNOFVIEEYAGPEPVIGLTHSD 86

RESULT 13
C8BLT4 PRELIMINARY; PRT; 340 AA.
ID C8BLT4.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone: A730013p10 product: CADHERIN-7 homolog.
GN Name=cdh7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawakita Y.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi U., Aizawa K., Akimura T., Aizawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokane T.,
RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 cadherin domains.
CC EMBL: AK042657; BAC1323.1; -
CC HSSP: P15116; INCT.
CC MGD: MGI:2442792; Cdh7.
CC GO: GO:0016020; C:membrane; IEA.
CC GO: GO:0005509; F:calcium ion binding; IEA.
CC GO: GO:0007156; P:homophilic cell adhesion; IEA.
CC InterPro: IPR002126; Cadherin.
CC Pfam: PF00028; Cadherin_3.
CC PRINTS: PR00205; CADHERIN.
CC SMART: SM00112; CA; 2.
CC PROSITE: PS00232; CADHERIN_1; 2.
CC PROSITE: PS0268; CADHERIN_2; 3.
CC KX Calcium-binding.
CC KX Calcium-binding.
CC SEQUENCE: 340 AA; 37654 MW; DBA9DCA0A5F7527 CRC64;
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Query Match 78.9%; Score 142; DB 2; Length 340;
 Best Local Similarity 74.2%; Pred. No. 1.5e-11;
 Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 3 RTRRSWVWVNFVIEYAGPEPVILGKXHS 33
 ||:|||||||:|||||||:|||||||:|||||||
 DB 44 RTKRSMVWVNFVIEYWGSDPLYGKXHS 74

RESULT 14

Q8AMW2 PRELIMINARY; PRT; 551 AA.
 ID Q8AMW2
 AC Q8AMW2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cadherin-7
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22344707; PubMed=13364338;
 RA Kawano R., Matsuo N., Tanaka H., Nasu M., Yoshitaka H., Shirabe K.,
 RT "Identification and characterization of a soluble cadherin-7 isoform
 produced by alternative splicing."
 RL J. Biol. Chem. 277:47679-47685(2002).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AY15555; AAM55476.1; -.
 DR HSP; P15116; INCI.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KX
 KW Calcium-binding.
 SQ SEQUENCE 551 AA; 60862 MW; ABBAC26BA2D65B7C CRC64;

Query Match 78.9%; Score 142; DB 2; Length 551;
 Best Local Similarity 74.2%; Pred. No. 2.4e-11;
 Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 3 RTRRSWVWVNFVIEYAGPEPVILGKXHS 33
 ||:|||||||:|||||||:|||||||:|||||||
 DB 44 RTKRSMVWVNFVIEYWGSDPLYGKXHS 74

RESULT 15

Q8IY78 PRELIMINARY; PRT; 630 AA.
 ID Q8IY78
 AC Q8IY78;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE CDH7 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.M.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravitz M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.,
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC036786; AAH36786.1; -.
 DR HSP; P15116; INCI.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 5.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KX
 KW Calcium-binding.
 SQ SEQUENCE 630 AA; 69217 MW; 1EB6FD87A21A61D3 CRC64;

Query Match 78.9%; Score 142; DB 2; Length 630;
 Best Local Similarity 74.2%; Pred. No. 2.7e-11;
 Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 3 RTRRSWVWVNFVIEYAGPEPVILGKXHS 33
 ||:|||||||:|||||||:|||||||:|||||||
 DB 44 RTKRSMVWVNFVIEYWGSDPLYGKXHS 74

Search completed: December 8, 2004, 10:24:38
 Job time : 13.2273 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 13.6558 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-10

Perfect score: 180
Sequence: 1 LILTRRSWVWVNFVIEYAGPEFVLIGKLHSD 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	100.0	33	7	ADD29451
2	180	100.0	493	5	AD116946
3	180	100.0	607	5	ABB53295
4	180	100.0	620	7	ADD29448
5	180	100.0	636	7	ADD29445
6	180	100.0	781	5	ABB53296
7	180	100.0	781	5	AAM48736
8	180	100.0	781	5	ABG34078
9	180	100.0	781	5	AD116604
10	180	100.0	781	5	AD116606
11	180	100.0	781	6	ABR40114
12	180	100.0	781	6	ADA01366
13	180	100.0	781	6	ADA43795
14	180	100.0	781	6	ADA43563
15	180	100.0	781	6	ADA01238
16	180	100.0	781	6	ADA01122
17	180	100.0	781	7	ADA43679
18	180	100.0	781	7	ADA06941
19	180	100.0	781	7	ADA09429
20	180	100.0	781	7	ADB99722
21	180	100.0	781	7	ADB87005
22	180	100.0	781	7	ADB66160
23	180	100.0	781	7	ADB99838
24	180	100.0	781	7	ADB99493
25	180	100.0	781	7	ADB66044

26	180	100.0	781	7	ADC23442	ADC23442 Human tra
27	180	100.0	781	7	ADC26135	ADC26135 Human PRO
28	180	100.0	781	7	ADE04962	ADE04962 Human PRO
29	180	100.0	781	7	ADE11268	ADE11268 Human PRO
30	180	100.0	781	7	ADD88199	ADD88199 Human PRO
31	180	100.0	781	7	ADD95494	ADD95494 Human sec
32	180	100.0	781	7	ADE06424	ADE06424 Human PRO
33	180	100.0	781	7	ADE38199	ADE38199 Human PRO
34	180	100.0	781	7	ADD88315	ADD88315 Human PRO
35	180	100.0	781	7	ADD90896	ADD90896 Human sec
36	180	100.0	781	7	ADP99451	ADP99451 Human sec
37	180	100.0	781	7	ADG06544	ADG06544 Human PRO
38	180	100.0	781	7	ADG05495	ADG05495 Human PRO
39	180	100.0	781	7	ADG82496	ADG82496 Human PRO
40	180	100.0	781	8	ADE51749	ADE51749 Human sec
41	180	100.0	781	8	ADE51865	ADE51865 Human sec
42	180	100.0	781	8	ADE37723	ADE37723 Human sec
43	180	100.0	781	8	ADE37607	ADE37607 Human sec
44	180	100.0	781	8	ADD95378	ADD95378 Human sec
45	180	100.0	781	8	ADE38078	ADE38078 Human PRO

ALIGNMENTS

RESULT 1
ADD29451
ID ADD29451 standard, protein, 33 AA.
XX
AC ADD29451;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq ID10.
XX
XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopetrotic; cancer;
XX osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.
XX
XX Homo sapiens.
XX
XX US2003144491-A1.
XX
XX 31-JUL-2003.
XX
XX 16-FEB-2001; 2001US-00788051.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX
XX (GDB/) GODBOLE S D.
XX (KLOC/) KUO C.
XX (ARTE/) ARTERBURN M C.
XX (YEUN/) YEUNG G.
XX (PALE/) PALENCIA S.
XX (TANG/) TANG Y T.
XX (LIUC/) LIU C.
XX (DRMA/) DRMANAC R T.
XX
XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
XX Liu C, Drmanac RT;
XX
XX WPI; 2003-829799/77.
XX
XX Novel isolated human secreted cadherin-like polypeptide useful for
XX treating diseases such as cancers, osteopetrosis, Paget's disease,
XX osteomalacia, hyperostosis, osteopetrosis.
XX
XX Claim 11; SEQ ID NO 10; 63bp; English.
XX
XX This invention relates to a novel isolated human secreted cadherin-like
XX protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopontin activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 33 AA:

Query Match	100.0%;	Score 180;	DB 7;	Length 33;
Best Local Similarity	100.0%;	Pred. No. 3.5e-21;		
Matches 33;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY

1 LLRTSRSWVWNOFFVIEEYAGEPVLIGKLHSD 33
|||||
|||

D6

1 LLRTSRSWVWNOFFVIEEYAGEPVLIGKLHSD 33
|||||
|||

RESULT 2
AD116946
ID AD116946 standard; protein; 493 AA.

AC ADI16946;

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue SeqID 482.

KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;

KW Alzheimer's disease; infection; str.

KW Alzheimer's disease; infection; str.

KW Alzheimer's disease; infection; str.

Os Homo sapiens.

PN WO200268649-A2

PD 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

XX	3-JAN-2001	2001US-0265395P
PR	31-JAN-2001	2001US-0265514P
PR	31-JAN-2001	2001US-0265514P
PR	31-JAN-2001	2001US-0265517P
PR	02-FEB-2001	2001US-0266406P
PR	05-FEB-2001	2001US-0266467P
PR	07-FEB-2001	2001US-0266575P
PR	07-FEB-2001	2001US-0267057P
PR	08-FEB-2001	2001US-0267459P
PR	09-FEB-2001	2001US-0267823P
PR	15-FEB-2001	2001US-0268937P
PR	26-FEB-2001	2001US-0271664P
PR	27-FEB-2001	2001US-0271855P
PR	27-FEB-2001	2001US-0271855P
PR	02-MAR-2001	2001US-0272788P
PR	02-MAR-2001	2001US-0273046P
PR	14-MAR-2001	2001US-0273525P
PR	14-MAR-2001	2001US-0275347P
PR	14-MAR-2001	2001US-0275590P
PR	15-MAR-2001	2001US-0275589P
PR	15-MAR-2001	2001US-0276448P
PR	15-MAR-2001	2001US-0276450P
PR	16-MAR-2001	2001US-0276397P
PR	16-MAR-2001	2001US-0276769P
PR	20-MAR-2001	2001US-0278562P
PR	26-MAR-2001	2001US-0278775P

PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279682P.
PR 29-MAR-2001; 2001US-0279684P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282922P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0290447P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299342P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312869P.
PR 16-AUG-2001; 2001US-0312808P.
PR 21-AUG-2001; 2001US-0313590P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 18-SEP-2001; 2001US-032379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
PA
XX
(CURA-) CURAGEN CORP.

(CURA-) CURAGEN CORP.

PI Tchernev VT, Spytek KA, Zernhsen BD, Paturajan M, Shimkets RA;
PI Li L, Gengoli EA, Padigan M, Anderson SD, Rastelli L, Miller CE;
PI Gerlach VL, Tupper RJ, Gusev VV, Colman SD, Wolanc AR, Pena CEA;
PI Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
WPI: 2002-706998/76.

PT New NOVA polypeptides and nucleic acids, useful for preventing or
PT treating NOVA-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

PS Disclosure; SEQ ID NO 482; 1498bp; English.

This invention relates to a novel nucleic acid, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism. Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, hemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, antistimatic, nephrotoxic, antiarthritic, hepatocytic, neuroprotective, nootropic, antibacterial, virucide, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.

Sequence 493 AA;

Query Match 100.0%; Score 180; DB 5; Length 493;
Best Local Similarity 100.0%; Pred. No. 8.5e-20;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRRSWMWNOFVIEYAGPEPVIGKLSHD 33
DB 39 LTRRSWMWNOFVIEYAGPEPVIGKLSHD 71

RESULT 3
ID ABB53295
AC ABB53295; protein: 607 AA.

12-FEB-2002 (first entry)

Human polypeptide #35.

Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
neuroleptic; tranquilizer; antihypertensive; cardiac; antidiabetic;
antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
cardiovascular disease; respiratory disease; liver disease;
renal disease; skeletal muscle disease; gastrointestinal disease;
placental disease; testicular cancer; male fertility; pancreatic disease.

Homo sapiens.
MO200181363-A1.

01-NOV-2001.

26-APR-2001; 2001WO-US013360.

27-APR-2000; 2000US-0199963P.

11-MAY-2000; 2000US-0203336P.

25-MAY-2000; 2000US-0207087P.

26-MAY-2000; 2000US-0207546P.

(SMIK) SMITHKLINE BEECHAM CORP.

(SMIK) SMITHKLINE BEECHAM PLC.

Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;

Lai Y, Xie Q;

WPI; 2002-04392/05.

N-PSDB; ABA90360.

Novel polypeptides and polynucleotides useful as a vaccine for preventing

disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

Claim 1; Page 106-108; 116pp; English.

The invention relates to an isolated polypeptide comprising a 277, 480,

581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,

844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,

784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as

given in the specification. The polypeptides, modulators of the

polypeptides and antibodies against the polypeptides are useful for

treating diseases such as neurological and psychiatric diseases including

myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention

Sequence 607 AA;

Query Match 100.0%; Score 180; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTRRSWMWNOFVIEYAGPEPVIGKLSHD 33
DB 39 LTRRSWMWNOFVIEYAGPEPVIGKLSHD 71

RESULT 4
ID ADD29448
AC ADD29448; protein: 620 AA.

15-JAN-2004 (first entry)

Human cadherin-like mature protein.

cadherin-like protein; transmembrane protein; cadherin domain;
homotypic cell-cell adhesion; cytostatic; osteoporosis; cancer;
osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
metastatic tumour; human.

Homo sapiens.

US2003144491-A1.

31-JUL-2003.

16-FEB-2001; 2001US-00788051.

03-FEB-2000; 2000US-00496934.

27-APR-2000; 2000US-00560875.

(GODEB/) GODOLE S D.

(KUOC/) KUO C.

(ARTE/) ARTERBURN M C.

(VEIN/) YEUNG G.

(PALE/) PALENCIA S.

(TANG/) TANG Y T.

(LITC/) LIT C.

(DRMA/) DRMANAC R T.

Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

Liu C, Drmanac RT;

WPI; 2003-829799/77.

Novel isolated human secreted cadherin-like polypeptide useful for

treating diseases such as cancers, osteoporosis, Paget's disease,

osteomalacia, hyperostosis, osteopetrosis.

Claim 11; SEQ ID NO 7; 63pp; English.

This invention relates to a novel isolated human secreted cadherin-like

protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their

extracellular region. The extracellular portion mediates homotypic cell-

cell adhesion that is calcium dependent. Modulators of the protein of the

invention may have cytostatic or osteoparic activity. The invention may

allow development of therapeutics useful for the treatment of diseases

such as cancers, osteoporosis, Paget's disease, osteomalacia,

hyperostosis and osteopetrosis. The protein and DNA sequence of the

CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the mature human secreted
 CC cadherin-like protein which was used during the exemplification of the
 CC invention.

XX SQ Sequence 620 AA;

QY Query Match 100.0%; Score 180; DB 7; Length 620;
 Db Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LLRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 33
 23 LLRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 55

RESULT 5
 ADD29445
 ID ADD29445 standard; protein, 636 AA.
 XX
 XX ADD29445;
 DT 15-JAN-2004 (first entry)
 XX
 DE Human cadherin-like protein amino acid sequence.
 XX
 KM cadherin-like protein; transmembrane protein; cadherin domain;
 KM homotypic cell adhesion; cytosolic; osteopetrotic; cancer;
 KM osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KM metastatic tumour; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..16
 FT /label= Signal_peptide
 FT Protein 17..636
 FT /label= Mature_human_cadherin-like_protein

US2003144491-A1.
 31-JUL-2003.
 16-FEB-2001; 2001US-0078051.
 03-FEB-2000; 2000US-00496914.
 27-APR-2000; 2000US-00560875.

PA (GDBE/) GDBOLE S D.
 PA (KUC/) KUO C.
 PA (ARTE/) ARTERBURN M C.
 PA (YEUN/) YEUNG G.
 PA (PALE/) PALENCIA S.
 PA (TANG/) TANG Y T.
 PA (LUC/) LUC C.
 PA (DRMA/) DRMANAC R T.

Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
 Liu C, Drmanac RT;
 WPI: 2003-829799/77.
 DR N-PSDB: ADD29461, ADD29446.
 XX
 PT Novel isolated human secreted cadherin-like polypeptide useful for
 PT treating diseases such as cancers, osteopetrosis, Paget's disease,
 PT osteomalacia, hyperostosis, osteopetrosis.
 XX
 PS Claim 11; SEQ ID NO 4; 636p; English.
 XX
 CC This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopetrotic activity. The invention may
 CC allow development of therapeutic useful for the treatment of diseases
 CC such as cancers, osteopetrosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the human secreted cadherin-like
 CC protein of the invention.

XX SQ Sequence 636 AA;

QY Query Match 100.0%; Score 180; DB 7; Length 636;
 Db Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LLRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 33
 39 LLRTRRSWWVWVNFVIEEYAGPEPVLIGKLSHD 71

RESULT 6
 ABB53296
 ID ABB53296 standard; protein, 781 AA.
 XX
 XX ABB53296;
 AC
 DT 12-FEB-2002 (first entry)
 XX
 DE Human polypeptide #36.
 XX
 KM Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquilizer; antiarrhythmic; cardiant; antiasthmatic;
 KM antiinflammatory; antihypertensive; hepatotropic; vitrucide; antidiabetic;
 KM nephrotoxic; anorectic; cytosolic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..16
 FT /label= Signal_peptide
 FT Protein 17..781
 FT /label= Mature_human_polypeptide #36

WO200181363-A1.
 01-NOV-2001.
 26-APR-2001; 2001WO-US013360.
 27-APR-2000; 2000US-0199963P.
 11-MAY-2000; 2000US-0203336P.
 25-MAY-2000; 2000US-0207087P.
 26-MAY-2000; 2000US-0207546P.

PA (SMK) SMITHLINE BECHAM CORP.
 PA (SMK) SMITHLINE BECHAM PLC.
 PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 Lai Y, Xie Q;
 WPI: 2002-041392/05.
 DR N-PSDB: ABA90361.
 XX
 PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated with the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX
 PS Claim 1; Page 108-109; 116p; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 886, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including

CC Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression, cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphogranuloma; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 33
DB 39 LRLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 71
RESULT 7
AA048736
ID AA048736 standard; protein; 781 AA.
XX
XX AA048736;
AC
XX
XX
DT 28-MAR-2002 (first entry)
XX
DE Human cadherin family member 57805 protein SEQ ID NO. 2.
XX
XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
XX antidiabetic; neuroprotective; antiarthritic; antitubercular;
XX dermatological; immunosuppressive; antiinflammatory; antipruritic;
XX antiaesthetic; antiallergic; antileptotic; haemostatic; antipruritic;
XX antithyroid; hypotensive; antiarteriosclerotic; cardiac; antiarrhythmic;
XX anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
XX gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200190145-A2.
EN
XX
XX 29-NOV-2001.
PD
XX
XX 18-MAY-2001; 2001WO-US016013.
PF
XX
XX 19-MAY-2000; 2000US-0205674P.
PR
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX
XX
PI Curtis RAJ;
XX
XX WPI; 2002-083082/11.
DR N-P8DB; ABA96406; ABA96407.
XX
XX
XX New human cadherin family protein and polynucleotides, useful for
XX PT diagnosing and treating disorders e.g. obstructive jaundice, multiple
XX PT sclerosis, encephalomyelitis and atherosclerosis and to identify
XX PT modulators of therapeutic use.
XX
XX Claim 9; Page 105; 11pp; English.

XX The invention relates to human cadherin family polypeptide designated
CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
CC neuroprotective, antiarthritic, antitubercular, dermatological,
CC immunosuppressive, antiinflammatory, antipruritic, antisthmatic,
CC antiallergic, antileptotic, haemostatic, antipruritic, antithyroid,
CC hypotensive, antiarteriosclerotic, cardiac, antiarrhythmic, anorectic,
CC immunomodulatory, vasotropic, virucide, cytostatic, thrombolytic,
CC analgesic and anabolic activity. The 57805 molecule are useful for
CC diagnosing and treating disorders which include disorders associated with
CC bone metabolism, immune disorders, cardiovascular disorders, liver
CC disorders, viral diseases, pain or metabolic disorders. Especially bone
CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
CC immune disorders including autoimmune disease including diabetes mellitus
CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
CC allergy; cardiovascular disorders, thrombus, hypertension,
CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
CC glycogen storage disease, vascular disorders, chronic heart failure,
CC portal vein thrombosis; viral diseases; metabolic or pain disorders
CC include obesity, anorexia nervosa and diabetes, inflammation, infection
CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
CC useful in gene therapy
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 33
DB 39 LRLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 71
RESULT 8
ABG34078
ID ABG34078 standard; protein; 781 AA.
XX
XX ABG34078;
AC
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Pro peptide #49.
XX
XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;
XX tumour; cancer.
XX
XX Homo sapiens.
OS
XX
XX WO200224888-A2.
EN
XX
XX 28-MAR-2002.
PD
XX
XX 29-AUG-2001; 2001WO-US027099.
PF
XX
XX 01-SEP-2000; 2000US-0229896P.
PR
XX
XX 05-SEP-2000; 2000US-0230621P.
PR
XX
XX 22-SEP-2000; 2000US-023547P.
PR
XX
XX 10-NOV-2000; 2000WO-US030873.
PR
XX
XX 12-JAN-2001; 2001US-0261878P.
PR
XX
XX 16-JAN-2001; 2001US-0261910P.
PR
XX
XX 16-JAN-2001; 2001US-0261939P.
PR
XX
XX 16-JAN-2001; 2001US-0262150P.
PR
XX
XX 25-JAN-2001; 2001US-0264395P.
PR
XX
XX 02-FEB-2001; 2001US-0266421P.
PR
XX
XX 09-FEB-2001; 2001US-0267623P.
PR
XX
XX 28-FEB-2001; 2001WO-US006520.
PR
XX
XX 09-MAR-2001; 2001US-0274399P.
PR
XX
XX 03-APR-2001; 2001US-0280982P.
PR
XX
XX 04-APR-2001; 2001US-0282129P.
PR
XX
XX 04-APR-2001; 2001US-0282199P.

PR 09-MAY-2001; 2001US-0230589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX WPI; 2002-362426/39.
XX N-PSDB; ABR70009.
XX
XX New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX
XX Claim 11, Fig 98, 218pp: English.
XX
XX This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. Polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a human PRO protein of the invention
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLRTRRSWVWVQPFVIEBYAGPEPVLLIGKLHSD 33
Db 39 LLRTRRSWVWVQPFVIEBYAGPEPVLLIGKLHSD 71
RESULT 9
AD116604
ID AD116604 standard; protein; 781 AA.
XX
XX AD116604;
AC
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Human NOXV protein to treat human pathological conditions SeqID140.
DE
XX
XX human; NOXV; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cyclostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
XX hamostatic; anti-HIV; antidiabetic; antiarteriosclerotic; antiparasitic;
XX antiautomatic; nephrotropic; antitachycardic; hepatotropic;
XX neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW

KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
KM single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX WO200268649-A2.
XX
XX 06-SEP-2002.
PD
XX
XX 31-JAN-2002; 2002WO-US002785.
PF
XX
XX 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273045P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282922P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296464P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernav VT, Szytek KA, Zernusen BD, Patturajan M, Shinkets RA;
PI Li L, Gargoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VG, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA,
PI Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX

DR WPI; 2002-706998/76.
 DR N-PSDB; AD116603.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

PS Claim 1; SEQ ID NO 140; 1498bp; English.

XX
 CC This invention relates to a novel nucleic acid, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytoskeletal, cardiac, antiinflammatory, immunosuppressive, antiallergic,
 CC hemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
 CC antiaesthetic, nephroprotective, antiarthritic, hepatotropic,
 CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticoagulant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a human NOVX protein of the
 CC invention.

XX Sequence 781 AA;

XX Query Match Best Local Similarity 100.0%; Score 180; DB 5; Length 781;

XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLRTSRGWMNQFVIEYAGPEPVLTIGKLHSD 33
 |||||
 Db 39 LLRTSRGWMNQFVIEYAGPEPVLTIGKLHSD 71

RESULT 10

AD116606
 ID AD116606 standard; protein; 781 AA.

AC AD116606;

DT 15-APR-2004 (first entry)

XX Human NOVX protein to treat human pathological conditions SeqID142.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 XX inflammation; autoimmune disorder; allergy; blood disorder;
 XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 XX immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 XX cytoskeletal; cardiac; antiinflammatory; immunosuppressive; antiallergic;
 XX haemostatic; anti-HIV; antidiabetic; antiatherosclerotic; anorectic;
 XX antiaesthetic; nephroprotective; antiarthritic; hepatotropic;
 XX neuroprotective; neurotropic; antibacterial; virucide; antiparasitic;
 XX relaxant; anticoagulant; neurogenesis; wound healing; angiogenesis;
 XX chromosome mapping; tissue typing; pharmacogenomic.

OS Homo sapiens.

XX WO200268649-A2.

XX
 PD 06-SEP-2002.

XX 31-JAN-2002; 2002WO-US002785.

XX 31-JAN-2001; 2001US-0265395P.

XX 31-JAN-2001; 2001US-0265412P.

XX 31-JAN-2001; 2001US-0265514P.

XX 02-FEB-2001; 2001US-0265517P.

XX 03-FEB-2001; 2001US-0265767P.

XX 07-FEB-2001; 2001US-0265975P.

XX 08-FEB-2001; 2001US-0267057P.

XX 09-FEB-2001; 2001US-0267459P.

XX 15-FEB-2001; 2001US-0268974P.

XX 26-FEB-2001; 2001US-0271664P.

XX 27-FEB-2001; 2001US-0271839P.

XX 27-FEB-2001; 2001US-0271855P.

XX 02-MAR-2001; 2001US-0273046P.

XX 14-MAR-2001; 2001US-0275925P.

XX 14-MAR-2001; 2001US-0275947P.

XX 14-MAR-2001; 2001US-0275950P.

XX 14-MAR-2001; 2001US-0275989P.

XX 15-MAR-2001; 2001US-0276448P.

XX 15-MAR-2001; 2001US-0276450P.

XX 16-MAR-2001; 2001US-0276397P.

XX 16-MAR-2001; 2001US-0276768P.

XX 20-MAR-2001; 2001US-0278552P.

XX 26-MAR-2001; 2001US-0278775P.

XX 26-MAR-2001; 2001US-0278778P.

XX 29-MAR-2001; 2001US-0279882P.

XX 30-MAR-2001; 2001US-0279884P.

XX 11-APR-2001; 2001US-0280147P.

XX 11-APR-2001; 2001US-0282992P.

XX 20-APR-2001; 2001US-0285133P.

XX 23-APR-2001; 2001US-0285749P.

XX 03-MAY-2001; 2001US-0288327P.

XX 03-MAY-2001; 2001US-0288504P.

XX 29-MAY-2001; 2001US-0294047P.

XX 30-MAY-2001; 2001US-0294473P.

XX 08-JUN-2001; 2001US-0296964P.

XX 18-JUN-2001; 2001US-0298959P.

XX 19-JUN-2001; 2001US-0299324P.

XX 13-AUG-2001; 2001US-0312020P.

XX 16-AUG-2001; 2001US-0312889P.

XX 16-AUG-2001; 2001US-0312908P.

XX 21-AUG-2001; 2001US-0313390P.

XX 28-AUG-2001; 2001US-0315470P.

XX 31-AUG-2001; 2001US-0315447P.

XX 07-SEP-2001; 2001US-0318115P.

XX 07-SEP-2001; 2001US-0318118P.

XX 12-SEP-2001; 2001US-0318740P.

XX 19-SEP-2001; 2001US-0323379P.

XX 18-OCT-2001; 2001US-0330245P.

XX 18-OCT-2001; 2001US-0330308P.

XX 14-NOV-2001; 2001US-0332701P.

XX (CURA-) CURAGEN CORP.

XX Tchernev VT, Spytek KA, Zethusen BD, Patrujan M, Shimkets RA;

XX Li L, Gangoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;

XX Gertsch VL, Taupier RJ, Gusev VY, Colman SD, Molenc AR, Pena CBA;

XX Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;

XX WPI; 2002-706998/76.

XX N-PSDB; AD116605.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.
XX
XX Claim 1; SEQ ID NO 142; 1498bp; English.
PS
CC This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC haemostatic, cardiac, anti-inflammatory, immunosuppressive, antiallergic,
CC antiaesthetic, nephrotropic, antidiabetic, antiarteriosclerotic, anorectic,
CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 180; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLRTSRWVWVNFVIEVYAGPEPVILGKLHSD 33
D5 39 LLRTSRWVWVNFVIEVYAGPEPVILGKLHSD 71
RESULT 11
ABR40114
ID ABR40114 standard; protein; 781 AA.
XX
AC ABR40114;
XX
DT 04-JUL-2003 (first entry)
XX
DE Human cell adhesion and extracellular matrix protein, CADECW-11.
XX
KW Human; anti-HIV; anti-allergic; cerebroprotective; antiparkinsonian;
KW anticonvulsant; neurotropic; neuroprotective; immunosuppressive;
KW dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KW gene therapy; cell adhesion; extracellular matrix; CADECW;
KW immune system disorder; AIDS; allergy; neurological disorder; stroke;
KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
KW atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO2003027230-A2.
XX
PD 03-APR-2003.
XX
PF 02-AUG-2002; 2002WO-US024649.
XX
PR 03-AUG-2001; 2001US-0309964P.
PR 03-AUG-2001; 2001US-0310119P.
PR 17-AUG-2001; 2001US-0313091P.

PR 31-AUG-2001; 2001US-0316771P.
PR 07-SEP-2001; 2001US-0317896P.
PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Burford N, Warren BA, Dugan BW, Mason PM, Richardson TW, Yue H;
PI Forsythe JF, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
PI Kallik Da, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
PI Wallia NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramesh Kumar U;
XX
XX WPI; 2003-354645/33.
DR N-PSDB; ACC000402.
DR
XX
XX New human cell adhesion and extracellular matrix proteins (CADECW),
PT useful for diagnosing, treating or preventing disorders associated with
PT aberrant CADECW expression, e.g. cancer, AIDS, atherosclerosis, allergies
PT or stroke.
XX
PS Claim 1; Page 192-194; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECW-1 to CADECW-22, and their coding
XX sequences (ACC000392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECW, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX proliferative disorders (e.g. cancer or atherosclerosis)
SQ
Sequence 781 AA;
Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLRTSRWVWVNFVIEVYAGPEPVILGKLHSD 33
D5 39 LLRTSRWVWVNFVIEVYAGPEPVILGKLHSD 71
RESULT 12
ADA01366
ID ADA01366 standard; protein; 781 AA.
XX
AC ADA01366;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #49.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003068779-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245107.
PR 09-MAY-2001; 2001US-0290589P.

PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi UC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX MPI: 2003-625484/59.
DR N-PSDB; ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
XX Claim 11; Fig 98; 307pp; English.
PS
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor- α (TNF- α) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping. In generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polypeptide of the invention.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLRTRRSWWNOFVIEEYAGPEPVILGKHS D 33
Db 39 LLRTRRSWWNOFVIEEYAGPEPVILGKHS D 71
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ADA43795
ID ADA43795 standard; protein; 781 AA.
XX
XX ADA43795;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO34009.
XX
XX Human; PRO; secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
XX
XX US2003064474-A1.
XX
XX PN
XX PD 03-APR-2003.

XX
XX 16-SEP-2002; 2002US-00245859.
XX
XX 29-AUG-2001; 2001WO-US027099.
XX
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi UC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX MPI: 2003-605867/57.
DR N-PSDB; ADA43794.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 11; Fig 98; 308pp; English.
PS
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO459, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO459, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLRTRRSWWNOFVIEEYAGPEPVILGKHS D 33
Db 39 LLRTRRSWWNOFVIEEYAGPEPVILGKHS D 71
RESULT 14
ADA43563
ID ADA43563 standard; protein; 781 AA.
XX
XX ADA43563;
XX
XX 20-NOV-2003 (first entry)
XX
XX

DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 XX Human; PRO, secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003073196-A1.
 PN
 XX
 XX 17-APR-2003.
 PD
 XX
 XX 18-SEP-2002; 2002US-00246210.
 PF
 XX
 XX 04-APR-2001; 2001US-0282199P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENENTECH INC.
 PA
 XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WT, Zhang Z,
 PI Fong S,
 PI
 XX WPI; 2003-743814/70.
 DR N-PSDB; ADA43562.
 DR
 XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 XX Claim 11; Fig 98; 307pp; English.
 PS
 XX
 XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO499, PRO308, PRO600,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO3133, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4987 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SO Sequence 781 AA.

QY 1 LKTRRSWMMNFYIEEYAGPEVLIGKLSHD 33
 DB 39 LKTRRSWMMNFYIEEYAGPEVLIGKLSHD 71
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 ADA01238
 ID ADA01238 strandand; protein; 781 AA.
 XX
 XX ADA01238;
 AC
 XX
 XX 06-NOV-2003 (first entry)
 DT
 XX
 XX Human PRO polypeptide #49.
 DE
 XX
 XX Human; PRO, secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; kidney; liver;
 KW microvascular endothelial cell; endothelial cell tube formation.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003068782-A1.
 PN
 XX
 XX 10-APR-2003.
 PD
 XX
 XX 16-SEP-2002; 2002US-00245851.
 PF
 XX
 XX 27-APR-1999; 99US-0131271P.
 PR 29-OCT-1999; 99US-0162506P.
 PR 02-DEC-1999; 99WO-US028551.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 XX (GENENTECH INC.
 PA
 XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WT, Zhang Z,
 PI Fong S,
 PI
 XX WPI; 2003-625487/59.
 DR N-PSDB; ADA01237.
 DR
 XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 PT
 XX
 XX Claim 11; Fig 98; 308pp; English.
 PS
 XX
 XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SO Sequence 781 AA;

Query Match 100.0%; Score 180; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1,5e-19;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Dec 8 11:46:16 2004

us-09-788-051-10.rag

Page 11

Query Match 100.0%; Score 180; DB 6; Length 781;
Best Local Similarity 100.0%; Pred.No.1.5e-19;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKRTSRWVWVNOFFVIEFYAGPEPVLIQKLSHSD 33
Db 39 LKRTSRWVWVNOFFVIEFYAGPEPVLIQKLSHSD 71

Search completed: December 8, 2004, 10:13:05
Job time : 13.6558 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 33.7208 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-10

Perfect score: 180
Sequence: 1 LTRTRSWWNOFVIEYAGPEPVLIGKLHSD 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 9: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/1/pubppaa/US09C_NEW_PUB.pep:*
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- 14: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
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- 16: /cgn2_6/prodata/1/pubppaa/US10C_PUBCOMB.pep:*
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- 19: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	100.0	33	US-09-788-051-10	Sequence 10, Appl
2	180	100.0	493	US-10-072-012-482	Sequence 482, App
3	180	100.0	607	US-10-258-951-74	Sequence 74, Appl
4	180	100.0	620	US-09-788-051-7	Sequence 7, Appl
5	180	100.0	636	US-09-788-051-4	Sequence 4, Appl
6	180	100.0	781	US-09-860-868-2	Sequence 2, Appl
7	180	100.0	781	US-10-245-752-98	Sequence 98, Appl
8	180	100.0	781	US-10-245-859-98	Sequence 98, Appl
9	180	100.0	781	US-10-245-103-98	Sequence 98, Appl
10	180	100.0	781	US-10-245-107-98	Sequence 98, Appl
11	180	100.0	781	US-10-245-143-98	Sequence 98, Appl
12	180	100.0	781	US-10-245-771-98	Sequence 98, Appl
13	180	100.0	781	US-10-245-851-98	Sequence 98, Appl

Result No.	Score	Query Match	Length	ID	Description
14	180	100.0	781	US-10-245-883-98	Sequence 98, Appl
15	180	100.0	781	US-10-237-535-98	Sequence 98, Appl
16	180	100.0	781	US-10-238-183-98	Sequence 98, Appl
17	180	100.0	781	US-10-238-263-98	Sequence 98, Appl
18	180	100.0	781	US-10-238-370-98	Sequence 98, Appl
19	180	100.0	781	US-10-245-055-98	Sequence 98, Appl
20	180	100.0	781	US-10-245-147-98	Sequence 98, Appl
21	180	100.0	781	US-10-245-30-98	Sequence 98, Appl
22	180	100.0	781	US-10-245-739-98	Sequence 98, Appl
23	180	100.0	781	US-10-246-210-98	Sequence 98, Appl
24	180	100.0	781	US-10-239-196-98	Sequence 98, Appl
25	180	100.0	781	US-10-243-024-98	Sequence 98, Appl
26	180	100.0	781	US-10-243-809-98	Sequence 98, Appl
27	180	100.0	781	US-10-245-621-98	Sequence 98, Appl
28	180	100.0	781	US-10-245-880-98	Sequence 98, Appl
29	180	100.0	781	US-10-245-033-98	Sequence 98, Appl
30	180	100.0	781	US-10-243-095-98	Sequence 98, Appl
31	180	100.0	781	US-10-245-185-98	Sequence 98, Appl
32	180	100.0	781	US-10-245-427-98	Sequence 98, Appl
33	180	100.0	781	US-10-245-473-98	Sequence 98, Appl
34	180	100.0	781	US-10-245-770-98	Sequence 98, Appl
35	180	100.0	781	US-10-245-577-98	Sequence 98, Appl
36	180	100.0	781	US-10-246-976-98	Sequence 98, Appl
37	180	100.0	781	US-10-243-320-98	Sequence 98, Appl
38	180	100.0	781	US-10-162-435-13	Sequence 13, Appl
39	180	100.0	781	US-10-242-743-98	Sequence 98, Appl
40	180	100.0	781	US-10-242-845-98	Sequence 98, Appl
41	180	100.0	781	US-10-237-636-98	Sequence 98, Appl
42	180	100.0	781	US-10-238-325-98	Sequence 98, Appl
43	180	100.0	781	US-10-238-446-98	Sequence 98, Appl
44	180	100.0	781	US-10-238-411-98	Sequence 98, Appl
45	180	100.0	781	US-10-243-124-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-10
Sequence 10, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radcoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 33
TYPE: PR
ORGANISM: Homo sapiens
US-09-788-051-10
Query Match 100.0% Score 180 DB 10 Length 33
Best Local Similarity 100.0% Pred. No. 9.8e-15
Matches 33 Conservative 0 Mismatches 0 Indels 0 Gaps 0
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RESULT 2
US-10-072-012-482
; Sequence 482, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchervnev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Futak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCES: 21402-258
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 482
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-482

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Best Local Similarity 100.0%; Pred. No. 1,7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 LLRTSRWVWVNFVIEVYAGPEPVLIIGKLHSD 33
Db      39 LLRTSRWVWVNFVIEVYAGPEPVLIIGKLHSD 71

RESULT 3
US-10-258-951-74
; Sequence 74, Application US/10258951
; Publication No. US20040033504A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnick, Karen
; APPLICANT: Lal, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCES: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-951-74

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Db      39 LLRTSRWVWVNFVIEVYAGPEPVLIIGKLHSD 71

RESULT 4
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US2003014491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaeyun
; APPLICANT: Attebury, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimanac, Radjoe T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
; FILE REFERENCES: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7
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? PRIOR APPLICATION NUMBER: 10/197942
? PRIOR FILING DATE: 2002-07-18
? PRIOR APPLICATION NUMBER: 60/059114
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/063046
? PRIOR FILING DATE: 1997-10-24
? PRIOR APPLICATION NUMBER: 60/065027
? PRIOR FILING DATE: 1997-11-10
? PRIOR APPLICATION NUMBER: 60/079689
? PRIOR FILING DATE: 1998-03-27
? PRIOR APPLICATION NUMBER: 60/086478
? PRIOR FILING DATE: 1998-05-22
? PRIOR APPLICATION NUMBER: 60/087607
? PRIOR FILING DATE: 1998-06-18
? PRIOR APPLICATION NUMBER: 60/089801
? PRIOR FILING DATE: 1998-06-18
? PRIOR APPLICATION NUMBER: 60/090557
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090689
? PRIOR FILING DATE: 1998-06-25
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 116
? SEQ ID NO 98
? LENGTH: 781
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-245-103-98

Query Match      100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY      1 LTRRSWYNQFVIEEYAGPEPVILGKLHSD 33
Db      39 LTRRSWYNQFVIEEYAGPEPVILGKLHSD 71

RESULT 10
US-10-245-107-98
? Sequence 98, Application US/10245107
? Publication No. US20030068779A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin
? APPLICANT: Baton, Dan
? APPLICANT: Elvaroff, Ellen
? APPLICANT: Goddard, Audrey
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin
? APPLICANT: Smith, Victoria
? APPLICANT: Stephan, Jean-Phillippe
? APPLICANT: Watanabe, Colin
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? APPLICANT: Fong, Sherman
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3630R.LC71
? CURRENT APPLICATION NUMBER: US/10/245,107
? PRIOR FILING DATE: 2002-09-16
? PRIOR APPLICATION NUMBER: 10/197942
? PRIOR FILING DATE: 2002-07-18
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? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/063046
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? PRIOR APPLICATION NUMBER: 60/065027
? PRIOR FILING DATE: 1997-11-10
? PRIOR APPLICATION NUMBER: 60/079689
? PRIOR FILING DATE: 1998-03-27
? PRIOR APPLICATION NUMBER: 60/086478
? PRIOR FILING DATE: 1998-05-22
? PRIOR APPLICATION NUMBER: 60/087607
? PRIOR FILING DATE: 1998-06-18
? PRIOR APPLICATION NUMBER: 60/089801
? PRIOR FILING DATE: 1998-06-18
? PRIOR APPLICATION NUMBER: 60/090557
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090689
? PRIOR FILING DATE: 1998-06-25
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 116
? SEQ ID NO 98
? LENGTH: 781
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-245-103-98

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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2,7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLRTSRWVWNOFVIEEYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 11

US-10-245-143-98
Sequence 98, Application US/10245143
Publication No. US20030068780A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bacon, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

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Best Local Similarity 100.0%; Pred. No. 2,7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLRTSRWVWNOFVIEEYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 12

US-10-245-771-98
Sequence 98, Application US/10245771
Publication No. US20030068781A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bacon, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-771-98

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Best Local Similarity 100.0%; Pred. No. 2,7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 LLRTSRWVWNOFVIEEYAGPEPVILGKLHSD 33
Db 39 LLRTSRWVWNOFVIEEYAGPEPVILGKLHSD 71

RESULT 13
US-10-245-851-98
Sequence 98, Application US/10245851
Publication No. US20030068782A1
GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/10/245,851
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
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; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98

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Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVNFVIEYAGPEPVLIGKLHSD 33
Db 39 LLRTSRWVWVNFVIEYAGPEPVLIGKLHSD 71

RESULT 14
US-10-245-863-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/10/237,535
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/059114
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; FILE REFERENCE: P3630R1C70
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; NUMBER OF SEQ ID NOS: 116
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; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 180; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRTSRWVWVNFVIEYAGPEPVLIGKLHSD 33
Db 39 LLRTSRWVWVNFVIEYAGPEPVLIGKLHSD 71

RESULT 15
US-10-237-535-98
; Sequence 98, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C3
; CURRENT APPLICATION NUMBER: US/10/237,535
; CURRENT FILING DATE: 2002-09-06
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Wed Dec 8 11:46:17 2004

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/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: 10/119480
/ PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 180; DB 14; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.7e-17;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTRTRSWVMNQFVIEBYAGPEPYLIGKLHSD 33
Db 39 LTRTRSWVMNQFVIEBYAGPEPYLIGKLHSD 71

Search completed: December 8, 2004, 11:34:29
Job time : 34.7208 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13, Search time 3.93506 Seconds
(without alignments)

556.152 Million cell updates/sec

Title: US-09-788-051-10

Perfect score: 180

Sequence: 1 LKTRRSWMNQFVIEYAGPEVILGKHSD 33

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/aa/6A.COMB.pep.*

5: /cgn2_6/ptodata/1/aa/6B.COMB.pep.*

6: /cgn2_6/ptodata/1/aa/backlist.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	152	84.4	615	2	US-08-738-349-12	Sequence 12, Appl
2	152	84.4	693	2	US-08-738-349-6	Sequence 6, Appl
3	152	84.4	693	4	US-09-919-487-55	Sequence 55, Appl
4	152	84.4	796	1	US-08-188-228-58	Sequence 58, Appl
5	152	84.4	796	1	US-08-332-643-52	Sequence 52, Appl
6	152	84.4	796	1	US-08-332-643-58	Sequence 58, Appl
7	152	84.4	796	2	US-08-738-349-2	Sequence 2, Appl
8	152	84.4	796	2	US-08-738-349-4	Sequence 2, Appl
9	152	84.4	796	4	US-09-654-378-2	Sequence 4, Appl
10	150	83.3	110	3	US-09-187-859-4	Sequence 4, Appl
11	150	83.3	110	4	US-09-839-542B-4	Sequence 4, Appl
12	150	83.3	110	4	US-09-535-852-4	Sequence 4, Appl
13	142	78.9	110	3	US-09-187-859-10	Sequence 10, Appl
14	142	78.9	110	4	US-09-839-542B-10	Sequence 10, Appl
15	142	78.9	110	4	US-09-535-852-10	Sequence 10, Appl
16	139	77.2	532	1	US-08-188-228-44	Sequence 44, Appl
17	139	77.2	532	1	US-08-332-643-44	Sequence 44, Appl
18	139	77.2	793	1	US-08-188-228-54	Sequence 54, Appl
19	139	77.2	793	1	US-08-332-643-48	Sequence 48, Appl
20	139	77.2	793	1	US-08-332-643-54	Sequence 54, Appl
21	139	77.2	799	1	US-08-188-228-42	Sequence 42, Appl
22	139	77.2	799	1	US-08-332-643-42	Sequence 42, Appl
23	139	76.7	110	3	US-09-187-859-13	Sequence 13, Appl
24	138	76.7	110	4	US-09-839-542B-13	Sequence 13, Appl
25	138	76.7	110	4	US-09-535-852-13	Sequence 13, Appl
26	137	76.1	106	3	US-09-187-859-44	Sequence 44, Appl
27	137	76.1	106	3	US-09-187-859-45	Sequence 45, Appl

28	137	76.1	106	4	US-09-305-927-1	Sequence 1, Appl
29	137	76.1	106	4	US-09-305-927-2	Sequence 2, Appl
30	137	76.1	106	4	US-09-305-927-3	Sequence 3, Appl
31	137	76.1	106	4	US-09-073-040-12	Sequence 12, Appl
32	137	76.1	106	4	US-09-073-040-13	Sequence 13, Appl
33	137	76.1	106	4	US-09-839-542B-44	Sequence 44, Appl
34	137	76.1	106	4	US-09-839-542B-45	Sequence 45, Appl
35	137	76.1	106	4	US-09-264-516A-1	Sequence 1, Appl
36	137	76.1	106	4	US-09-264-516A-2	Sequence 2, Appl
37	137	76.1	106	4	US-09-264-516A-3	Sequence 3, Appl
38	137	76.1	106	4	US-09-234-395-4	Sequence 4, Appl
39	137	76.1	106	4	US-09-234-395-5	Sequence 5, Appl
40	137	76.1	106	4	US-09-305-928-4	Sequence 4, Appl
41	137	76.1	106	4	US-09-305-928-5	Sequence 5, Appl
42	136	75.6	110	3	US-09-187-859-22	Sequence 22, Appl
43	136	75.6	110	4	US-09-839-542B-22	Sequence 22, Appl
44	136	75.6	110	4	US-09-535-852-22	Sequence 22, Appl
45	134	74.4	110	3	US-09-187-859-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-738-349-12
Sequence 12, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amanu, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE: US 08/112,061
APPLICATION NUMBER: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-738-349-12

Query Match 84.4%; Score 152; DB 2; Length 615;
Best Local Similarity 75.8%; Pred. No. 8.3e-16;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 33
Db 42 LQSKRGWVWVNFVIEEYTGPDVVLVGRHSD 74

RESULT 2
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Aman, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

TITLE OF INVENTION: Process for Its Production

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &

ADDRESSEE: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE:

APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481,1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 693 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-738-349-6

Query Match 84.4%; Score 152; DB 2; Length 693;
Best Local Similarity 75.8%; Pred. No. 9.5e-16;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 33
Db 48 LQSKRGWVWVNFVIEEYTGPDVVLVGRHSD 80

RESULT 3
US-09-919-497-55

Sequence 55, Application US/09919497

Patent No. 6773883

GENERAL INFORMATION:

APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 84.4%; Score 152; DB 4; Length 693;
Best Local Similarity 75.8%; Pred. No. 9.5e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLTRRSWVWVNFVIEEYAGPEPVLLIGKLHSD 33
Db 48 LQSKRGWVWVNFVIEEYTGPDVVLVGRHSD 80

RESULT 4
US-08-188-228-58

Sequence 58, Application US/08188228

Patent No. 5597725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,460

FILING DATE: 19 APR 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5597725and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-188-228-58

Query Match 84.4%; Score 152; DB 1; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;

Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LKTRSRWVWNOFFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWNOFFVIEEYTGPDVVLVGRHSD 80

RESULT 5
US-08-332-643-52

; Sequence 52, Application US/08332643

; Patent No. 5639634

; GENERAL INFORMATION:

; APPLICANT: Suzuki, Shintaro

; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: Two First National Plaza, 20 South Clark

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/332,643

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/872,643

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5639634and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/30795

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 346-5750

; TELEFAX: (312) 984-9740

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 796 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-332-643-52

QY 1 LKTRSRWVWNOFFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWNOFFVIEEYTGPDVVLVGRHSD 80

RESULT 6
US-08-332-638-58

; Sequence 58, Application US/08332638

; Patent No. 5646250

; GENERAL INFORMATION:

; APPLICANT: Suzuki, Shintaro

; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/332,638

; FILING DATE: 01-NOV-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/872,643

; FILING DATE: 17 APR 1992

; APPLICATION NUMBER: US/08/049,460

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5646250and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31340

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 796 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-332-638-58

QY 1 LKTRSRWVWNOFFVIEEYAGPEPVLIGKLHSD 33
DB 48 LQSKRGWVWNOFFVIEEYTGPDVVLVGRHSD 80

RESULT 7
US-08-738-349-2

; Sequence 2, Application US/08738349

; Patent No. 5869638

; GENERAL INFORMATION:

; APPLICANT: Takeshita, Sunao

; APPLICANT: Okazaki, Makoto

; APPLICANT: Kawai, Shinji

; APPLICANT: Tsujimura, Atsushi

; APPLICANT: Asanum, Egon

; TITLE OF INVENTION: Bone-Related Cadherin-like Protein and

; PROCESS FOR ITS PRODUCTION

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/738,349

; FILING DATE: 25-OCT-1996

; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWVWNOFVIEEYAGPEPYLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGPDYLVGRLHSD 80

RESULT 8
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shingji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
ATTORNEY/AGENT INFORMATION:
FILING DATE: 26-AUG-1993
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-4

Query Match
Best Local Similarity 84.4%; Score 152; DB 2; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWVWNOFVIEEYAGPEPYLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGPDYLVGRLHSD 80

RESULT 9
US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
APPLICANT: Valencia, Xavier
TITLE OF INVENTION: Methods and Compositions for Treatment
TITLE OF INVENTION: of Inflammatory Disease Using Cadherin-11 Modulating Agents
FILE REFERENCE: B0801/7187/RRP/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match
Best Local Similarity 84.4%; Score 152; DB 4; Length 796;
Best Local Similarity 75.8%; Pred. No. 1.1e-15;
Matches 25; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 LRTSRWVWNOFVIEEYAGPEPYLIGKLHSD 33
DB 48 LQSKRGWVWNOFVIEEYTGPDYLVGRLHSD 80

RESULT 10
US-09-187-859-4
Sequence 4, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-4

Query Match
Best Local Similarity 83.3%; Score 150; DB 3; Length 110;
Best Local Similarity 77.4%; Pred. No. 2.3e-16;
Matches 24; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RTRSRWVWNOFVIEEYAGPEPYLIGKLHSD 33

Db 1 RSKRGWVWNOFFVLEETGPPVLVGRLHSD 31

RESULT 11
US-09-839-542B-4

; Sequence 4, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-4

Query Match 83.3%; Score 150; DB 4; Length 110;
Best Local Similarity 77.4%; Pred. No. 2.3e-16;
Matches 24; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Cy 3 RTRRSWVWNOFFVLEETGPPVLVGRLHSD 33
Db 1 RSKRGWVWNOFFVLEETGPPVLVGRLHSD 31

RESULT 12

US-09-535-852-4
; Sequence 4, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-852-4

Query Match 83.3%; Score 150; DB 4; Length 110;
Best Local Similarity 77.4%; Pred. No. 2.3e-16;
Matches 24; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Cy 3 RTRRSWVWNOFFVLEETGPPVLVGRLHSD 33
Db 1 RSKRGWVWNOFFVLEETGPPVLVGRLHSD 31

RESULT 13
US-09-187-859-10
; Sequence 10, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-187-859-10

Query Match 78.9%; Score 142; DB 3; Length 110;
Best Local Similarity 74.2%; Pred. No. 4.5e-15;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Cy 3 RTRRSWVWNOFFVLEETGPPVLVGRLHSD 33
Db 1 RSKRGWVWNOFFVLEETGPPVLVGRLHSD 31

RESULT 14

US-09-839-542B-10
; Sequence 10, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-839-542B-10

Query Match 78.9%; Score 142; DB 4; Length 110;
Best Local Similarity 74.2%; Pred. No. 4.5e-15;
Matches 23; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Cy 3 RTRRSWVWNOFFVLEETGPPVLVGRLHSD 33
Db 1 RSKRGWVWNOFFVLEETGPPVLVGRLHSD 31

RESULT 15

US-09-535-852-10
; Sequence 10, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-535-852-10

Query Match 78.9%; Score 142; DB 4; Length 110;
Best Local Similarity 74.2%; Pred. No. 4.5e-15;

Wed Dec 8 11:46:17 2004

us-09-788-051-10.rat

Page 6

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Db		1	RTRRSWMNQFFVLEBYMGSDPLYGVKLS	D	31					

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Job time : 3.93506 secs
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Job time : 3.93506 secs
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